



SEQUENCE LISTING

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<120> CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS
INVOLVED IN CARBON METABOLISM AND ENERGY
PRODUCTION

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<141> 2000-06-23

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cgc gca cgc gat act gaa gat ttg gtt gca cag gct gcc tcc aaa ttc	163	
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Ile Glu Val Val Glu Ala Ala Thr Ala Asn Asn Gly Thr Ala Gln Val		
	25 30 35	
gtg ctc acc ggt ggt ggc gcc ggc atc aag ttg ctg gaa aag ctc agc	259	
Val Leu Thr Gly Gly Gly Ala Gly Ile Lys Leu Leu Glu Lys Leu Ser		
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gtt gat gcg gct gac ctt gcc tgg gat cgc att cat gtg ttc ttc ggc	307	
Val Asp Ala Ala Asp Leu Ala Trp Asp Arg Ile His Val Phe Phe Gly		
	55 60 65	
gat gag cgc aat gtc cct gtc agt gat tct gag tcc aat gag ggc cag	355	
Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu Ser Asn Glu Gly Gln		
	70 75 80 85	
gct cgt gag gca ctg ttg tcc aag gtt tct atc cct gaa gcc aac att	403	
Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile Pro Glu Ala Asn Ile		
	90 95 100	
cac gga tat ggt ctc ggc gac gta gat ctt gca gag gca gcc cgc gct	451	
His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala Glu Ala Ala Arg Ala		
	105 110 115	
tac gaa gct gtg ttg gat gaa ttc gca cca aac ggc ttt gat ctt cac	499	
Tyr Glu Ala Val Leu Asp Glu Phe Ala Pro Asn Gly Phe Asp Leu His		
	120 125 130	
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Leu Leu Gly Met Gly Gly Glu Gly His Ile Asn Ser Leu Phe Pro His		
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Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu Thr Leu Pro Ala Val		
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50 55 60

His Val Phe Phe Gly Asp Glu Arg Asn Val Pro Val Ser Asp Ser Glu
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Ser Asn Glu Gly Gln Ala Arg Glu Ala Leu Leu Ser Lys Val Ser Ile
85 90 95

Pro Glu Ala Asn Ile His Gly Tyr Gly Leu Gly Asp Val Asp Leu Ala
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Ser Leu Phe Pro His Thr Asp Ala Val Lys Glu Ser Ser Ala Lys Val
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Ile Ala Val Phe Asp Ser Pro Lys Pro Pro Ser Glu Arg Ala Thr Leu
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Thr Leu Pro Ala Val His Ser Ala Lys Arg Val Trp Leu Leu Val Ser
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Gly Ala Glu Lys Ala Glu Ala Ala Ala Ala Ile Val Asn Gly Glu Pro
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cag atg tgc aaa atg cag cgc att att gaa cta gca gga act gcc gaa 259
 Gln Met Cys Lys Met Gln Arg Ile Ile Glu Leu Ala Gly Thr Ala Glu
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 Gly Asp Val Val Thr Gly Ala Gly Val Ile Gly Gly Ser Asn Phe Gln
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ctg aat aac gag cca aat gaa gtg gtt ccc cat cca gat acc tat gcg 355
 Leu Asn Asn Glu Pro Asn Glu Val Val Pro His Pro Asp Thr Tyr Ala
 70 75 80 85

gat ttc ccc gat atc aag gcg gtt gtt atc tcc gcg gag act ttt gaa 403
 Asp Phe Pro Asp Ile Lys Ala Val Val Ile Ser Ala Glu Thr Phe Glu
 90 95 100

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Pro Leu Ile Ala Pro Ser Ile Leu Ala Ala Asp Phe Ser Arg Leu Gly
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Glu Gln Val Leu Ala Val Pro Asp Ala Asp Trp Ile His Val Asp Ile
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Met Asp Gly His Phe Val Pro Asn Leu Ser Phe Gly Ala Asp Ile Thr
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Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr Ile Asp Ala Gly Ala
70 75 80 85

gac tgc att gtt ttc cac gtt gaa gcc acc gaa ggt cac gtt gag ttg 403
Asp Cys Ile Val Phe His Val Glu Ala Thr Glu Gly His Val Glu Leu
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Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp Leu Glu His Phe Asp
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aag acc atc aag cag gct gcc gac gct ggc gtg gat gcc ttc gtt gca 691
 Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val Asp Ala Phe Val Ala
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 35 40 45

Gly Ala Asp Ile Thr Ala Ala Val Asn Arg Val Thr Asp Lys Glu Leu
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Asp Val His Leu Met Ile Glu Asn Pro Glu Lys Trp Val Asp Asn Tyr
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Ile Asp Ala Gly Ala Asp Cys Ile Val Phe His Val Glu Ala Thr Glu
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Gly His Val Glu Leu Ala Lys Tyr Ile Arg Ser Lys Gly Val Arg Ala
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Gly Phe Ser Leu Arg Pro Gly Thr Pro Ile Glu Asp Tyr Leu Asp Asp
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Leu Glu His Phe Asp Glu Val Ile Val Met Ser Val Glu Pro Gly Phe
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Arg Lys Val Ile Asp Glu Arg Gly Leu Asn Thr Val Ile Glu Ile Asp
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Gly Gly Ile Ser Ala Lys Thr Ile Lys Gln Ala Ala Asp Ala Gly Val
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 Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val Leu Gly Gly Ser Gly
 55 60 65

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 Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys Gly Ala Arg Cys Ala
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ctt gct tgg tct gtt gaa act gca cgc ctc gcc cgc gag cac aac aat 403
 Leu Ala Trp Ser Val Glu Thr Ala Arg Leu Ala Arg Glu His Asn Asn
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Glu Ala Ala Ser Arg Thr Val Asn Asp Pro Gly Ser Leu Gly Ile Val
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Leu Gly Gly Ser Gly Asn Gly Glu Gln Ile Ala Ala Asn Lys Val Lys
      65           70           75           80

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Glu Thr Thr Arg Pro Glu Phe Ile His Pro Val Ser Val Leu Pro Glu
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Val Ser Ala Gly Thr Val Leu Asp Ala Ala Glu Pro Ala Gly Val Pro
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acc aaa gat atg tgg gaa tac caa aaa gac cac atg aac ctg gtc tcc 259
Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His Met Asn Leu Val Ser
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Pro Leu Asn Arg Arg Lys Phe Arg Val Leu Val Val Gly Thr Gly Leu
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Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg Ala His Ser Ile Ala			
	90	95	100
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Gly Arg Glu Ser Asp Cys Trp Arg Leu Ala Val Glu Ser Val Arg Val			
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Ile Asp His Met Asn Ala Ile Gly Ala Pro Phe Ala Arg Glu Tyr Gly			
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Tyr Tyr Thr Arg Gly Gln Thr Gly Gln Gln Leu Gln Phe Ser Thr Ala			
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Arg Cys Glu Gly Leu Ile Met Arg Asn Leu Ile Thr Gly Glu Leu Thr			
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Pro Ala Gly Val Pro Thr Lys Asp Met Trp Glu Tyr Gln Lys Asp His
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Val Gly Thr Gly Leu Ser Gly Gly Ala Ala Ala Ala Ala Leu Gly Glu
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Leu Gly Tyr Asp Val Lys Ala Phe Thr Tyr His Asp Ala Pro Arg Arg
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Ala His Ser Ile Ala Ala Gln Gly Gly Val Asn Ser Ala Arg Gly Lys
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Lys Val Asp Asn Asp Gly Ala Tyr Arg His Val Lys Asp Thr Val Lys
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 Thr Leu Pro Phe Thr Ile Pro Asn Tyr Leu Gly Pro Leu Leu Gly Ser
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Gln	Ala	Ala	Ile	Ala	Arg	Ala	Gln	Ala	Arg	Ile	Asp	Arg	Leu	Met	Gly		
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 Asp Asp Phe Trp Lys Asn Met Arg Ile Thr Gly Ser Thr Asp Glu Met
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Gly	Ala	Ser	Ala	Ser																		

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Ile	Glu	Gly	Ala	Met	Gly	Ala	Lys	Met	Arg	Asn	Ile	Gly	Glu	Ala	Cys	
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Thr	Ala	Ala	Asn	Arg	Phe	Leu	Val	His	Glu	Ser	Val	Ala	Asp	Glu	Phe	
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1593

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Met Lys Leu Thr Leu
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Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr	
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Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu	
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Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala	
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Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro	
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Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg	
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Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys	
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Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys	
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Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu	
185 190 195	
cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc	739
Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys	
200 205 210	
tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg	787
Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu	
215 220 225	
acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga	835
Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg	
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<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 16

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20 25 30

Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
35 40 45

Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
50 55 60

Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
65 70 75 80

Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
85 90 95

Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
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Arg Ala Ala Phe Arg Gly Lys Asp Asp
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<211> 1530

<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1507)

<223> RXA01535

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ttc cgt att gag cac gac acc atg ggt gaa gtg aag gtt cca gca aag 163
Phe Arg Ile Glu His Asp Thr Met Gly Glu Val Lys Val Pro Ala Lys
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gct ctg tgg cag gca cag acc cag cgc gct gtt gag aac ttc cct atc 211
Ala Leu Trp Gln Ala Gln Thr Gln Arg Ala Val Glu Asn Phe Pro Ile
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tct ggt cgt ggt ctg gaa tcc gca cag atc cgc gca atg ggt ctg ctg 259
Ser Gly Arg Gly Leu Glu Ser Ala Gln Ile Arg Ala Met Gly Leu Leu
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Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser Gly Ala Leu Asp Ala
                               55                               60                               65

gag aag gca gat gcc atc att gca gct ggt aag gag atc gcg tcc ggt 355
Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys Glu Ile Ala Ser Gly
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aag cat gac gct gag ttc cca att gat gtg ttc cag act ggt tcc ggt 403
Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe Gln Thr Gly Ser Gly
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act tcc tcc aac atg aac acc aat gag gtt atc gct tcc atc gcg aag 451
Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile Ala Ser Ile Ala Lys
                               105                               110                               115

gct aac ggc gtt gag gtt cac cca aat gac cac gtc aac atg ggt cag 499
Ala Asn Gly Val Glu Val His Pro Asn Asp His Val Asn Met Gly Gln
                               120                               125                               130

tcc tcc aat gac acc ttc cct act gca act cac gtt gct gca acc gaa 547
Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His Val Ala Ala Thr Glu
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gct gct gtc aat gac ctc atc cca ggc ctg aag gtt ctg cac gag tct 595
Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys Val Leu His Glu Ser
                               150                               155                               160                               165

ttg gcg aag aag gct aac gag tgg tct gag gtt gtt aag tcc ggc cgc 643
Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val Val Lys Ser Gly Arg
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acc cac ctg atg gac gct gtt cca gta acc ctg ggc cag gag ttc ggt 691
Thr His Leu Met Asp Ala Val Pro Val Thr Leu Gly Gln Glu Phe Gly

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Leu	Pro	Arg	Leu	Gly	Glu	Leu	Ala	Ile	Gly	Gly	Thr	Ala	Ala	Gly	Thr	
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Gly	Ile	Asn	Thr	Ser	Ala	Asp	Phe	Gly	Gly	Lys	Val	Val	Ala	Glu	Leu	
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Ile	Asn	Leu	Thr	Asp	Val	Lys	Glu	Leu	Lys	Glu	Ala	Glu	Asn	His	Phe	
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Glu	Ala	Gln	Ala	Ala	Arg	Asp	Ala	Leu	Val	Glu	Phe	Ser	Gly	Ala	Met	
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cgc	gtt	atc	gct	gtc	tcc	ttg	tac	aag	atc	gct	aac	gat	atc	cgc	ctc	979
Arg	Val	Ile	Ala	Val	Ser	Leu	Tyr	Lys	Ile	Ala	Asn	Asp	Ile	Arg	Leu	
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atg	ggc	tcc	ggc	cca	ctg	acc	ggt	ctt	ggc	gag	atc	cgt	ctc	cca	gac	1027
Met	Gly	Ser	Gly	Pro	Leu	Thr	Gly	Leu	Gly	Glu	Ile	Arg	Leu	Pro	Asp	
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ctg	cag	cca	ggt	tcc	tcc	atc	atg	cca	ggc	aag	gtc	aac	cca	gtt	ctc	1075
Leu	Gln	Pro	Gly	Ser	Ser	Ile	Met	Pro	Gly	Lys	Val	Asn	Pro	Val	Leu	
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Cys	Glu	Thr	Ala	Thr	Gln	Val	Ser	Ala	Gln	Val	Ile	Gly	Asn	Asp	Ala	
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gct	gtt	gcg	ttc	tcc	ggc	acc	cag	ggc	cag	ttc	gag	ctc	aac	gtg	ttc	1171
Ala	Val	Ala	Phe	Ser	Gly	Thr	Gln	Gly	Gln	Phe	Glu	Leu	Asn	Val	Phe	
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Ile	Pro	Val	Met	Ala	Arg	Asn	Val	Leu	Glu	Ser	Ala	Arg	Leu	Leu	Ala	
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Asn	Thr	Ser	Arg	Val	Phe	Ala	Thr	Arg	Leu	Val	Asp	Gly	Ile	Glu	Pro	
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aac	gag	gca	cac	atg	aag	gag	ctc	gct	gag	tct	tca	cct	tcc	atc	gtt	1315
Asn	Glu	Ala	His	Met	Lys	Glu	Leu	Ala	Glu	Ser	Ser	Pro	Ser	Ile	Val	
390				395				400				405				
acc	cca	ctg	aac	tct	gca	atc	ggc	tac	gaa	gct	gct	gca	aag	gtg	gct	1363
Thr	Pro	Leu	Asn	Ser	Ala	Ile	Gly	Tyr								

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 440 445 450

cgc ctc gac gtt ctt gct atg gct cac acc gag cgc gag aac aag ttc 1507
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taaaactaga acccgataaa taa 1530

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<213> Corynebacterium glutamicum

<400> 18

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 35 40 45

Ala Met Gly Leu Leu Lys Ala Ala Cys Ala Gln Val Asn Lys Asp Ser
 50 55 60

Gly Ala Leu Asp Ala Glu Lys Ala Asp Ala Ile Ile Ala Ala Gly Lys
 65 70 75 80

Glu Ile Ala Ser Gly Lys His Asp Ala Glu Phe Pro Ile Asp Val Phe
 85 90 95

Gln Thr Gly Ser Gly Thr Ser Ser Asn Met Asn Thr Asn Glu Val Ile
 100 105 110

Ala Ser Ile Ala Lys Ala Asn Gly Val Glu Val His Pro Asn Asp His
 115 120 125

Val Asn Met Gly Gln Ser Ser Asn Asp Thr Phe Pro Thr Ala Thr His
 130 135 140

Val Ala Ala Thr Glu Ala Ala Val Asn Asp Leu Ile Pro Gly Leu Lys
 145 150 155 160

Val Leu His Glu Ser Leu Ala Lys Lys Ala Asn Glu Trp Ser Glu Val
 165 170 175

Val Lys Ser Gly Arg Thr His Leu Met Asp Ala Val Pro Val Thr Leu
 180 185 190

Gly Gln Glu Phe Gly Gly Tyr Ala Arg Gln Ile Gln Leu Gly Ile Glu
 195 200 205

Arg Val Glu Ala Thr Leu Pro Arg Leu Gly Glu Leu Ala Ile Gly Gly
 210 215 220

Thr Ala Ala Gly Thr Gly Ile Asn Thr Ser Ala Asp Phe Gly Gly Lys


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225                230                235                240
Val Val Ala Glu Leu Ile Asn Leu Thr Asp Val Lys Glu Leu Lys Glu
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Ala Glu Asn His Phe Glu Ala Gln Ala Ala Arg Asp Ala Leu Val Glu
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Phe Ser Gly Ala Met Arg Val Ile Ala Val Ser Leu Tyr Lys Ile Ala
                275                280                285
Asn Asp Ile Arg Leu Met Gly Ser Gly Pro Leu Thr Gly Leu Gly Glu
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Ile Arg Leu Pro Asp Leu Gln Pro Gly Ser Ser Ile Met Pro Gly Lys
305                310                315                320
Val Asn Pro Val Leu Cys Glu Thr Ala Thr Gln Val Ser Ala Gln Val
                325                330                335
Ile Gly Asn Asp Ala Ala Val Ala Phe Ser Gly Thr Gln Gly Gln Phe
                340                345                350
Glu Leu Asn Val Phe Ile Pro Val Met Ala Arg Asn Val Leu Glu Ser
                355                360                365
Ala Arg Leu Leu Ala Asn Thr Ser Arg Val Phe Ala Thr Arg Leu Val
                370                375                380
Asp Gly Ile Glu Pro Asn Glu Ala His Met Lys Glu Leu Ala Glu Ser
385                390                395                400
Ser Pro Ser Ile Val Thr Pro Leu Asn Ser Ala Ile Gly Tyr Glu Ala
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Ala Ala Lys Val Ala Lys Thr Ala Leu Ala Glu Gly Lys Thr Ile Arg
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Gln Thr Val Ile Asp Leu Gly Leu Val Asp Gly Glu Lys Leu Thr Glu
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<212> DNA

<213> Corynebacterium glutamicum

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<222> (101)..(1141)

<223> RXA00517

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Val Asn Ala Gln Gln Leu Thr Val Leu Cys Thr Asp Ile Leu Thr Lys									
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act gga gta cct gca gca gac gcc cat ctt gtc ggt gat agt ttg gtg	211								
Thr Gly Val Pro Ala Ala Asp Ala His Leu Val Gly Asp Ser Leu Val									
	25	30	35						
cag gct gat ctt tgg ggt cac ccc tcc cac ggt gtg ctt cga ctg cct	259								
Gln Ala Asp Leu Trp Gly His Pro Ser His Gly Val Leu Arg Leu Pro									
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Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met Thr Thr His Ala His									
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gtg gag gtt ctc aat gat ttg ggt gcc gtg ttg gcg ttg gat gga cac	355								
Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu Ala Leu Asp Gly His									
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aat gga atc ggc caa gtt tta gct gat cat gct cgt aaa gaa gca gtg	403								
Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala Arg Lys Glu Ala Val									
	90	95	100						
act agg gca atg atg ttc ggc atc ggt gcg gtg tcg gtg cgc aac tcc	451								
Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val Ser Val Arg Asn Ser									
	105	110	115						
aat cat ttt gga act gcc atg tac tac acc cgg aaa gcg gca gcg caa	499								
Asn His Phe Gly Thr Ala Met Tyr Thr Arg Lys Ala Ala Ala Gln									
	120	125	130						
gga tgt gtt tcc att ctc acc acc aat gca tct ccg gcg atg gcg ccc	547								
Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser Pro Ala Met Ala Pro									
	135	140	145						
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Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn Pro Trp Ser Ile Ala									
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Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp Ile Ala Asn Thr Ala									
	170	175	180						
gtt gcg cgc gga aag atc tac cac gca cga cag aca aac atg ccc att	691								
Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln Thr Asn Met Pro Ile									
	185	190	195						
cct gag act tgg gcg atc acg agt gag ggc gca ccc acc acg gat cct	739								
Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala Pro Thr Thr Asp Pro									
	200	205	210						
gct gag gca atc aac ggt gtc gtc ctt ccc atg gct ggt cac aaa ggt	787								
Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met Ala Gly His Lys Gly									
	215	220	225						
tat gcg att agc ttc atg atg gat gtg ctt tct gga gtt ctc act ggt	835								

Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser Gly Val Leu Thr Gly
 230 235 240 245
 tcc cag cac agc acc aag gta cat ggt ccg tat gat ccc act ccc cca 883
 Ser Gln His Ser Thr Lys Val His Gly Pro Tyr Asp Pro Thr Pro Pro
 250 255 260
 ggt gga gct ggc cac ttg ttc atc gcg ttg gat gtt gca gcg ttt cgc 931
 Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp Val Ala Ala Phe Arg
 265 270 275
 gat cca caa gat ttc gat gac gca ctc agc gat ctg gtt ggg gaa gtt 979
 Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp Leu Val Gly Glu Val
 280 285 290
 aaa tcc act ccg aaa gca caa aac acc gag gag att ttc tac ccc ggt 1027
 Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu Ile Phe Tyr Pro Gly
 295 300 305
 gaa tcg gaa gac cgt gcg cat cgg aaa aac tct gcg cac ggt att tca 1075
 Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser Ala His Gly Ile Ser
 310 315 320 325
 ttg cct gaa aaa acg tgg atg gaa ctg caa gaa ctg gca atc gag aac 1123
 Leu Pro Glu Lys Thr Trp Met Glu Leu Gln Glu Leu Ala Ile Glu Asn
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 His Val Val Thr His Arg
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<211> 347

<212> PRT

<213> Corynebacterium glutamicum

<400> 20

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 20 25 30
 Gly Asp Ser Leu Val Gln Ala Asp Leu Trp Gly His Pro Ser His Gly
 35 40 45
 Val Leu Arg Leu Pro Trp Tyr Val Arg Arg Leu His Ser Gly Ala Met
 50 55 60
 Thr Thr His Ala His Val Glu Val Leu Asn Asp Leu Gly Ala Val Leu
 65 70 75 80
 Ala Leu Asp Gly His Asn Gly Ile Gly Gln Val Leu Ala Asp His Ala
 85 90 95
 Arg Lys Glu Ala Val Thr Arg Ala Met Met Phe Gly Ile Gly Ala Val
 100 105 110
 Ser Val Arg Asn Ser Asn His Phe Gly Thr Ala Met Tyr Tyr Thr Arg
 115 120 125

Lys Ala Ala Ala Gln Gly Cys Val Ser Ile Leu Thr Thr Asn Ala Ser
 130 135 140
 Pro Ala Met Ala Pro Trp Gly Gly Arg Glu Lys Arg Ile Gly Thr Asn
 145 150 155 160
 Pro Trp Ser Ile Ala Ala Pro Phe Gly Glu Thr Ala Thr Val Val Asp
 165 170 175
 Ile Ala Asn Thr Ala Val Ala Arg Gly Lys Ile Tyr His Ala Arg Gln
 180 185 190
 Thr Asn Met Pro Ile Pro Glu Thr Trp Ala Ile Thr Ser Glu Gly Ala
 195 200 205
 Pro Thr Thr Asp Pro Ala Glu Ala Ile Asn Gly Val Val Leu Pro Met
 210 215 220
 Ala Gly His Lys Gly Tyr Ala Ile Ser Phe Met Met Asp Val Leu Ser
 225 230 235 240
 Gly Val Leu Thr Gly Ser Gln His Ser Thr Lys Val His Gly Pro Tyr
 245 250 255
 Asp Pro Thr Pro Pro Gly Gly Ala Gly His Leu Phe Ile Ala Leu Asp
 260 265 270
 Val Ala Ala Phe Arg Asp Pro Gln Asp Phe Asp Asp Ala Leu Ser Asp
 275 280 285
 Leu Val Gly Glu Val Lys Ser Thr Pro Lys Ala Gln Asn Thr Glu Glu
 290 295 300
 Ile Phe Tyr Pro Gly Glu Ser Glu Asp Arg Ala His Arg Lys Asn Ser
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1084)
 <223> RXA01350

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 Met Asn Ser Pro Gln
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Asn Val Ser Thr Lys Lys Val Thr Val Thr Gly Ala Ala Gly Gln Ile	
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Ser Tyr Ser Leu Leu Trp Arg Ile Ala Asn Gly Glu Val Phe Gly Thr	
25 30 35	
gac acc cct gta gaa ctg aaa ctt ctg gag atc cct cag gct ctt ggc	259
Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile Pro Gln Ala Leu Gly	
40 45 50	
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Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp Ser Ala Phe Pro Leu	
55 60 65	
ctg cga aac atc acc atc acc gcg gat gcc aat gag gca ttc gac ggc	355
Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn Glu Ala Phe Asp Gly	
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gct aat gcg gcg ttt ttg gtc ggt gcg aag cct cgc gga aaa ggc gaa	403
Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro Arg Gly Lys Gly Glu	
90 95 100	
gag cgc gca gat ttg ctg gct aac aac ggc aag att ttc gga cct caa	451
Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys Ile Phe Gly Pro Gln	
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ggt aaa gct atc aat gac aac gcc gca gat gac att cgt gtc cta gtt	499
Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp Ile Arg Val Leu Val	
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gtt gga aac cca gcg aac acc aac gcg ttg att gct tca gct gcg gcc	547
Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile Ala Ser Ala Ala Ala	
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Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met Met Arg Leu Asp His	
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Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu Gly Arg Gly Ser Ala	
170 175 180	
gaa ttt aac aac att gtg gtc tgg gga aat cac tcc gca acc cag ttc	691
Glu Phe Asn Asn Ile Val Val Trp Gly Asn His Ser Ala Thr Gln Phe	
185 190 195	
cca gac atc acc tac gca acc gtt ggt gga gaa aag gtc act gac ctg	739
Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu Lys Val Thr Asp Leu	
200 205 210	
gtt gat cac gat tgg tat gtg gag gag ttc att cct cgc gtg gct aac	787
Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile Pro Arg Val Ala Asn	
215 220 225	
cgt ggc gct gaa atc att gag gtc cgt gga aag tct tct gca gct tct	835
Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys Ser Ser Ala Ala Ser	
230 235 240 245	
gca gca tcc tct gcg att gat cac atg cgc gat tgg gta cag ggc acc	883

Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp Trp Val Gln Gly Thr
 250 255 260

gag gcg tgg tcc tct gcg gca att cct tcc acc ggt gca tac ggc att 931
 Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr Gly Ala Tyr Gly Ile
 265 270 275

cct gag ggc att ttt gtc ggt ctg cca acc gta tcc cgc aac ggt gag 979
 Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val Ser Arg Asn Gly Glu
 280 285 290

tgg gaa atc gtt gaa ggc ctg gag att tcc gat ttc cag cgc gcc cgc 1027
 Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp Phe Gln Arg Ala Arg
 295 300 305

atc gac gcg aat gct cag gaa ttg cag gcc gag cgc gag gca gtg cgc 1075
 Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu Arg Glu Ala Val Arg
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 Asp Leu Leu

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 22

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Glu Val Phe Gly Thr Asp Thr Pro Val Glu Leu Lys Leu Leu Glu Ile
 35 40 45

Pro Gln Ala Leu Gly Gly Ala Glu Gly Val Ala Met Glu Leu Leu Asp
 50 55 60

Ser Ala Phe Pro Leu Leu Arg Asn Ile Thr Ile Thr Ala Asp Ala Asn
 65 70 75 80

Glu Ala Phe Asp Gly Ala Asn Ala Ala Phe Leu Val Gly Ala Lys Pro
 85 90 95

Arg Gly Lys Gly Glu Glu Arg Ala Asp Leu Leu Ala Asn Asn Gly Lys
 100 105 110

Ile Phe Gly Pro Gln Gly Lys Ala Ile Asn Asp Asn Ala Ala Asp Asp
 115 120 125

Ile Arg Val Leu Val Val Gly Asn Pro Ala Asn Thr Asn Ala Leu Ile
 130 135 140

Ala Ser Ala Ala Ala Pro Asp Val Pro Ala Ser Arg Phe Asn Ala Met
 145 150 155 160

Met Arg Leu Asp His Asn Arg Ala Ile Ser Gln Leu Ala Thr Lys Leu

	165	170	175
Gly Arg Gly Ser Ala Glu Phe Asn Asn Ile Val Val Trp Gly Asn His	180	185	190
Ser Ala Thr Gln Phe Pro Asp Ile Thr Tyr Ala Thr Val Gly Gly Glu	195	200	205
Lys Val Thr Asp Leu Val Asp His Asp Trp Tyr Val Glu Glu Phe Ile	210	215	220
Pro Arg Val Ala Asn Arg Gly Ala Glu Ile Ile Glu Val Arg Gly Lys	225	230	235
Ser Ser Ala Ala Ser Ala Ala Ser Ser Ala Ile Asp His Met Arg Asp	245	250	255
Trp Val Gln Gly Thr Glu Ala Trp Ser Ser Ala Ala Ile Pro Ser Thr	260	265	270
Gly Ala Tyr Gly Ile Pro Glu Gly Ile Phe Val Gly Leu Pro Thr Val	275	280	285
Ser Arg Asn Gly Glu Trp Glu Ile Val Glu Gly Leu Glu Ile Ser Asp	290	295	300
Phe Gln Arg Ala Arg Ile Asp Ala Asn Ala Gln Glu Leu Gln Ala Glu	305	310	315
Arg Glu Ala Val Arg Asp Leu Leu	325		

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 <223> RXA02149

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 Met Pro Gln Lys Pro
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 gcc agt ttc gcg gtg ggc ttt gac atc ggc ggc acc aac atg cga gcc 163
 Ala Ser Phe Ala Val Gly Phe Asp Ile Gly Gly Thr Asn Met Arg Ala
 10 15 20
 ggg ctt gtc gac gaa tcc ggg cgc atc gtg acc agt ttg tcg gcg ccg 211
 Gly Leu Val Asp Glu Ser Gly Arg Ile Val Thr Ser Leu Ser Ala Pro
 25 30 35
 tcg ccg cgc acg acg cag gca atg gaa cag ggg att ttt gat cta gtc 259
 Ser Pro Arg Thr Thr Gln Ala Met Glu Gln Gly Ile Phe Asp Leu Val
 40 45 50

gaa cag ctc aag gcc gaa tac ccg gtt ggt gct gtg gga ctt gcc gtc Glu Gln Leu Lys Ala Glu Tyr Pro Val Gly Ala Val Gly Leu Ala Val 55 60 65	307
gcg gga ttt ttg gat cct gag tgc gag gtt gtt cga ttt gcc ccg cac Ala Gly Phe Leu Asp Pro Glu Cys Glu Val Val Arg Phe Ala Pro His 70 75 80 85	355
ctt cct tgg cgc gat gag cca gtg cgt gaa aag ttg gaa aac ctt ttg Leu Pro Trp Arg Asp Glu Pro Val Arg Glu Lys Leu Glu Asn Leu Leu 90 95 100	403
ggc ctg cct gtt cgt ttg gaa cat gat gcc aac tca gca gcg tgg ggt Gly Leu Pro Val Arg Leu Glu His Asp Ala Asn Ser Ala Ala Trp Gly 105 110 115	451
gag cat cgt ttt ggt gca gct caa ggc gct gac aac tgg gtt ttg ttg Glu His Arg Phe Gly Ala Ala Gln Gly Ala Asp Asn Trp Val Leu Leu 120 125 130	499
gca ctc ggc act gga att ggt gca gcg ctg att gaa aaa ggc gaa att Ala Leu Gly Thr Gly Ile Gly Ala Ala Leu Ile Glu Lys Gly Glu Ile 135 140 145	547
tac cgt ggt gca tat ggc acg gca cca gaa ttt ggt cat ttg cgt gtt Tyr Arg Gly Ala Tyr Gly Thr Ala Pro Glu Phe Gly His Leu Arg Val 150 155 160 165	595
gtt cgt ggc gga cgc gca tgt gcg tgt ggc aaa gaa ggc tgc ctg gag Val Arg Gly Gly Arg Ala Cys Ala Cys Gly Lys Glu Gly Cys Leu Glu 170 175 180	643
cgt tac tgt tcc ggt act gcc ttg gtt tac act gcg cgt gaa ttg gct Arg Tyr Cys Ser Gly Thr Ala Leu Val Tyr Thr Ala Arg Glu Leu Ala 185 190 195	691
tcg cat ggc tca ttc cgc aac agc ggg ctg ttt gac aag atc aaa gcc Ser His Gly Ser Phe Arg Asn Ser Gly Leu Phe Asp Lys Ile Lys Ala 200 205 210	739
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ggc gaa act ttg gcg atc att gct gat gtc ctt gac cca ggc atg atc Gly Glu Thr Leu Ala Ile Ile Ala Asp Val Leu Asp Pro Gly Met Ile 250 255 260	883
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Ser	Leu	Ser	Ala	Pro	Ser	Pro	Arg	Thr	Thr	Gln	Ala	Met	Glu	Gln	Gly	
		35					40					45				
Ile	Phe	Asp	Leu	Val	Glu	Gln	Leu	Lys	Ala	Glu	Tyr	Pro	Val	Gly	Ala	
	50					55					60					
Val	Gly	Leu	Ala	Val	Ala	Gly	Phe	Leu	Asp	Pro	Glu	Cys	Glu	Val	Val	
65					70					75					80	
Arg	Phe	Ala	Pro	His	Leu	Pro	Trp	Arg	Asp	Glu	Pro	Val	Arg	Glu	Lys	
				85					90					95		
Leu	Glu	Asn	Leu	Leu	Gly	Leu	Pro	Val	Arg	Leu	Glu	His	Asp	Ala	Asn	
			100					105					110			
Ser	Ala	Ala	Trp	Gly	Glu	His	Arg	Phe	Gly	Ala	Ala	Gln	Gly	Ala	Asp	
		115					120					125				
Asn	Trp	Val	Leu	Leu	Ala	Leu	Gly	Thr	Gly	Ile	Gly	Ala	Ala	Leu	Ile	
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Glu	Lys	Gly	Glu	Ile	Tyr	Arg	Gly	Ala	Tyr	Gly	Thr	Ala	Pro	Glu	Phe	
145				150						155					160	
Gly	His	Leu	Arg	Val	Val	Arg	Gly	Gly	Arg	Ala	Cys	Ala	Cys	Gly	Lys	
				165					170					175		
Glu	Gly	Cys	Leu	Glu	Arg	Tyr	Cys	Ser	Gly	Thr	Ala	Leu	Val	Tyr	Thr	
			180					185					190			
Ala	Arg	Glu	Leu	Ala	Ser	His	Gly	Ser	Phe	Arg	Asn	Ser	Gly	Leu	Phe	
		195					200					205				
Asp	Lys	Ile	Lys	Ala	Asp	Pro	Asn	Ser	Ile	Asn	Gly	Lys	Thr	Ile	Thr	
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Met Ala His Glu Arg																115
1 5																
gcc ggg caa ctc gcc caa cca gaa gat ctc atc gat gtt gcg gaa ctg																163
Ala Gly Gln Leu Ala Gln Pro Glu Asp Leu Ile Asp Val Ala Glu Leu																
10 15 20																
gtc acc gca tat ttc acc cgc aag ccg gac gtg aac aac cct gat cag																211
Val Thr Ala Tyr Phe Thr Arg Lys Pro Asp Val Asn Asn Pro Asp Gln																
25 30 35																
cag gtc gct ttc ggc acc tcc gga cac cgt ggc ttc gcg ctg gac agc																259
Gln Val Ala Phe Gly Thr Ser Gly His Arg Gly Phe Ala Leu Asp Ser																
40 45 50																
gct ttc aac gag gac cac atc ctg gca acc acc cag gcg atc gtc gac																307
Ala Phe Asn Glu Asp His Ile Leu Ala Thr Thr Gln Ala Ile Val Asp																
55 60 65																
tac cgc aac cag cag cca aaa aac tgg gtc ggc ccg ctg ttt atc ggc																355
Tyr Arg Asn Gln Gln Pro Lys Asn Trp Val Gly Pro Leu Phe Ile Gly																
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cgc gat acg cac gcg ctg tcc gaa cca gcg atg atc agc gcg ctt gag																403
Arg Asp Thr His Ala Leu Ser Glu Pro Ala Met Ile Ser Ala Leu Glu																
90 95 100																

gtc ctc att gcc aac gac gtc gaa gtg ctt gtc gac gcc gac ggc cgc	451
Val Leu Ile Ala Asn Asp Val Glu Val Leu Val Asp Ala Asp Gly Arg	
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Tyr Thr Pro Thr Pro Ala Val Ser His Ala Ile Leu Arg His Asn Asp	
120 125 130	
ggc atc atc ctt ggc acc gca gga ccc tcc cgc ccc tac gcc gac ggc	547
Gly Ile Ile Leu Gly Thr Ala Gly Pro Ser Arg Pro Tyr Ala Asp Gly	
135 140 145	
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Ile Val Ile Thr Pro Ser His Asn Pro Pro Arg Asp Gly Gly Phe Lys	
150 155 160 165	
tac aac cca gcc aac ggt ggc cct gca gat acc gac gcc acc gac tgg	643
Tyr Asn Pro Ala Asn Gly Gly Pro Ala Asp Thr Asp Ala Thr Asp Trp	
170 175 180	
atc gcc aac cgc gcc aac gat att ctg cgc ggc gac ctt gca gac gtg	691
Ile Ala Asn Arg Ala Asn Asp Ile Leu Arg Gly Asp Leu Ala Asp Val	
185 190 195	
aag cga gtt cca gtt tcc ggt gtc ctc gac gag cgc acc act gcc tac	739
Lys Arg Val Pro Val Ser Gly Val Leu Asp Glu Arg Thr Thr Ala Tyr	
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gac ttc aag ggc att tac atc gct gac ctg cca aac gtg gtc aac atc	787
Asp Phe Lys Gly Ile Tyr Ile Ala Asp Leu Pro Asn Val Val Asn Ile	
215 220 225	
gat gcc atc cgc gaa gct ggt gtt cga atc ggc gca gac cca atg ggt	835
Asp Ala Ile Arg Glu Ala Gly Val Arg Ile Gly Ala Asp Pro Met Gly	
230 235 240 245	
ggc gca tcc gtg gat tac tgg ggt gcc atc gca gaa acc cat ggc ctc	883
Gly Ala Ser Val Asp Tyr Trp Gly Ala Ile Ala Glu Thr His Gly Leu	
250 255 260	
aac ctc acc gtg gtc aac cca cac gtt gat tcc acc ttc cgc ttc atg	931
Asn Leu Thr Val Val Asn Pro His Val Asp Ser Thr Phe Arg Phe Met	
265 270 275	
aca ttg gac acc gac ggc aag atc cgc atg gac tgc tcc agc cca cac	979
Thr Leu Asp Thr Asp Gly Lys Ile Arg Met Asp Cys Ser Ser Pro His	
280 285 290	
gca atg gca tcg ctg att gac aac cga gac aag ttc gat gtg gca acc	1027
Ala Met Ala Ser Leu Ile Asp Asn Arg Asp Lys Phe Asp Val Ala Thr	
295 300 305	
ggc aac gac gcc gac gcc gac cgc cac ggc atc gtc acc cca gac gct	1075
Gly Asn Asp Ala Asp Ala Asp Arg His Gly Ile Val Thr Pro Asp Ala	
310 315 320 325	
ggc ttg atg aac ccc aac cac tac ctc gca gta gca att gag tac ctc	1123
Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val Ala Ile Glu Tyr Leu	
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Phe	Ala	His	Arg	Pro	Gly	Trp	Ser	Ala	Asp	Thr	Ala	Val	Gly	Lys	Thr		
			345					350					355				
ctg	gtc	agc	tcc	tcc	atg	atc	gac	cgc	gtt	gtg	gcg	cag	ctt	ggc	cgc	1219	
Leu	Val	Ser	Ser	Ser	Met	Ile	Asp	Arg	Val	Val	Ala	Gln	Leu	Gly	Arg		
		360					365					370					
acc	ctc	gtt	gag	gtt	cca	gtc	gga	ttc	aag	tgg	ttt	gtc	cca	ggg	ttg	1267	
Thr	Leu	Val	Glu	Val	Pro	Val	Gly	Phe	Lys	Trp	Phe	Val	Pro	Gly	Leu		
		375				380					385						
atc	tcc	ggc	gaa	atc	gga	ttc	ggg	ggg	gaa	gaa	tcc	gca	ggg	gca	tcc	1315	
Ile	Ser	Gly	Glu	Ile	Gly	Phe	Gly	Gly	Glu	Glu	Ser	Ala	Gly	Ala	Ser		
390					395				400						405		
ttc	ctc	cgc	atg	gac	ggc	acc	acc	tgg	tcc	acc	gac	aag	gac	ggc	ctc	1363	
Phe	Leu	Arg	Met	Asp	Gly	Thr	Thr	Trp	Ser	Thr	Asp	Lys	Asp	Gly	Leu		
			410					415						420			
atc	ctt	gac	ctc	ctg	gca	gct	gag	atc	att	gca	gta	acc	ggc	aag	acc	1411	
Ile	Leu	Asp	Leu	Leu	Ala	Ala	Glu	Ile	Ile	Ala	Val	Thr	Gly	Lys	Thr		
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cca	tca	cag	cgc	tac	gca	gaa	ctc	gcc	gaa	gaa	ttc	ggg	gca	cct	gcc	1459	
Pro	Ser	Gln	Arg	Tyr	Ala	Glu	Leu	Ala	Glu	Glu	Phe	Gly	Ala	Pro	Ala		
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Tyr	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Asn	Arg	Glu	Gln	Lys	Ala	Ile	Leu		
		455				460					465						
aag	gca	ctg	tcc	cca	gaa	cag	gtc	acc	gcc	acc	gaa	cta	gcc	ggc	gaa	1555	
Lys	Ala	Leu	Ser	Pro	Glu	Gln	Val	Thr	Ala	Thr	Glu	Leu	Ala	Gly	Glu		
470					475				480					485			
gca	atc	acc	gct	aag	ctc	acc	gaa	gct	ccc	ggc	aat	ggc	gca	gcc	atc	1603	
Ala	Ile	Thr	Ala	Lys	Leu	Thr	Glu	Ala	Pro	Gly	Asn	Gly	Ala	Ala	Ile		
			490					495					500				
gga	gga	cta	aaa	gtg	acc	acc	gaa	aac	gcc	tgg	ttc	gca	gca	cgc	cca	1651	
Gly	Gly	Leu	Lys	Val	Thr	Thr	Glu	Asn	Ala	Trp	Phe	Ala	Ala	Arg	Pro		
		505						510				515					
tcc	ggc	acc	gaa	gac	aag	tac	aag	atc	tac	gca	gaa	tcc	ttc	aag	ggc	1699	
Ser	Gly	Thr	Glu	Asp	Lys	Tyr	Lys	Ile	Tyr	Ala	Glu	Ser	Phe	Lys	Gly		
		520					525					530					
gaa	gag	cac	ctc	gcc	cag	gtt	cag	aag	gaa	gcc	caa	gcg	ttg	gtc	agc	1747	
Glu	Glu	His	Leu	Ala	Gln	Val	Gln	Lys	Glu	Ala	Gln	Ala	Leu	Val	Ser		
		535				540					545						
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Glu	Val	Leu	Gly	Gln													
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<211> 554

<212> PRT

<213> Corynebacterium glutamicum

<400> 26

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Asn	Asn	Pro	Asp	Gln	Gln	Val	Ala	Phe	Gly	Thr	Ser	Gly	His	Arg	Gly	35	40	45	
Phe	Ala	Leu	Asp	Ser	Ala	Phe	Asn	Glu	Asp	His	Ile	Leu	Ala	Thr	Thr	50	55	60	
Gln	Ala	Ile	Val	Asp	Tyr	Arg	Asn	Gln	Gln	Pro	Lys	Asn	Trp	Val	Gly	65	70	75	80
Pro	Leu	Phe	Ile	Gly	Arg	Asp	Thr	His	Ala	Leu	Ser	Glu	Pro	Ala	Met	85	90	95	
Ile	Ser	Ala	Leu	Glu	Val	Leu	Ile	Ala	Asn	Asp	Val	Glu	Val	Leu	Val	100	105	110	
Asp	Ala	Asp	Gly	Arg	Tyr	Thr	Pro	Thr	Pro	Ala	Val	Ser	His	Ala	Ile	115	120	125	
Leu	Arg	His	Asn	Asp	Gly	Ile	Ile	Leu	Gly	Thr	Ala	Gly	Pro	Ser	Arg	130	135	140	
Pro	Tyr	Ala	Asp	Gly	Ile	Val	Ile	Thr	Pro	Ser	His	Asn	Pro	Pro	Arg	145	150	155	160
Asp	Gly	Gly	Phe	Lys	Tyr	Asn	Pro	Ala	Asn	Gly	Gly	Pro	Ala	Asp	Thr	165	170	175	
Asp	Ala	Thr	Asp	Trp	Ile	Ala	Asn	Arg	Ala	Asn	Asp	Ile	Leu	Arg	Gly	180	185	190	
Asp	Leu	Ala	Asp	Val	Lys	Arg	Val	Pro	Val	Ser	Gly	Val	Leu	Asp	Glu	195	200	205	
Arg	Thr	Thr	Ala	Tyr	Asp	Phe	Lys	Gly	Ile	Tyr	Ile	Ala	Asp	Leu	Pro	210	215	220	
Asn	Val	Val	Asn	Ile	Asp	Ala	Ile	Arg	Glu	Ala	Gly	Val	Arg	Ile	Gly	225	230	235	240
Ala	Asp	Pro	Met	Gly	Gly	Ala	Ser	Val	Asp	Tyr	Trp	Gly	Ala	Ile	Ala	245	250	255	
Glu	Thr	His	Gly	Leu	Asn	Leu	Thr	Val	Val	Asn	Pro	His	Val	Asp	Ser	260	265	270	
Thr	Phe	Arg	Phe	Met	Thr	Leu	Asp	Thr	Asp	Gly	Lys	Ile	Arg	Met	Asp	275	280	285	
Cys	Ser	Ser	Pro	His	Ala	Met	Ala	Ser	Leu	Ile	Asp	Asn	Arg	Asp	Lys	290	295	300	
Phe	Asp	Val	Ala	Thr	Gly	Asn	Asp	Ala	Asp	Ala	Asp	Arg	His	Gly	Ile	305	310	315	320

Val Thr Pro Asp Ala Gly Leu Met Asn Pro Asn His Tyr Leu Ala Val
 325 330 335
 Ala Ile Glu Tyr Leu Phe Ala His Arg Pro Gly Trp Ser Ala Asp Thr
 340 345 350
 Ala Val Gly Lys Thr Leu Val Ser Ser Ser Met Ile Asp Arg Val Val
 355 360 365
 Ala Gln Leu Gly Arg Thr Leu Val Glu Val Pro Val Gly Phe Lys Trp
 370 375 380
 Phe Val Pro Gly Leu Ile Ser Gly Glu Ile Gly Phe Gly Gly Glu Glu
 385 390 395 400
 Ser Ala Gly Ala Ser Phe Leu Arg Met Asp Gly Thr Thr Trp Ser Thr
 405 410 415
 Asp Lys Asp Gly Leu Ile Leu Asp Leu Leu Ala Ala Glu Ile Ile Ala
 420 425 430
 Val Thr Gly Lys Thr Pro Ser Gln Arg Tyr Ala Glu Leu Ala Glu Glu
 435 440 445
 Phe Gly Ala Pro Ala Tyr Ala Arg Thr Asp Ala Glu Ala Asn Arg Glu
 450 455 460
 Gln Lys Ala Ile Leu Lys Ala Leu Ser Pro Glu Gln Val Thr Ala Thr
 465 470 475 480
 Glu Leu Ala Gly Glu Ala Ile Thr Ala Lys Leu Thr Glu Ala Pro Gly
 485 490 495
 Asn Gly Ala Ala Ile Gly Gly Leu Lys Val Thr Thr Glu Asn Ala Trp
 500 505 510
 Phe Ala Ala Arg Pro Ser Gly Thr Glu Asp Lys Tyr Lys Ile Tyr Ala
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 <223> RXN02803

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Gln Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val	
20 25 30	
gca ttc ctc acc gat gat tat ggc gct gac atg ggc gtg atg att tct	144
Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser	
35 40 45	
gca tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca	192
Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala	
50 55 60	
ggt gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt	240
Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val	
65 70 75 80	
atg gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt	288
Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg	
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gtc atc gaa gaa gca acc gat gca cag gac cgt tac cta gag cac ctg	336
Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu	
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aag gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat	384
Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp	
115 120 125	
gca gcc aat ggt gcg gca agt gtt gta gct cca acg gct tat gag gct	432
Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala	
130 135 140	
gcg ggt gca act gta att gct att cat aac aag cca gac tca tac aac	480
Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn	
145 150 155 160	
atc aac atg gac tgc ggt tcc acc cac att gat cag gcg cag ccg cca	528
Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro	
165 170 175	
gtc ttg aag cac ggt gct gac ctt gga ctc gcg cat gac ggt gat gct	576
Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala	
180 185 190	
gac cgt tgt ttg gct gtg aac aag gat gcc aac ctt gtt gat ggt gac	624
Asp Arg Cys Leu Ala Val Asn Lys Asp Ala Asn Leu Val Asp Gly Asp	
195 200 205	
caa atc atg gcg ctg tta gcc att gcg atg aaa taaaacggcg agctgcgcaa	677
Gln Ile Met Ala Leu Leu Ala Ile Ala Met Lys	
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gaa	680

<210> 28

<211> 219

<212> PRT

<213> Corynebacterium glutamicum

<400> 28

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 Ala Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser
 35 40 45
 Ala Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala
 50 55 60
 Gly Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val
 65 70 75 80
 Met Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg
 85 90 95
 Val Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu
 100 105 110
 Lys Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp
 115 120 125
 Ala Ala Asn Gly Ala Ala Ser Val Val Ala Pro Thr Ala Tyr Glu Ala
 130 135 140
 Ala Gly Ala Thr Val Ile Ala Ile His Asn Lys Pro Asp Ser Tyr Asn
 145 150 155 160
 Ile Asn Met Asp Cys Gly Ser Thr His Ile Asp Gln Ala Gln Pro Pro
 165 170 175
 Val Leu Lys His Gly Ala Asp Leu Gly Leu Ala His Asp Gly Asp Ala
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 Gly Val Asp Val Ile Arg Val Gly Val Ile Pro Thr Pro Ala Val Ala
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Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
      35              40              45

tcc cac aac cca atg ccg gac aac gga atc aag ttc ttt tct gca ggt 192
Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
      50              55              60

gga cac aag ctt cca gac cat gtg gaa gac gag att gag cgt gtt atg 240
Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
      65              70              75

gac agc ttg cca gca gaa ggc cca aca ggg cat gga gtt ggc cgt gtc 288
Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
      85              90              95

atc gaa gaa gca acc gat gca cag gac cgc tac cta gag cac ctg aag 336
Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
      100              105              110

gaa gct gtt cct acg tca ctt gaa ggc atc aag att gtt gtg gat gca 384
Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
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Ala Asn Gly Ala Ala
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<212> PRT

<213> Corynebacterium glutamicum

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Phe Leu Thr Asp Asp Tyr Gly Ala Asp Met Gly Val Met Ile Ser Ala
      35              40              45

Ser His Asn Pro Met Pro Asp Asn Gly Ile Lys Phe Phe Ser Ala Gly
      50              55              60

Gly His Lys Leu Pro Asp His Val Glu Asp Glu Ile Glu Arg Val Met
      65              70              75

Asp Ser Leu Pro Ala Glu Gly Pro Thr Gly His Gly Val Gly Arg Val
      85              90              95

Ile Glu Glu Ala Thr Asp Ala Gln Asp Arg Tyr Leu Glu His Leu Lys
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Glu Ala Val Pro Thr Ser Leu Glu Gly Ile Lys Ile Val Val Asp Ala
      115              120              125

Ala Asn Gly Ala Ala

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Met Asp Glu Ser Arg 5															
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Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala 20															
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Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val 35															
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Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu 40															
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Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp 55															
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Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His 70															
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Val Thr Leu Leu Pro Thr Pro Ser Pro Thr Pro Leu Ile Pro Trp Leu 105															
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Val Asn Lys His Gly Leu Asp Ala Gly Val Gln Ile Thr Ala Ser His 120															
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Gln Leu Tyr Ser Glu Leu Glu Pro Glu Leu Glu Ala His Ile Asn Ala 150															
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Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	Arg	Gly	Asn	Leu	Arg	
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Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	Ala	Lys	Glu	Lys	Asn	
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Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Ser	Gln	Leu	Leu	
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Ala	Phe	Ala	Tyr	Glu	Glu	Ala	Val	Gly	Thr	Cys	Pro	Val	Pro	Asp	Val	
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Val	Pro	Asp	Lys	Asp	Gly	Ile	Ser	Thr	Ala	Leu	Phe	Met	Ala	Ser	Trp	
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gct	gcc	gaa	ctg	aag	gct	cag	ggc	gca	agc	ctg	cag	caa	aaa	ctc	aat	1363
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Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His	Trp	Ile	Ala	His	Pro					
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Gln	Gln	Glu	Leu	Ile	Gly	Val	Ser	Val	Thr	Pro	His	Ile	Leu	Pro	Glu					
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Lys	Gln	Gly	Ile	Ala	Leu	His	Gly	Gln	Val	Gly	His	Val	His	Ile	Arg					
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Glu	Val	Gly	Gln	Ala	Ser	Ser	His	Asp	Glu	Ala	Ala	Gln	Leu	Leu	His					
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Thr	Thr	Ala	Gly	Val	Ala	Ser	Trp	Leu	Ala	Glu	Arg	Ala	Ala	Leu	Asn
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Leu	Tyr	Pro	Gln	Asp	Gly	Pro	Leu	Arg	Val	Val	Val	Gly	Tyr	Asp	Ala
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Arg	Tyr	Gly	Ser	His	Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala
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Gly	Ala	Gly	Phe	Glu	Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro
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Ala	His	Ile	Asn	Ala	Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr
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Phe	Pro	Asn	Pro	Glu	Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg
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Ala	Lys	Glu	Lys	Asn	Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala
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Glu	Tyr	Ser	Gly	Glu	Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val
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Ser	Ser	Gln	Leu	Leu	Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr
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Phe	Met	Ala	Ser	Trp	Ala	Ala	Glu	Leu	Lys	Ala	Gln	Gly	Ala	Ser	Leu
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Gln	Gln	Lys	Leu	Asn	Glu	Leu	Tyr	Arg	Arg	Tyr	Gly	Tyr	Phe	Ala	Ser
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Ser	Gln	Ile	Ala	Val	Arg	Thr	Ser	Ser	Pro	Arg	Glu	Leu	Val	Asp	His
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Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
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 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
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 <223> FRXA02854

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 Gln Leu Ser Phe Gly Thr Ala Gly Leu Arg Ala Pro Val Gly Pro Ala
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 cgc cat cag atg aat gtt ttg cag gta acc aga act aca gca ggt gtt 211
 Arg His Gln Met Asn Val Leu Gln Val Thr Arg Thr Thr Ala Gly Val
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 gct agt tgg ttg gca gaa cgt gcg gca cta aat cca gtg ccg cat ttg 259
 Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn Pro Val Pro His Leu
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 Val Pro Glu Asp Glu Thr Gly Ile Gly Arg Ala Leu Tyr Pro Gln Asp
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 ggt ccg ttg cgg gtc gtt gtg ggg tat gac gct cgc tat ggt tcg cat 355
 Gly Pro Leu Arg Val Val Val Gly Tyr Asp Ala Arg Tyr Gly Ser His
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 act ttt gct gca acc act gcg gag gtg ttc gcg ggt gct ggt ttt gag 403
 Thr Phe Ala Ala Thr Thr Ala Glu Val Phe Ala Gly Ala Gly Phe Glu
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Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	Leu	Ser	Asn	Gly	Arg	
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Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	Ala	His	Ile	Asn	Ala	
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Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	Ser	Ser	Gln	Leu	Leu	
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 Gly Phe Lys Asn Leu Ser Arg Ala Ala Asp Gly Leu Asp Gly Pro Leu
 360 365 370
 gct ttc gct tat gag gaa gct gtg ggc acc tgc ccg gtt cca gat gtc 1267
 Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys Pro Val Pro Asp Val
 375 380 385
 gtg ccg gat aag gac ggc atc tct aca gcg ttg ttc atg gcg tcg tgg 1315
 Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu Phe Met Ala Ser Trp
 390 395 400 405
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 gag ttg tat cgc cga tat ggg tat ttt gcg tcc tcg caa att gct gtg 1411
 Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser Ser Gln Ile Ala Val
 425 430 435
 cgc acg agc agt cca cgc gag tta gtt gat cac tgg att gcg cat cct 1459
 Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His Trp Ile Ala His Pro
 440 445 450
 cag caa gaa ctc att gga gtg tct gtc acc cca cat att ctt cct gaa 1507
 Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro His Ile Leu Pro Glu
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 aaa cag ggc att gct ttg cat ggc cag gtg ggg cat gtg cat atc cgt 1555
 Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly His Val His Ile Arg
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<212> PRT

<213> Corynebacterium glutamicum

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Thr Thr Ala Gly Val Ala Ser Trp Leu Ala Glu Arg Ala Ala Leu Asn

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Arg	Tyr	Gly	Ser	His	Thr	Phe	Ala	Ala	Thr	Thr	Ala	Glu	Val	Phe	Ala	
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Gly	Ala	Gly	Phe	Glu	Val	Thr	Leu	Leu	Pro	Thr	Pro	Ser	Pro	Thr	Pro	
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Leu	Ile	Pro	Trp	Leu	Val	Asn	Lys	His	Gly	Leu	Asp	Ala	Gly	Val	Gln	
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Ile	Thr	Ala	Ser	His	Asn	Gly	Ala	Ala	Asp	Asn	Gly	Tyr	Lys	Val	Phe	
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Leu	Ser	Asn	Gly	Arg	Gln	Leu	Tyr	Ser	Glu	Leu	Glu	Pro	Glu	Leu	Glu	
145					150					155					160	
Ala	His	Ile	Asn	Ala	Val	Glu	Asp	Pro	Ile	Arg	Val	Pro	Arg	Val	Thr	
165					170					175						
Val	Arg	Pro	Thr	Ala	Asp	Gln	Leu	Arg	Arg	Tyr	Val	Asp	Glu	Met	Val	
180					185					190						
Ser	Leu	Val	Thr	Pro	Asp	Gln	Ala	Asp	Leu	Leu	Arg	Val	Asn	Ser	Glu	
195					200					205						
Arg	Gly	Asn	Leu	Arg	Val	Val	Tyr	Thr	Ala	Leu	His	Gly	Val	Gly	Gly	
210					215					220						
Arg	Ala	Met	Ala	Asn	Ala	Phe	Gln	Phe	Ala	Gly	Phe	Pro	His	Thr	His	
225					230					235					240	
Gly	Val	Lys	Ala	Gln	Gln	Tyr	Pro	Asp	Pro	Thr	Phe	Pro	Thr	Val	Ala	
245					250					255						
Phe	Pro	Asn	Pro	Glu	Glu	Pro	Ser	Ala	Ile	Glu	Leu	Leu	Leu	Glu	Arg	
260					265					270						
Ala	Lys	Glu	Lys	Asn	Ala	Asp	Ile	Leu	Phe	Ala	Leu	Asp	Pro	Asp	Ala	
275					280					285						
Asp	Arg	Cys	Ala	Val	Gly	Ile	Arg	Thr	Ala	Asp	Gly	Gly	His	Arg	Met	
290					295					300						
Leu	Ser	Gly	Asp	Glu	Val	Gly	Thr	Leu	Leu	Ala	Thr	Arg	Leu	Val	Pro	
305					310					315					320	
Glu	Tyr	Ser	Gly	Glu	Gly	Pro	Arg	Pro	Val	Val	Ala	Thr	Thr	Val	Val	
325					330					335						
Ser	Ser	Gln	Leu	Leu	Gly	Ile	Ile	Ala	Glu	Asp	Lys	Gly	Trp	Asp	Tyr	
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Ser	Glu	Thr	Leu	Thr	Gly	Phe	Lys	Asn	Leu	Ser	Arg	Ala	Ala	Asp	Gly	
355					360					365						

Leu Asp Gly Pro Leu Ala Phe Ala Tyr Glu Glu Ala Val Gly Thr Cys
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 Pro Val Pro Asp Val Val Pro Asp Lys Asp Gly Ile Ser Thr Ala Leu
 385 390 395 400
 Phe Met Ala Ser Trp Ala Ala Glu Leu Lys Ala Gln Gly Ala Ser Leu
 405 410 415
 Gln Gln Lys Leu Asn Glu Leu Tyr Arg Arg Tyr Gly Tyr Phe Ala Ser
 420 425 430
 Ser Gln Ile Ala Val Arg Thr Ser Ser Pro Arg Glu Leu Val Asp His
 435 440 445
 Trp Ile Ala His Pro Gln Gln Glu Leu Ile Gly Val Ser Val Thr Pro
 450 455 460
 His Ile Leu Pro Glu Lys Gln Gly Ile Ala Leu His Gly Gln Val Gly
 465 470 475 480
 His Val His Ile Arg Ala Ile Gly Arg Val Ser Gly Thr Glu Ala Lys
 485 490 495
 Ala Lys Leu Tyr Leu Glu Val Gly Gln Ala Ser Ser His Asp Glu Ala
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 Ala Gln Leu Leu His Gln Leu Glu Asp Glu Val Gln Ser Trp Leu Ser
 515 520 525

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 <213> Corynebacterium glutamicum

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 <222> (1)..(513)
 <223> RXA00511

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 Leu Lys Ile Ala Met Asp Glu Ala Gly Ile Thr Leu Arg Thr Thr Lys
 20 25 30
 gta gga gac cgc tac gtg ctg gaa gac ctc aat gca ggt gga ttc agc 144
 Val Gly Asp Arg Tyr Val Leu Glu Asp Leu Asn Ala Gly Gly Phe Ser
 35 40 45
 ctg ggc ggc gag caa tct ggc cac att gtt ctt cca gat cat ggc acc 192
 Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60

act ggc gat gga act ttg act ggt ctt tcc atc atg gcg cgc atg gct 240
 Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80

gaa acc gga aag tcc ttg ggc gag ttg gca caa gct atg acg gtg ctg 288
 Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95

cca cag gtt ctg atc aat gtg cca gtt tcc gat aag tcc acc atc gtg 336
 Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110

agc cac cca agc gtt gtg gct gcg atc gcg gaa gca gaa gct gag ttg 384
 Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125

ggc gcc acc ggt cgc gtt ctt ctt cgt gct tct ggc acc gaa gag ctt 432
 Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
 130 135 140

ttc cgc gtg atg gtt gag gct gga gac aag gaa caa gct cgt cgt atc 480
 Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
 145 150 155 160

gcg gga cgt ctt gct gca gtg gtt gca gaa gtc taattcactt cagtcacagc 533
 Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
 165 170

gca 536

<210> 36

<211> 171

<212> PRT

<213> Corynebacterium glutamicum

<400> 36

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 35 40 45

Leu Gly Gly Glu Gln Ser Gly His Ile Val Leu Pro Asp His Gly Thr
 50 55 60

Thr Gly Asp Gly Thr Leu Thr Gly Leu Ser Ile Met Ala Arg Met Ala
 65 70 75 80

Glu Thr Gly Lys Ser Leu Gly Glu Leu Ala Gln Ala Met Thr Val Leu
 85 90 95

Pro Gln Val Leu Ile Asn Val Pro Val Ser Asp Lys Ser Thr Ile Val
 100 105 110

Ser His Pro Ser Val Val Ala Ala Ile Ala Glu Ala Glu Ala Glu Leu
 115 120 125

Gly Ala Thr Gly Arg Val Leu Leu Arg Ala Ser Gly Thr Glu Glu Leu
130 135 140

Phe Arg Val Met Val Glu Ala Gly Asp Lys Glu Gln Ala Arg Arg Ile
145 150 155 160

Ala Gly Arg Leu Ala Ala Val Val Ala Glu Val
165 170

<210> 37

<211> 1497

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1474)

<223> RXN01365

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Met Arg Thr Arg Glu
1 5

tct gtc aca gct gta att aag gcg tat gac gtc cgt ggt gtt gtt ggt 163
Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
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gtc gat att gat gct gat ttc att tct gag act ggc gct gcc ttt ggt 211
Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
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cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
40 45 50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
55 60 65

act gca cag ggt ttg gat gtt gtt cat ttg gga ctg act tct act gat 355
Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
70 75 80 85

gag ctg tac ttt gcg tcc gga acc ttg aag tgt gct ggt gcg atg ttt 403
Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
90 95 100

act gcg tcg cat aac ccc gct gag tac aac ggc atc aag ttg tgt cgt 451
Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
105 110 115

gcg ggt gct cgt ccg gtc ggt cag gat tct ggt ttg gcc aac atc att 499
Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
120 125 130

gat gat ctg gtt gag ggt gtt cca gcg ttt gat ggt gag tca ggt tcg 547

Asp	Asp	Leu	Val	Glu	Gly	Val	Pro	Ala	Phe	Asp	Gly	Glu	Ser	Gly	Ser	
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Val	Ser	Glu	Gln	Asp	Leu	Leu	Ser	Ala	Tyr	Ala	Glu	Tyr	Leu	Asn	Glu	
150					155					160					165	
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Leu	Val	Asp	Leu	Lys	Asn	Ile	Arg	Pro	Met	Lys	Val	Ala	Val	Asp	Ala	
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gca	aac	ggc	atg	ggt	ggg	ttc	act	gtc	cct	gag	gta	ttc	aag	ggt	ctg	691
Ala	Asn	Gly	Met	Gly	Gly	Phe	Thr	Val	Pro	Glu	Val	Phe	Lys	Gly	Leu	
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Pro	Leu	Asp	Val	Ala	Pro	Leu	Tyr	Phe	Glu	Leu	Asp	Gly	Asn	Phe	Pro	
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Asn	His	Glu	Ala	Asn	Pro	Leu	Glu	Pro	Ala	Asn	Leu	Val	Asp	Leu	Gln	
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aag	ttt	acc	gta	gag	acc	gga	tct	gat	atc	ggt	ttg	gcg	ttc	gac	ggc	835
Lys	Phe	Thr	Val	Glu	Thr	Gly	Ser	Asp	Ile	Gly	Leu	Ala	Phe	Asp	Gly	
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Asp	Ala	Asp	Arg	Cys	Phe	Val	Val	Asp	Glu	Lys	Gly	Gln	Pro	Val	Ser	
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cct	tcg	gcg	atc	tgt	gcg	atc	gta	gcg	gag	cgt	tac	ttg	gag	aag	ctt	931
Pro	Ser	Ala	Ile	Cys	Ala	Ile	Val	Ala	Glu	Arg	Tyr	Leu	Glu	Lys	Leu	
			265					270					275			
ccg	ggt	tcc	acc	atc	atc	cac	aac	ctg	att	acc	tct	aag	gct	gtg	cct	979
Pro	Gly	Ser	Thr	Ile	Ile	His	Asn	Leu	Ile	Thr	Ser	Lys	Ala	Val	Pro	
		280					285					290				
gag	gtg	att	gct	gaa	aac	ggt	ggc	act	gcg	gtg	cgt	act	cgc	gtg	ggt	1027
Glu	Val	Ile	Ala	Glu	Asn	Gly	Gly	Thr	Ala	Val	Arg	Thr	Arg	Val	Gly	
	295					300					305					
cac	tcc	ttc	atc	aag	gcg	aag	atg	gca	gag	acc	ggt	gcg	gcc	ttt	ggt	1075
His	Ser	Phe	Ile	Lys	Ala	Lys	Met	Ala	Glu	Thr	Gly	Ala	Ala	Phe	Gly	
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ggc	gag	cac	tct	gcg	cac	tac	tac	ttc	act	gag	ttc	ttc	aat	gcg	gac	1123
Gly	Glu	His	Ser	Ala	His	Tyr	Tyr	Phe	Thr	Glu	Phe	Phe	Asn	Ala	Asp	
				330					335					340		
tcc	ggc	att	ttg	gct	gcg	atg	cac	gtg	ctg	gct	gcg	ctg	gga	agc	cag	1171
Ser	Gly	Ile	Leu	Ala	Ala	Met	His	Val	Leu	Ala	Ala	Leu	Gly	Ser	Gln	
			345					350					355			
gac	cag	cca	ctc	agt	gag	atg	atg	gct	agg	tat	aac	cgg	tac	ggt	gct	1219
Asp	Gln	Pro	Leu	Ser	Glu	Met	Met	Ala	Arg	Tyr	Asn	Arg	Tyr	Val	Ala	
		360					365					370				
tca	ggc	gag	ttg	aac	tcc	cgt	ttg	gct	aat	gca	gag	gcg	cag	caa	gag	1267
Ser	Gly	Glu	Leu	Asn	Ser	Arg	Leu	Ala	Asn	Ala	Glu	Ala	Gln	Gln	Glu	

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cgc acc cag gct gtg ctc gat gcg ttc gct gat cgc acc gag tcc gtg 1315
Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp Arg Thr Glu Ser Val
390      395      400      405

gac acc ctt gac ggc gtg act gtg gaa ctc aag gac acc tcc gcg tgg 1363
Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys Asp Thr Ser Ala Trp
      410      415      420

ttc aac gtg cgt gcg tcc aac acc gag ccg ctg ctt cgc ctc aat gtt 1411
Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu Leu Arg Leu Asn Val
      425      430      435

gaa gct gca tcg aag gaa gaa gtc gat gcg ttg gta gcg gag att cta 1459
Glu Ala Ala Ser Lys Glu Glu Val Asp Ala Leu Val Ala Glu Ile Leu
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ggg att atc cgc gca taatccatt ttccggcggg cat 1497
Gly Ile Ile Arg Ala
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<210> 38
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<212> PRT
<213> Corynebacterium glutamicum

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Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
      35      40      45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
      50      55      60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
      65      70      75      80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
      85      90      95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
      100      105      110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
      115      120      125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
      130      135      140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
      145      150      155      160

Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
      165      170      175

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Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
 260 265 270
 Tyr Leu Glu Lys Leu Pro Gly Ser Thr Ile Ile His Asn Leu Ile Thr
 275 280 285
 Ser Lys Ala Val Pro Glu Val Ile Ala Glu Asn Gly Gly Thr Ala Val
 290 295 300
 Arg Thr Arg Val Gly His Ser Phe Ile Lys Ala Lys Met Ala Glu Thr
 305 310 315 320
 Gly Ala Ala Phe Gly Gly Glu His Ser Ala His Tyr Tyr Phe Thr Glu
 325 330 335
 Phe Phe Asn Ala Asp Ser Gly Ile Leu Ala Ala Met His Val Leu Ala
 340 345 350
 Ala Leu Gly Ser Gln Asp Gln Pro Leu Ser Glu Met Met Ala Arg Tyr
 355 360 365
 Asn Arg Tyr Val Ala Ser Gly Glu Leu Asn Ser Arg Leu Ala Asn Ala
 370 375 380
 Glu Ala Gln Gln Glu Arg Thr Gln Ala Val Leu Asp Ala Phe Ala Asp
 385 390 395 400
 Arg Thr Glu Ser Val Asp Thr Leu Asp Gly Val Thr Val Glu Leu Lys
 405 410 415
 Asp Thr Ser Ala Trp Phe Asn Val Arg Ala Ser Asn Thr Glu Pro Leu
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<211> 994

<212> DNA

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<222> (101)..(994)

<223> FRXA01365

<400> 39

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Ser Val Thr Ala Val Ile Lys Ala Tyr Asp Val Arg Gly Val Val Gly
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Val Asp Ile Asp Ala Asp Phe Ile Ser Glu Thr Gly Ala Ala Phe Gly
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cgg ctc atg cgt agt gag ggt gaa acc acc gtt gct att ggc cat gac 259
Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val Ala Ile Gly His Asp
                        40 45 50

atg cgt gat tcc tcc cct gaa ttg gcc aag gcg ttt gcc gat ggc gtg 307
Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala Phe Ala Asp Gly Val
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Thr Ala Gln Gly Leu Asp Val Val His Leu Gly Leu Thr Ser Thr Asp
                        70 75 80 85

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Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys Ala Gly Ala Met Phe
                        90 95 100

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Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly Ile Lys Leu Cys Arg
                        105 110 115

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Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly Leu Ala Asn Ile Ile
                        120 125 130

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Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp Gly Glu Ser Gly Ser
                        135 140 145

gtt tct gag cag gat ttg ctg agc gca tat gcc gag tac ctc aat gag 595
Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala Glu Tyr Leu Asn Glu
                        150 155 160 165

ctt gtt gat ctg aag aac atc cgc ccg atg aag gtt gct gtg gat gcg 643
Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys Val Ala Val Asp Ala
                        170 175 180

gca aac ggc atg ggt ggg ttc act gtc cct gag gta ttc aag ggt ctg 691
Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu Val Phe Lys Gly Leu
                        185 190 195

cca ctt gat gtt gcg cca ctg tat ttt gag ctt gac ggc aat ttc ccc 739

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 Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn Leu Val Asp Leu Gln
 215 220 225

aag ttt acc gta gag acc gga tct gat atc ggt ttg gcg ttc gac ggc 835
 Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly Leu Ala Phe Asp Gly
 230 235 240 245

gat gcg gat cgt tgc ttc gtg gtc gat gag aag ggc cag cca gtc agc 883
 Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys Gly Gln Pro Val Ser
 250 255 260

cct tcg gcg atc tgt gcg atc gta gcg gag cgt tac ttg gag aag ctt 931
 Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg Tyr Leu Glu Lys Leu
 265 270 275

ccg ggt tcc acc atc atc cac aac ctg att acc tct aag gct gtg cct 979
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gag gtg att gct gaa 994
 Glu Val Ile Ala Glu
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<210> 40

<211> 298

<212> PRT

<213> Corynebacterium glutamicum

<400> 40

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Gly Ala Ala Phe Gly Arg Leu Met Arg Ser Glu Gly Glu Thr Thr Val
 35 40 45

Ala Ile Gly His Asp Met Arg Asp Ser Ser Pro Glu Leu Ala Lys Ala
 50 55 60

Phe Ala Asp Gly Val Thr Ala Gln Gly Leu Asp Val Val His Leu Gly
 65 70 75 80

Leu Thr Ser Thr Asp Glu Leu Tyr Phe Ala Ser Gly Thr Leu Lys Cys
 85 90 95

Ala Gly Ala Met Phe Thr Ala Ser His Asn Pro Ala Glu Tyr Asn Gly
 100 105 110

Ile Lys Leu Cys Arg Ala Gly Ala Arg Pro Val Gly Gln Asp Ser Gly
 115 120 125

Leu Ala Asn Ile Ile Asp Asp Leu Val Glu Gly Val Pro Ala Phe Asp
 130 135 140

Gly Glu Ser Gly Ser Val Ser Glu Gln Asp Leu Leu Ser Ala Tyr Ala
 145 150 155 160
 Glu Tyr Leu Asn Glu Leu Val Asp Leu Lys Asn Ile Arg Pro Met Lys
 165 170 175
 Val Ala Val Asp Ala Ala Asn Gly Met Gly Gly Phe Thr Val Pro Glu
 180 185 190
 Val Phe Lys Gly Leu Pro Leu Asp Val Ala Pro Leu Tyr Phe Glu Leu
 195 200 205
 Asp Gly Asn Phe Pro Asn His Glu Ala Asn Pro Leu Glu Pro Ala Asn
 210 215 220
 Leu Val Asp Leu Gln Lys Phe Thr Val Glu Thr Gly Ser Asp Ile Gly
 225 230 235 240
 Leu Ala Phe Asp Gly Asp Ala Asp Arg Cys Phe Val Val Asp Glu Lys
 245 250 255
 Gly Gln Pro Val Ser Pro Ser Ala Ile Cys Ala Ile Val Ala Glu Arg
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 Ser Lys Ala Val Pro Glu Val Ile Ala Glu
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 <213> Corynebacterium glutamicum

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 <222> (101)..(1720)
 <223> RXA00098

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 Met Ala Asp Ile Ser
 1 5
 acc acc cag gtt tgg caa gac ctg acc gat cat tac tca aac ttc cag 163
 Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His Tyr Ser Asn Phe Gln
 10 15 20
 gca acc act ctg cgt gaa ctt ttc aag gaa gaa aac cgc gcc gag aag 211
 Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu Asn Arg Ala Glu Lys
 25 30 35
 tac acc ttc tcc gcg gct ggc ctc cac gtc gac ctg tcg aag aat ctg 259
 Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp Leu Ser Lys Asn Leu
 40 45 50
 ctt gac gac gcc acc ctc acc aag ctc ctt gca ctg acc gaa gaa tct 307

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Gly	Leu	Arg	Glu	Arg	Ile	Asp	Ala	Met	Phe	Ala	Gly	Glu	His	Leu	Asn	
70					75					80					85	
aac	acc	gaa	gac	cgc	gct	gtc	ctc	cac	acc	gcg	ctg	cgc	ctt	cct	gcc	403
Asn	Thr	Glu	Asp	Arg	Ala	Val	Leu	His	Thr	Ala	Leu	Arg	Leu	Pro	Ala	
				90					95					100		
gaa	gct	gat	ctg	tca	gta	gat	ggc	caa	gat	gtt	gct	gct	gat	gtc	cac	451
Glu	Ala	Asp	Leu	Ser	Val	Asp	Gly	Gln	Asp	Val	Ala	Ala	Asp	Val	His	
			105					110					115			
gaa	gtt	ttg	gga	cgc	atg	cgt	gac	ttc	gct	act	gcg	ctg	cgc	tca	ggc	499
Glu	Val	Leu	Gly	Arg	Met	Arg	Asp	Phe	Ala	Thr	Ala	Leu	Arg	Ser	Gly	
	120						125				130					
aac	tgg	ttg	gga	cac	acc	ggc	cac	acg	atc	aag	aag	atc	gtc	aac	att	547
Asn	Trp	Leu	Gly	His	Thr	Gly	His	Thr	Ile	Lys	Lys	Ile	Val	Asn	Ile	
	135					140					145					
ggt	atc	ggt	ggc	tct	gac	ctc	gga	cca	gcc	atg	gct	acg	aag	gct	ctg	595
Gly	Ile	Gly	Gly	Ser	Asp	Leu	Gly	Pro	Ala	Met	Ala	Thr	Lys	Ala	Leu	
150					155				160						165	
cgt	gca	tac	gcg	acc	gct	ggg	atc	tca	gca	gaa	ttc	gtc	tcc	aac	gtc	643
Arg	Ala	Tyr	Ala	Thr	Ala	Gly	Ile	Ser	Ala	Glu	Phe	Val	Ser	Asn	Val	
				170					175					180		
gac	cca	gca	gac	ctc	gtt	tct	gtg	ttg	gaa	gac	ctc	gat	gca	gaa	tcc	691
Asp	Pro	Ala	Asp	Leu	Val	Ser	Val	Leu	Glu	Asp	Leu	Asp	Ala	Glu	Ser	
			185					190					195			
aca	ttg	ttc	gtg	atc	gct	tcg	aaa	act	ttc	acc	acc	cag	gag	acg	ctg	739
Thr	Leu	Phe	Val	Ile	Ala	Ser	Lys	Thr	Phe	Thr	Thr	Gln	Glu	Thr	Leu	
	200						205					210				
tcc	aac	gct	cgt	gca	gct	cgt	gct	tgg	ctg	gta	gag	aag	ctc	ggg	gaa	787
Ser	Asn	Ala	Arg	Ala	Ala	Arg	Ala	Trp	Leu	Val	Glu	Lys	Leu	Gly	Glu	
	215					220				225						
gag	gct	gtc	gcg	aag	cac	ttc	gtc	gca	gtg	tcc	acc	aat	gct	gaa	aag	835
Glu	Ala	Val	Ala	Lys	His	Phe	Val	Ala	Val	Ser	Thr	Asn	Ala	Glu	Lys	
230					235				240						245	
gtc	gca	gag	ttc	ggg	atc	gac	acg	gac	aac	atg	ttc	ggc	ttc	tgg	gac	883
Val	Ala	Glu	Phe	Gly	Ile	Asp	Thr	Asp	Asn	Met	Phe	Gly	Phe	Trp	Asp	
				250					255					260		
tgg	gtc	gga	ggg	cgt	tac	tcc	gtg	gac	tcc	gca	gtt	ggg	ctt	tcc	ctc	931
Trp	Val	Gly	Gly	Arg	Tyr	Ser	Val	Asp	Ser	Ala	Val	Gly	Leu	Ser	Leu	
			265					270					275			
atg	gca	gtg	atc	ggc	cct	cgc	gac	ttc	atg	cgt	ttc	ctc	ggg	gga	ttc	979
Met	Ala	Val	Ile	Gly	Pro	Arg	Asp	Phe	Met	Arg	Phe	Leu	Gly	Gly	Phe	
	280						285					290				
cac	gcg	atg	gat	gaa	cac	ttc	cgc	acc	acc	aag	ttc	gaa	gag	aac	gtt	1027
His	Ala	Met	Asp	Glu	His	Phe	Arg	Thr	Thr	Lys	Phe	Glu	Glu	Asn	Val	

295	300	305	
cca atc ttg atg gct ctg ctc ggt gtc tgg tac tcc gat ttc tat ggt Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr Ser Asp Phe Tyr Gly 310 315 320 325			1075
gca gaa acc cac gct gtc cta cct tat tcc gag gat ctc agc cgt ttt Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu Asp Leu Ser Arg Phe 330 335 340			1123
gct gct tac ctc cag cag ctg acc atg gaa tca aat ggc aag tca gtc Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser Asn Gly Lys Ser Val 345 350 355			1171
cac cgc gac ggc tcc cct gtt tcc act ggc act ggc gaa att tac tgg His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr Gly Glu Ile Tyr Trp 360 365 370			1219
ggt gag cct ggc aca aat ggc cag cac gct ttc ttc cag ctg atc cac Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe Phe Gln Leu Ile His 375 380 385			1267
cag ggc act cgc ctt gtt cca gct gat ttc att ggt ttc gct cgt cca Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile Gly Phe Ala Arg Pro 390 395 400 405			1315
aag cag gat ctt cct gcc ggt gag cgc acc atg cat gac ctt ttg atg Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met His Asp Leu Leu Met 410 415 420			1363
agc aac ttc ttc gca cag acc aag gtt ttg gct ttc ggt aag aac gct Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala Phe Gly Lys Asn Ala 425 430 435			1411
gaa gag atc gct gcg gaa ggt gtc gca cct gag ctg gtc aac cac aag Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu Leu Val Asn His Lys 440 445 450			1459
gtc atg cca ggt aat cgc cca acc acc acc att ttg gcg gag gaa ctt Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile Leu Ala Glu Glu Leu 455 460 465			1507
acc cct tct att ctc ggt gcg ttg atc gct ttg tac gaa cac atc gtg Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu Tyr Glu His Ile Val 470 475 480 485			1555
atg gtt cag ggc gtg att tgg gac atc aac tcc ttc gac caa tgg ggt Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser Phe Asp Gln Trp Gly 490 495 500			1603
gtt gaa ctg ggc aaa cag cag gca aat gac ctc gct ccg gct gtc tct Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu Ala Pro Ala Val Ser 505 510 515			1651
ggt gaa gag gat gtt gac tcg gga gat tct tcc act gat tca ctg att Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser Thr Asp Ser Leu Ile 520 525 530			1699
aag tgg tac cgc gca aat agg tagtcgcttg cttatagggt cag Lys Trp Tyr Arg Ala Asn Arg 535 540			1743

<210> 42

<211> 540

<212> PRT

<213> Corynebacterium glutamicum

<400> 42

Met Ala Asp Ile Ser Thr Thr Gln Val Trp Gln Asp Leu Thr Asp His
 1 5 10 15

Tyr Ser Asn Phe Gln Ala Thr Thr Leu Arg Glu Leu Phe Lys Glu Glu
 20 25 30

Asn Arg Ala Glu Lys Tyr Thr Phe Ser Ala Ala Gly Leu His Val Asp
 35 40 45

Leu Ser Lys Asn Leu Leu Asp Asp Ala Thr Leu Thr Lys Leu Leu Ala
 50 55 60

Leu Thr Glu Glu Ser Gly Leu Arg Glu Arg Ile Asp Ala Met Phe Ala
 65 70 75 80

Gly Glu His Leu Asn Asn Thr Glu Asp Arg Ala Val Leu His Thr Ala
 85 90 95

Leu Arg Leu Pro Ala Glu Ala Asp Leu Ser Val Asp Gly Gln Asp Val
 100 105 110

Ala Ala Asp Val His Glu Val Leu Gly Arg Met Arg Asp Phe Ala Thr
 115 120 125

Ala Leu Arg Ser Gly Asn Trp Leu Gly His Thr Gly His Thr Ile Lys
 130 135 140

Lys Ile Val Asn Ile Gly Ile Gly Gly Ser Asp Leu Gly Pro Ala Met
 145 150 155 160

Ala Thr Lys Ala Leu Arg Ala Tyr Ala Thr Ala Gly Ile Ser Ala Glu
 165 170 175

Phe Val Ser Asn Val Asp Pro Ala Asp Leu Val Ser Val Leu Glu Asp
 180 185 190

Leu Asp Ala Glu Ser Thr Leu Phe Val Ile Ala Ser Lys Thr Phe Thr
 195 200 205

Thr Gln Glu Thr Leu Ser Asn Ala Arg Ala Ala Arg Ala Trp Leu Val
 210 215 220

Glu Lys Leu Gly Glu Glu Ala Val Ala Lys His Phe Val Ala Val Ser
 225 230 235 240

Thr Asn Ala Glu Lys Val Ala Glu Phe Gly Ile Asp Thr Asp Asn Met
 245 250 255

Phe Gly Phe Trp Asp Trp Val Gly Gly Arg Tyr Ser Val Asp Ser Ala
 260 265 270

Val Gly Leu Ser Leu Met Ala Val Ile Gly Pro Arg Asp Phe Met Arg
 275 280 285

Phe Leu Gly Gly Phe His Ala Met Asp Glu His Phe Arg Thr Thr Lys
 290 295 300
 Phe Glu Glu Asn Val Pro Ile Leu Met Ala Leu Leu Gly Val Trp Tyr
 305 310 315 320
 Ser Asp Phe Tyr Gly Ala Glu Thr His Ala Val Leu Pro Tyr Ser Glu
 325 330 335
 Asp Leu Ser Arg Phe Ala Ala Tyr Leu Gln Gln Leu Thr Met Glu Ser
 340 345 350
 Asn Gly Lys Ser Val His Arg Asp Gly Ser Pro Val Ser Thr Gly Thr
 355 360 365
 Gly Glu Ile Tyr Trp Gly Glu Pro Gly Thr Asn Gly Gln His Ala Phe
 370 375 380
 Phe Gln Leu Ile His Gln Gly Thr Arg Leu Val Pro Ala Asp Phe Ile
 385 390 395 400
 Gly Phe Ala Arg Pro Lys Gln Asp Leu Pro Ala Gly Glu Arg Thr Met
 405 410 415
 His Asp Leu Leu Met Ser Asn Phe Phe Ala Gln Thr Lys Val Leu Ala
 420 425 430
 Phe Gly Lys Asn Ala Glu Glu Ile Ala Ala Glu Gly Val Ala Pro Glu
 435 440 445
 Leu Val Asn His Lys Val Met Pro Gly Asn Arg Pro Thr Thr Thr Ile
 450 455 460
 Leu Ala Glu Glu Leu Thr Pro Ser Ile Leu Gly Ala Leu Ile Ala Leu
 465 470 475 480
 Tyr Glu His Ile Val Met Val Gln Gly Val Ile Trp Asp Ile Asn Ser
 485 490 495
 Phe Asp Gln Trp Gly Val Glu Leu Gly Lys Gln Gln Ala Asn Asp Leu
 500 505 510
 Ala Pro Ala Val Ser Gly Glu Glu Asp Val Asp Ser Gly Asp Ser Ser
 515 520 525
 Thr Asp Ser Leu Ile Lys Trp Tyr Arg Ala Asn Arg
 530 535 540

<210> 43

<211> 630

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(630)

<223> RXA01989

<400> 43

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Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser	
1 5 10 15	
gac ttc tta ggc tgg gtt gat tta cca gtt gat tac gac aaa gaa gaa	96
Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu	
20 25 30	
ttt tca aga att gtt gaa gca tca aaa cgc att aaa gaa aat tct gat	144
Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp	
35 40 45	
gtt tta gta gtc atc ggt att ggt ggt tct tac tta ggt gca cgt gca	192
Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala	
50 55 60	
gca atc gaa atg tta acg tca tca ttt aga aac agc aat gaa tac cct	240
Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro	
65 70 75 80	
gaa att gta ttt gtt ggt aat cac tta tca tca aca tat acg aaa gag	288
Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu	
85 90 95	
tta gtt gat tat tta gca gac aaa gat ttc tct gta aac gtt att tct	336
Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser	
100 105 110	
aaa tct ggt aca act aca gaa cca gca gtt gca ttt aga ttg ttc aaa	384
Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys	
115 120 125	
caa tta gtt gaa gaa aga tac ggt aaa gaa gaa gca caa aaa cgt ata	432
Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile	
130 135 140	
ttt gca aca acg gat aaa gaa aaa ggt gct tta aaa cag ttg gct aca	480
Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr	
145 150 155 160	
aac gaa ggt tat gaa acg ttt atc gta cct gat gat gta ggt gga aga	528
Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg	
165 170 175	
tat tct gtt tta aca gca gta gga tta tta cca att gca aca gct gga	576
Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly	
180 185 190	
att aac atc gaa gct atg atg att ggt gct gca aaa gca cgt gaa gaa	624
Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu	
195 200 205	
tta tct	630
Leu Ser	
210	

<210> 44

<211> 210

<212> PRT

<213> Corynebacterium glutamicum

<400> 44

Val Lys Ser Ile His Lys Thr Ile His Glu Gly Thr Gly Ala Gly Ser
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Asp Phe Leu Gly Trp Val Asp Leu Pro Val Asp Tyr Asp Lys Glu Glu
 20 25 30

Phe Ser Arg Ile Val Glu Ala Ser Lys Arg Ile Lys Glu Asn Ser Asp
 35 40 45

Val Leu Val Val Ile Gly Ile Gly Gly Ser Tyr Leu Gly Ala Arg Ala
 50 55 60

Ala Ile Glu Met Leu Thr Ser Ser Phe Arg Asn Ser Asn Glu Tyr Pro
 65 70 75 80

Glu Ile Val Phe Val Gly Asn His Leu Ser Ser Thr Tyr Thr Lys Glu
 85 90 95

Leu Val Asp Tyr Leu Ala Asp Lys Asp Phe Ser Val Asn Val Ile Ser
 100 105 110

Lys Ser Gly Thr Thr Thr Glu Pro Ala Val Ala Phe Arg Leu Phe Lys
 115 120 125

Gln Leu Val Glu Glu Arg Tyr Gly Lys Glu Glu Ala Gln Lys Arg Ile
 130 135 140

Phe Ala Thr Thr Asp Lys Glu Lys Gly Ala Leu Lys Gln Leu Ala Thr
 145 150 155 160

Asn Glu Gly Tyr Glu Thr Phe Ile Val Pro Asp Asp Val Gly Gly Arg
 165 170 175

Tyr Ser Val Leu Thr Ala Val Gly Leu Leu Pro Ile Ala Thr Ala Gly
 180 185 190

Ile Asn Ile Glu Ala Met Met Ile Gly Ala Ala Lys Ala Arg Glu Glu
 195 200 205

Leu Ser
 210

<210> 45

<211> 1269

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1246)

<223> RXA00340

<400> 45

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ctcttacctc atcactgaca tctcttagaa agaccacca gtg aaa tta gtc atc 115
 Val Lys Leu Val Ile
 1 5

gag gcc gac ggc ggc tcc cgc gga aac ccc ggc gtc gcc ggc tcc ggc	163
Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly Val Ala Gly Ser Gly	
10 15 20	
acc gtg gtg tac tcc gac aac aaa gca gaa gtt ctc aaa gaa atc gcc	211
Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val Leu Lys Glu Ile Ala	
25 30 35	
tat gtt gtc gga aca aaa gcc acc aac aac gtc gcc gaa tac cgc gga	259
Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val Ala Glu Tyr Arg Gly	
40 45 50	
cta ctc gaa ggc ctc aaa gca gcc cgc gag ctc ggc gct acc tcc gtg	307
Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu Gly Ala Thr Ser Val	
55 60 65	
gat gtc tac atg gac tcc aaa ctt gtc gtt gaa caa atg tcc ggc cgg	355
Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu Gln Met Ser Gly Arg	
70 75 80 85	
tgg aaa atc aaa cac ccc gac atg aaa gtt cta gcg atc gaa gcc aag	403
Trp Lys Ile Lys His Pro Asp Met Lys Val Leu Ala Ile Glu Ala Lys	
90 95 100	
gag att gct tcc gaa atc ggg tcc gtt tct tat acg tgg att ccg cgt	451
Glu Ile Ala Ser Glu Ile Gly Ser Val Ser Tyr Thr Trp Ile Pro Arg	
105 110 115	
gag aaa aac aaa cga gct gac gca ttg tcc aac gtg gcg atg gat gct	499
Glu Lys Asn Lys Arg Ala Asp Ala Leu Ser Asn Val Ala Met Asp Ala	
120 125 130	
gca gcg gca ggt aag ccg gta ggt gtt gta ggg gat tct gct tct gta	547
Ala Ala Ala Gly Lys Pro Val Gly Val Val Gly Asp Ser Ala Ser Val	
135 140 145	
tct tct gct tct tcg gtt gcg ggc tca gag aaa gaa gac ctc aac tgc	595
Ser Ser Ala Ser Ser Val Ala Gly Ser Glu Lys Glu Asp Leu Asn Cys	
150 155 160 165	
acc gaa acc aaa ccc acc aac tgg aac ggc gca acc aca gat ccc act	643
Thr Glu Thr Lys Pro Thr Asn Trp Asn Gly Ala Thr Thr Asp Pro Thr	
170 175 180	
cgt ttc ttg ttg ctt cgc cac ggc caa act gct atg tca gtg gca cgc	691
Arg Phe Leu Leu Leu Arg His Gly Gln Thr Ala Met Ser Val Ala Arg	
185 190 195	
ctt tac tcc ggt agg tcc aac cca gag ctg tct gaa ctt ggt gaa aaa	739
Leu Tyr Ser Gly Arg Ser Asn Pro Glu Leu Ser Glu Leu Gly Glu Lys	
200 205 210	
caa gca gca gcg gca gca cga cga ctc gct caa acc ggt ggc atc gac	787
Gln Ala Ala Ala Ala Ala Arg Arg Leu Ala Gln Thr Gly Gly Ile Asp	
215 220 225	
gct att gtg agt tct ccg ctc acc cgc acg atg caa acc gca gaa gca	835
Ala Ile Val Ser Ser Pro Leu Thr Arg Thr Met Gln Thr Ala Glu Ala	
230 235 240 245	

gca gcg gcc gca ctg gga atg aaa gta cgt gtt atc gat gat ctc atc 883
 Ala Ala Ala Ala Leu Gly Met Lys Val Arg Val Ile Asp Asp Leu Ile
 250 255 260

gaa act gac ttt gga ctg tgg gat gga aaa tca ttt tca gaa gcc cac 931
 Glu Thr Asp Phe Gly Leu Trp Asp Gly Lys Ser Phe Ser Glu Ala His
 265 270 275

gaa caa gat cca gaa ctg cac acc aag tgg ctc act gac tca tct gta 979
 Glu Gln Asp Pro Glu Leu His Thr Lys Trp Leu Thr Asp Ser Ser Val
 280 285 290

gcc cca ccc ggt ggt gag tcc ctg cag acg gtt aat cga cgt gtg aaa 1027
 Ala Pro Pro Gly Gly Glu Ser Leu Gln Thr Val Asn Arg Arg Val Lys
 295 300 305

aag gct cgt gaa agc ctc caa cgc gaa tac ggt gca gcg aat gtt ttg 1075
 Lys Ala Arg Glu Ser Leu Gln Arg Glu Tyr Gly Ala Ala Asn Val Leu
 310 315 320 325

gtg gtc agc cac gtc acc cca atc aaa gcc atc atg agg caa gca ttg 1123
 Val Val Ser His Val Thr Pro Ile Lys Ala Ile Met Arg Gln Ala Leu
 330 335 340

gac gca ggc cca tcc ttc ttt cag aag gca cac ctt gac ttg gcg tcg 1171
 Asp Ala Gly Pro Ser Phe Phe Gln Lys Ala His Leu Asp Leu Ala Ser
 345 350 355

ctg tcg atc gca gag ttt tac gaa gac ggc cca acc tgc gta aga ctg 1219
 Leu Ser Ile Ala Glu Phe Tyr Glu Asp Gly Pro Thr Cys Val Arg Leu
 360 365 370

ttc aac gac acc tca cac ctg gaa gcg tgacgacagt ctgacggaag 1266
 Phe Asn Asp Thr Ser His Leu Glu Ala
 375 380

ctc 1269

<210> 46

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 46

Val Lys Leu Val Ile Glu Ala Asp Gly Gly Ser Arg Gly Asn Pro Gly
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Val Ala Gly Ser Gly Thr Val Val Tyr Ser Asp Asn Lys Ala Glu Val
 20 25 30

Leu Lys Glu Ile Ala Tyr Val Val Gly Thr Lys Ala Thr Asn Asn Val
 35 40 45

Ala Glu Tyr Arg Gly Leu Leu Glu Gly Leu Lys Ala Ala Arg Glu Leu
 50 55 60

Gly Ala Thr Ser Val Asp Val Tyr Met Asp Ser Lys Leu Val Val Glu
 65 70 75 80

Gln Met Ser Gly Arg Trp Lys Ile Lys His Pro Asp Met Lys Val Leu

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<210> 47
<211> 840
<212> DNA
<213> Corynebacterium glutamicum
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<220>

<221> CDS

<222> (101)..(817)

<223> RXA02492

<400> 47

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aaacgcgcgt cgtggaacat aaagtggcaa actagtagctt atg act aac gga aaa 115
                                         Met Thr Asn Gly Lys
                                         1 5

ttg att ctt ctt cgt cac ggt cag agc gaa tgg aac gca tcc aac cag 163
Leu Ile Leu Leu Arg His Gly Gln Ser Glu Trp Asn Ala Ser Asn Gln
                        10 15 20

ttc act gga tgg gtc gac gtc aat ctg acc gaa cag ggt gag gct gag 211
Phe Thr Gly Trp Val Asp Val Asn Leu Thr Glu Gln Gly Glu Ala Glu
                        25 30 35

gcc aaa ggc gtc ctc cca ggc gtt gta tac acc tcc ttg ctg cgt cgc 259
Ala Lys Gly Val Leu Pro Gly Val Val Tyr Thr Ser Leu Leu Arg Arg
                        40 45 50

gcg atc cgc act gca aac atc gca ctg aac gct gca gac cgc cac tgg 307
Ala Ile Arg Thr Ala Asn Ile Ala Leu Asn Ala Ala Asp Arg His Trp
                        55 60 65

atc cca gtg atc cgc gac tgg cgc ctc aac gag cgt cac tac ggc gca 355
Ile Pro Val Ile Arg Asp Trp Arg Leu Asn Glu Arg His Tyr Gly Ala
                        70 75 80 85

ctg cag ggc ctt gac aag gct gca acc aag gaa aaa tac ggc gac gac 403
Leu Gln Gly Leu Asp Lys Ala Ala Thr Lys Glu Lys Tyr Gly Asp Asp
                        90 95 100

cag ttc atg gaa tgg cgc cgc tcc tac gac acc cca cca cca gag ctc 451
Gln Phe Met Glu Trp Arg Arg Ser Tyr Asp Thr Pro Pro Pro Glu Leu
                        105 110 115

gcg gat gac gca gag tac tcc cag gca aat gac cct cgt tac gcg gac 499
Ala Asp Asp Ala Glu Tyr Ser Gln Ala Asn Asp Pro Arg Tyr Ala Asp
                        120 125 130

ctc gac gta gtt cca cgc acc gaa tgc ctc aag gac gtt gtg gtt cgt 547
Leu Asp Val Val Pro Arg Thr Glu Cys Leu Lys Asp Val Val Val Arg
                        135 140 145

ttt gtt cct tac ttc gag gaa gaa atc ctg cca cgc gca aag aag ggc 595
Phe Val Pro Tyr Phe Glu Glu Glu Ile Leu Pro Arg Ala Lys Lys Gly
                        150 155 160 165

gaa acc gtc ctc atc gca gca cac ggc aac tcc ctg cgt gcg ctg gtt 643
Glu Thr Val Leu Ile Ala Ala His Gly Asn Ser Leu Arg Ala Leu Val
                        170 175 180

aag cac ctt gac ggc atc tcc gat gct gat atc gca gag ctc aac atc 691
Lys His Leu Asp Gly Ile Ser Asp Ala Asp Ile Ala Glu Leu Asn Ile
                        185 190 195

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ctc 840

Glu Asp Gly Ser Val Val Asn Pro Gly Gly Thr Tyr Leu Asp Pro Glu

210 215 220

Ala Ala Ala Ala Gly Ala Ala Ala Val Ala Asn Gln Gly Asn Lys
 225 230 235

<210> 49
 <211> 729
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(706)
 <223> RXA00381

<400> 49
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 Met Thr Gln Thr Ile
 1 5

gtc cat cta gtt cgc cac ggc gaa gtc cac aac cca gag aaa atc ctg 163
 Val His Leu Val Arg His Gly Glu Val His Asn Pro Glu Lys Ile Leu
 10 15 20

tac gga cgc atg ccc gga tac agg ttg tct tcc cgt gga cgc agc caa 211
 Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser Arg Gly Arg Ser Gln
 25 30 35

gcc gcc cgc act gca gct tct ttt gaa ggc cac gat gtc acc tac att 259
 Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His Asp Val Thr Tyr Ile
 40 45 50

gcg gcc tcc cca ttg cag cgt gtg cag gaa acc tcc gaa ccg ttc atc 307
 Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr Ser Glu Pro Phe Ile
 55 60 65

aag gtc aca ggc cta gaa ctg atc acc gac gag gat ctt ctg gaa gca 355
 Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu Asp Leu Leu Glu Ala
 70 75 80 85

ggc aac cgt ttc gaa ggc ctg cgc acc aaa ggt tgg cgt tcc cag ttg 403
 Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly Trp Arg Ser Gln Leu
 90 95 100

tgg aac ccc gtg cgt tgg cct ttg atg tac aac ccc acg ctt ccc agc 451
 Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn Pro Thr Leu Pro Ser
 105 110 115

tgg ggc gaa cac tac acc gac att ttg gaa aga atg atg gcg gct gtg 499
 Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg Met Met Ala Ala Val
 120 125 130

gaa cga gct cgg gtg gca gcg gaa gga cac gaa gca atc ctg gtg acc 547
 Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu Ala Ile Leu Val Thr
 135 140 145

cac cag ttg ccg atc gtg tgc gtg caa cgc cac gcc cgc gga caa agc 595
 His Gln Leu Pro Ile Val Cys Val Gln Arg His Ala Arg Gly Gln Ser

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150          155          160          165
ctg tcc cat aac cca gcg acc agg caa tgc gac ctc gcc tca gtg aca 643
Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp Leu Ala Ser Val Thr
          170          175          180

tcc ttg gtg ttc caa gac gat caa att gtc ggc gtg cat tac aac gaa 691
Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly Val His Tyr Asn Glu
          185          190          195

cca gct cag gag att tgatcactcg tgcgtttgac caa 729
Pro Ala Gln Glu Ile
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<210> 50
<211> 202
<212> PRT
<213> Corynebacterium glutamicum

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<400> 50
Met Thr Gln Thr Ile Val His Leu Val Arg His Gly Glu Val His Asn
  1          5          10          15

Pro Glu Lys Ile Leu Tyr Gly Arg Met Pro Gly Tyr Arg Leu Ser Ser
          20          25          30

Arg Gly Arg Ser Gln Ala Ala Arg Thr Ala Ala Ser Phe Glu Gly His
          35          40          45

Asp Val Thr Tyr Ile Ala Ala Ser Pro Leu Gln Arg Val Gln Glu Thr
          50          55          60

Ser Glu Pro Phe Ile Lys Val Thr Gly Leu Glu Leu Ile Thr Asp Glu
          65          70          75          80

Asp Leu Leu Glu Ala Gly Asn Arg Phe Glu Gly Leu Arg Thr Lys Gly
          85          90          95

Trp Arg Ser Gln Leu Trp Asn Pro Val Arg Trp Pro Leu Met Tyr Asn
          100          105          110

Pro Thr Leu Pro Ser Trp Gly Glu His Tyr Thr Asp Ile Leu Glu Arg
          115          120          125

Met Met Ala Ala Val Glu Arg Ala Arg Val Ala Ala Glu Gly His Glu
          130          135          140

Ala Ile Leu Val Thr His Gln Leu Pro Ile Val Cys Val Gln Arg His
          145          150          155          160

Ala Arg Gly Gln Ser Leu Ser His Asn Pro Ala Thr Arg Gln Cys Asp
          165          170          175

Leu Ala Ser Val Thr Ser Leu Val Phe Gln Asp Asp Gln Ile Val Gly
          180          185          190

Val His Tyr Asn Glu Pro Ala Gln Glu Ile
          195          200

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<222> (101)..(799)  
<223> RXA02122
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ccttttttta agtgggcggt caggaatttt tcgcacaggt atg ctg cat gtc atg															115
Met Leu His Val Met															5
1															
aag ccg ggt tca cac gca gct gcc gaa aag act caa tcc act gtg gtt	163														
Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr Gln Ser Thr Val Val															
10 15 20															
tta ctc att cgg cat ggg caa acc cca aca act ggt cag gtt ctg cct	211														
Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr Gly Gln Val Leu Pro															
25 30 35															
ggt cag acg ccg ggt tta cac ctg tct gat aag ggt gaa gag cag gcg	259														
Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys Gly Glu Glu Gln Ala															
40 45 50															
cgg gag gtg gca cag cgt ctg gcg gag gtg ccg att acc gct gtg tat	307														
Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro Ile Thr Ala Val Tyr															
55 60 65															
tca tcg ccg atg gag cgt gcg cag gaa aca gca gca ccg acg gtc agc	355														
Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala Ala Pro Thr Val Ser															
70 75 80 85															
gct cat ggc ctc gag ttg acg gtg gaa cct ggg ctt att gaa tgc gat	403														
Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly Leu Ile Glu Cys Asp															
90 95 100															
ttc ggc gag tgg acg ggc cgg aaa cta act gag ctc aat gcc cta gag	451														
Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu Leu Asn Ala Leu Glu															
105 110 115															
gag tgg aaa gcg gtg cag aag aca ccg tct acc ttc agg ttt cca ggt	499														
Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr Phe Arg Phe Pro Gly															
120 125 130															
ggt gag agt ttc gtg gaa atg cag gat cgg atg gtg gag gct atc ggc	547														
Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met Val Glu Ala Ile Gly															
135 140 145															
aac att gcg cag cag cat ccg gga gaa atc gtt gct gcg ttt agt cat	595														
Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val Ala Ala Phe Ser His															
150 155 160 165															
gcc gac acg atc aag gct gcg gtg gct cat ttt gta ggc act cca ctg	643														
Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe Val Gly Thr Pro Leu															
170 175 180															

gat tct ttt cag cgc att ttc atc gac acg gcg tca att tcc gca gtg 691
 Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala Ser Ile Ser Ala Val
 185 190 195

gaa ttt acc ggg aaa tct tca ggc gtc tcc tcc cat atg ctg ctg aca 739
 Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser His Met Leu Leu Thr
 200 205 210

aat tcc aga aca gga tcg ttg gga tac ctt cga gac aaa ctt ccg aaa 787
 Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg Asp Lys Leu Pro Lys
 215 220 225

gct ccg caa cca tgatcacctc accatttgag cgc 822
 Ala Pro Gln Pro
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<210> 52

<211> 233

<212> PRT

<213> Corynebacterium glutamicum

<400> 52

Met Leu His Val Met Lys Pro Gly Ser His Ala Ala Ala Glu Lys Thr
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Gln Ser Thr Val Val Leu Leu Ile Arg His Gly Gln Thr Pro Thr Thr
 20 25 30

Gly Gln Val Leu Pro Gly Gln Thr Pro Gly Leu His Leu Ser Asp Lys
 35 40 45

Gly Glu Glu Gln Ala Arg Glu Val Ala Gln Arg Leu Ala Glu Val Pro
 50 55 60

Ile Thr Ala Val Tyr Ser Ser Pro Met Glu Arg Ala Gln Glu Thr Ala
 65 70 75 80

Ala Pro Thr Val Ser Ala His Gly Leu Glu Leu Thr Val Glu Pro Gly
 85 90 95

Leu Ile Glu Cys Asp Phe Gly Glu Trp Thr Gly Arg Lys Leu Thr Glu
 100 105 110

Leu Asn Ala Leu Glu Glu Trp Lys Ala Val Gln Lys Thr Pro Ser Thr
 115 120 125

Phe Arg Phe Pro Gly Gly Glu Ser Phe Val Glu Met Gln Asp Arg Met
 130 135 140

Val Glu Ala Ile Gly Asn Ile Ala Gln Gln His Pro Gly Glu Ile Val
 145 150 155 160

Ala Ala Phe Ser His Ala Asp Thr Ile Lys Ala Ala Val Ala His Phe
 165 170 175

Val Gly Thr Pro Leu Asp Ser Phe Gln Arg Ile Phe Ile Asp Thr Ala
 180 185 190

Ser Ile Ser Ala Val Glu Phe Thr Gly Lys Ser Ser Gly Val Ser Ser
 195 200 205

His Met Leu Leu Thr Asn Ser Arg Thr Gly Ser Leu Gly Tyr Leu Arg
 210 215 220

Asp Lys Leu Pro Lys Ala Pro Gln Pro
 225 230

<210> 53

<211> 1161

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1138)

<223> RXA00206

<400> 53

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tgggtgattg ttccggcgcg ggtgttgtga tgggtttaat atg gaa gac atg cga 115
 Met Glu Asp Met Arg
 1 5

att gct act ctc acg tca ggc ggc gac tgc ccc gga cta aac gcc gtc 163
 Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro Gly Leu Asn Ala Val
 10 15 20

atc cga gga atc gtc cgc aca gcc agc aat gaa ttt ggc tcc acc gtc 211
 Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu Phe Gly Ser Thr Val
 25 30 35

gtt ggt tat caa gac ggt tgg gaa gga ctg tta ggc gat cgt cgc gta 259
 Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu Gly Asp Arg Arg Val
 40 45 50

cag ctg tat gac gat gaa gat att gac cga atc ctc ctt cga ggc ggc 307
 Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile Leu Leu Arg Gly Gly
 55 60 65

acc att ttg ggc act ggt cgc ctc cat ccg gac aag ttt aag gcc gga 355
 Thr Ile Leu Gly Thr Arg Leu His Pro Asp Lys Phe Lys Ala Gly
 70 75 80 85

att gat cag att aag gcc aac tta gaa gac gcc ggc atc gat gcc ctt 403
 Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala Gly Ile Asp Ala Leu
 90 95 100

atc cca atc ggt ggc gaa gga acc ctg aag ggt gcc aag tgg ctg tct 451
 Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly Ala Lys Trp Leu Ser
 105 110 115

gat aac ggt atc cct gtt gtc ggt gtc cca aag acc att gac aat gac 499
 Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys Thr Ile Asp Asn Asp
 120 125 130

gtg aat ggc act gac ttc acc ttc ggt ttc gat act gct gtg gca gtg 547
 Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp Thr Ala Val Ala Val
 135 140 145

gct acc gac gct gtt gac cgc ctg cac acc acc gct gaa tct cac aac 595
 Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr Ala Glu Ser His Asn
 150 155 160 165

cgt gtg atg atc gtg gag gtc atg ggc cgc cac gtg ggt tgg att gct 643
 Arg Val Met Ile Val Glu Val Met Gly Arg His Val Gly Trp Ile Ala
 170 175 180

ctg cac gca ggt atg gcc ggc ggt gct cac tac acc gtt att cca gaa 691
 Leu His Ala Gly Met Ala Gly Gly Ala His Tyr Thr Val Ile Pro Glu
 185 190 195

gta cct ttc gat att gca gag atc tgc aag gcg atg gaa cgt cgc ttc 739
 Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala Met Glu Arg Arg Phe
 200 205 210

cag atg ggc gag aag tac ggc att atc gtc gtt gcg gaa ggt gcg ttg 787
 Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val Ala Glu Gly Ala Leu
 215 220 225

cca cgc gaa ggc acc atg gag ctt cgt gaa ggc cac att gac cag ttc 835
 Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly His Ile Asp Gln Phe
 230 235 240 245

ggt cac aag acc ttc acg gga att gga cag cag atc gct gat gag atc 883
 Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln Ile Ala Asp Glu Ile
 250 255 260

cac gtg cgc ctc ggc cac gat gtt cgt acg acc gtt ctt ggc cac att 931
 His Val Arg Leu Gly His Asp Val Arg Thr Thr Val Leu Gly His Ile
 265 270 275

caa cgt ggt gga acc cca act gct ttc gac cgt gtt ctg gcc act cgt 979
 Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg Val Leu Ala Thr Arg
 280 285 290

tat ggt gtt cgt gca gct cgt gcg tgc cat gag gga agc ttt gac aag 1027
 Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu Gly Ser Phe Asp Lys
 295 300 305

gtt gtt gct ttg aag ggt gag agc att gag atg atc acc ttt gaa gaa 1075
 Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met Ile Thr Phe Glu Glu
 310 315 320 325

gca gtc gga acc ttg aag gaa gtt cca ttc gaa cgc tgg gtt act gcc 1123
 Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu Arg Trp Val Thr Ala
 330 335 340

cag gca atg ttt gga tagtttttcg ggctttttatc aac 1161
 Gln Ala Met Phe Gly
 345

<210> 54

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 54

Met Glu Asp Met Arg Ile Ala Thr Leu Thr Ser Gly Gly Asp Cys Pro
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Gly Leu Asn Ala Val Ile Arg Gly Ile Val Arg Thr Ala Ser Asn Glu
 20 25 30
 Phe Gly Ser Thr Val Val Gly Tyr Gln Asp Gly Trp Glu Gly Leu Leu
 35 40 45
 Gly Asp Arg Arg Val Gln Leu Tyr Asp Asp Glu Asp Ile Asp Arg Ile
 50 55 60
 Leu Leu Arg Gly Gly Thr Ile Leu Gly Thr Gly Arg Leu His Pro Asp
 65 70 75 80
 Lys Phe Lys Ala Gly Ile Asp Gln Ile Lys Ala Asn Leu Glu Asp Ala
 85 90 95
 Gly Ile Asp Ala Leu Ile Pro Ile Gly Gly Glu Gly Thr Leu Lys Gly
 100 105 110
 Ala Lys Trp Leu Ser Asp Asn Gly Ile Pro Val Val Gly Val Pro Lys
 115 120 125
 Thr Ile Asp Asn Asp Val Asn Gly Thr Asp Phe Thr Phe Gly Phe Asp
 130 135 140
 Thr Ala Val Ala Val Ala Thr Asp Ala Val Asp Arg Leu His Thr Thr
 145 150 155 160
 Ala Glu Ser His Asn Arg Val Met Ile Val Glu Val Met Gly Arg His
 165 170 175
 Val Gly Trp Ile Ala Leu His Ala Gly Met Ala Gly Gly Ala His Tyr
 180 185 190
 Thr Val Ile Pro Glu Val Pro Phe Asp Ile Ala Glu Ile Cys Lys Ala
 195 200 205
 Met Glu Arg Arg Phe Gln Met Gly Glu Lys Tyr Gly Ile Ile Val Val
 210 215 220
 Ala Glu Gly Ala Leu Pro Arg Glu Gly Thr Met Glu Leu Arg Glu Gly
 225 230 235 240
 His Ile Asp Gln Phe Gly His Lys Thr Phe Thr Gly Ile Gly Gln Gln
 245 250 255
 Ile Ala Asp Glu Ile His Val Arg Leu Gly His Asp Val Arg Thr Thr
 260 265 270
 Val Leu Gly His Ile Gln Arg Gly Gly Thr Pro Thr Ala Phe Asp Arg
 275 280 285
 Val Leu Ala Thr Arg Tyr Gly Val Arg Ala Ala Arg Ala Cys His Glu
 290 295 300
 Gly Ser Phe Asp Lys Val Val Ala Leu Lys Gly Glu Ser Ile Glu Met
 305 310 315 320
 Ile Thr Phe Glu Glu Ala Val Gly Thr Leu Lys Glu Val Pro Phe Glu
 325 330 335

Arg Trp Val Thr Ala Gln Ala Met Phe Gly
340 345

<210> 55
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXA01243

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agcagttgcg agaacgcgat gtagaagttg tgattgcaga atg att ctt aca gtc 115
Met Ile Leu Thr Val
1 5
act gca agt ccg tat ctg ttg agc acc aat gag ctt gac ggc acc atc 163
Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu Leu Asp Gly Thr Ile
10 15 20
gaa att ggc gaa gca aac aaa atc cgg cag gtt tcc act gtt gcc ggt 211
Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val Ser Thr Val Ala Gly
25 30 35
ggt ttt ggc acc ggt gtg gct gcc acc ttg ttt tat ggc ggc aat gaa 259
Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe Tyr Gly Gly Asn Glu
40 45 50
act ttt gca gtt ttt ccc gct cca gaa atc tct cat tac atg cgc ctg 307
Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser His Tyr Met Arg Leu
55 60 65
gtg acg ttt gct ggg ttg cct cat gaa att att ccg gtg gca ggt ccc 355
Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile Pro Val Ala Gly Pro
70 75 80 85
atc ccc atg cat ttg acc atg cgt gat gca gag ggc aat gag act aag 403
Ile Pro Met His Leu Thr Met Arg Asp Ala Glu Gly Asn Glu Thr Lys
90 95 100
ttc aaa gac tcc ccc atg cct ttg gat gtg tcc cag ttg gca att ctt 451
Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser Gln Leu Ala Ile Leu
105 110 115
cgt gat cta gtg gtg cgt cga gcc gaa gat gcc gcg tgg gtg ttg ttg 499
Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala Ala Trp Val Leu Leu
120 125 130
ggt ggc aat ttg ccg tct atc gcg cct gct gcg tgg ttt gtg gat gtg 547
Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala Trp Phe Val Asp Val
135 140 145
gtg aga tca ctt cgc ttg tac cac cct cat gtg aag gta gct atc gca 595
Val Arg Ser Leu Arg Leu Tyr His Pro His Val Lys Val Ala Ile Ala
150 155 160 165

gca act ggt gct gcg ttg cgt gcg gtt att cga cag ctt gca gct acg 643
 Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg Gln Leu Ala Ala Thr
 170 175 180

tcc ccg gat gcg ctg att gtg gct gcg gaa gaa atc gaa att gcc act 691
 Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu Ile Glu Ile Ala Thr
 185 190 195

gga tta gaa ccc aaa acc ttg aga ggt cca tgg gta gag gga gat ctc 739
 Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp Val Glu Gly Asp Leu
 200 205 210

tcc ccg act gtg gcg gca gcg cgc gct tta att gat agc ggt gtc acc 787
 Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile Asp Ser Gly Val Thr
 215 220 225

gag gtg ttg gtt acc aac aag cgg acg gaa tct ttg tat gtt tcc gag 835
 Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser Leu Tyr Val Ser Glu
 230 235 240 245

tct gaa tca ctg tta gcc agc tac gac agc acc cct ggt aag cag ggc 883
 Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr Pro Gly Lys Gln Gly
 250 255 260

gtg aat tgg cgg gaa tct ttt act gca gga ttc ttg gca gca tcc aat 931
 Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe Leu Ala Ala Ser Asn
 265 270 275

gat gga aaa tcc act gag gac agc gtg atc aac gcg gtt gct tac gcc 979
 Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn Ala Val Ala Tyr Ala
 280 285 290

aac gct gaa ggc agt gag tgg gac aac tac att ccc aca ccc gat aag 1027
 Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile Pro Thr Pro Asp Lys
 295 300 305

ctt cgg gcg gag cac gtg gtc atc aaa tcg ctt tagaccacgc aaaaagcctc 1080
 Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
 310 315 320

aaa 1083

<210> 56

<211> 320

<212> PRT

<213> Corynebacterium glutamicum

<400> 56

Met Ile Leu Thr Val Thr Ala Ser Pro Tyr Leu Leu Ser Thr Asn Glu
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Leu Asp Gly Thr Ile Glu Ile Gly Glu Ala Asn Lys Ile Arg Gln Val
 20 25 30

Ser Thr Val Ala Gly Gly Phe Gly Thr Gly Val Ala Ala Thr Leu Phe
 35 40 45

Tyr Gly Gly Asn Glu Thr Phe Ala Val Phe Pro Ala Pro Glu Ile Ser
 50 55 60

His Tyr Met Arg Leu Val Thr Phe Ala Gly Leu Pro His Glu Ile Ile
 65 70 75 80
 Pro Val Ala Gly Pro Ile Pro Met His Leu Thr Met Arg Asp Ala Glu
 85 90 95
 Gly Asn Glu Thr Lys Phe Lys Asp Ser Pro Met Pro Leu Asp Val Ser
 100 105 110
 Gln Leu Ala Ile Leu Arg Asp Leu Val Val Arg Arg Ala Glu Asp Ala
 115 120 125
 Ala Trp Val Leu Leu Gly Gly Asn Leu Pro Ser Ile Ala Pro Ala Ala
 130 135 140
 Trp Phe Val Asp Val Val Arg Ser Leu Arg Leu Tyr His Pro His Val
 145 150 155 160
 Lys Val Ala Ile Ala Ala Thr Gly Ala Ala Leu Arg Ala Val Ile Arg
 165 170 175
 Gln Leu Ala Ala Thr Ser Pro Asp Ala Leu Ile Val Ala Ala Glu Glu
 180 185 190
 Ile Glu Ile Ala Thr Gly Leu Glu Pro Lys Thr Leu Arg Gly Pro Trp
 195 200 205
 Val Glu Gly Asp Leu Ser Pro Thr Val Ala Ala Ala Arg Ala Leu Ile
 210 215 220
 Asp Ser Gly Val Thr Glu Val Leu Val Thr Asn Lys Arg Thr Glu Ser
 225 230 235 240
 Leu Tyr Val Ser Glu Ser Glu Ser Leu Leu Ala Ser Tyr Asp Ser Thr
 245 250 255
 Pro Gly Lys Gln Gly Val Asn Trp Arg Glu Ser Phe Thr Ala Gly Phe
 260 265 270
 Leu Ala Ala Ser Asn Asp Gly Lys Ser Thr Glu Asp Ser Val Ile Asn
 275 280 285
 Ala Val Ala Tyr Ala Asn Ala Glu Gly Ser Glu Trp Asp Asn Tyr Ile
 290 295 300
 Pro Thr Pro Asp Lys Leu Arg Ala Glu His Val Val Ile Lys Ser Leu
 305 310 315 320

<210> 57

<211> 1113

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1090)

<223> RXA01882

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Met Ile Ile Thr Phe															5
1															
acc cca aac ccg agt att gat tcc acg ctg tcg ctc ggc gaa gag ctc	163														
Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser Leu Gly Glu Glu Leu	20														
10 15															
tcc cgt gga tcc gtc caa cga ctt gat tcc gtc acc gct gtc gca ggt	211														
Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val Thr Ala Val Ala Gly	35														
25 30															
ggt aaa ggc atc aat gtc gcc cac gct gtc ttg ctt gcg ggc ttt gaa	259														
Gly Lys Gly Ile Asn Val Ala His Ala Val Leu Leu Ala Gly Phe Glu	50														
40 45															
acc ttg gct gtg ttc cca gcc ggc aag ctc gac ccc ttc gtc cca ctg	307														
Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp Pro Phe Val Pro Leu	60														
55 65															
gtc cgc gac atc ggc ttg ccc gtg gaa act gtt gtg atc aac aag aac	355														
Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val Val Ile Asn Lys Asn	85														
70 75															
gtc cgc acc aac acc aca gtc acc gaa ccg gac ggc acc acc acc aag	403														
Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp Gly Thr Thr Thr Lys	95														
90 100															
ctc aac ggc ccc ggc gcg ccg ctc agc gag cag aag ctc cgt agc ttg	451														
Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln Lys Leu Arg Ser Leu	105														
110 115															
gaa aag gtg ctt atc gac gcg ctc cgc ccc gaa gtc acc tgg gtt gtc	499														
Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu Val Thr Trp Val Val	120														
125 130															
ctg gcg ggc tcg ctg cca cca ggg gca cca gtt gac tgg tac gcg cgt	547														
Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val Asp Trp Tyr Ala Arg	135														
140 145															
ctc acc gcg ttg atc cat tca gca cgc cct gac gtt cgc gtg gct gtc	595														
Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp Val Arg Val Ala Val	150														
155 160															
gat acc tca gac aag cca ctg atg gcg ttg ggc gag agc ttg gat aca	643														
Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly Glu Ser Leu Asp Thr	170														
175 180															
cct ggc gct gct ccg aac ctg att aag cca aat ggt ctg gaa ctg ggc	691														
Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn Gly Leu Glu Leu Gly	185														
190 195															
cag ctg gct aac act gat ggt gaa gag ctg gag gcg cgt gct gcg caa	739														
Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu Ala Arg Ala Ala Gln	200														
205 210															
ggc gat tac gac gcc atc atc gca gct gcg gac gta ctg gtt aac cgt	787														

Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp Val Leu Val Asn Arg
 215 220 225
 ggc atc gaa cag gtg ctt gtc acc ttg ggt gcc gca gga gcg gtg ttg 835
 Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala Ala Gly Ala Val Leu
 230 235 240 245
 gtc aac gca gaa ggt gcg tgg act gct act tct cca aag att gat gtt 883
 Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser Pro Lys Ile Asp Val
 250 255 260
 gta tcc acc gtt gga gct gga gac tgt gct ctt gca ggt ttt gtt atg 931
 Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu Ala Gly Phe Val Met
 265 270 275
 gca cgt tcc cag aag aaa aca ctg gag gaa tct ctg ctg aat gcc gtg 979
 Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser Leu Leu Asn Ala Val
 280 285 290
 tct tac ggc tcg act gcg gcg tct ctt cct ggc act acc att cct cgt 1027
 Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly Thr Thr Ile Pro Arg
 295 300 305
 cct gac caa ctc gcc aca gct ggt gca acg gtc acc caa gtc aaa gga 1075
 Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val Thr Gln Val Lys Gly
 310 315 320 325
 ttg aaa gaa tca gca tgaatagcgt aaataattcc tcg 1113
 Leu Lys Glu Ser Ala
 330

<210> 58

<211> 330

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 58

Met Ile Ile Thr Phe Thr Pro Asn Pro Ser Ile Asp Ser Thr Leu Ser
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Leu Gly Glu Glu Leu Ser Arg Gly Ser Val Gln Arg Leu Asp Ser Val
 20 25 30

Thr Ala Val Ala Gly Gly Lys Gly Ile Asn Val Ala His Ala Val Leu
 35 40 45

Leu Ala Gly Phe Glu Thr Leu Ala Val Phe Pro Ala Gly Lys Leu Asp
 50 55 60

Pro Phe Val Pro Leu Val Arg Asp Ile Gly Leu Pro Val Glu Thr Val
 65 70 75 80

Val Ile Asn Lys Asn Val Arg Thr Asn Thr Thr Val Thr Glu Pro Asp
 85 90 95

Gly Thr Thr Thr Lys Leu Asn Gly Pro Gly Ala Pro Leu Ser Glu Gln
 100 105 110

Lys Leu Arg Ser Leu Glu Lys Val Leu Ile Asp Ala Leu Arg Pro Glu
 115 120 125

Val Thr Trp Val Val Leu Ala Gly Ser Leu Pro Pro Gly Ala Pro Val
130 135 140

Asp Trp Tyr Ala Arg Leu Thr Ala Leu Ile His Ser Ala Arg Pro Asp
145 150 155 160

Val Arg Val Ala Val Asp Thr Ser Asp Lys Pro Leu Met Ala Leu Gly
165 170 175

Glu Ser Leu Asp Thr Pro Gly Ala Ala Pro Asn Leu Ile Lys Pro Asn
180 185 190

Gly Leu Glu Leu Gly Gln Leu Ala Asn Thr Asp Gly Glu Glu Leu Glu
195 200 205

Ala Arg Ala Ala Gln Gly Asp Tyr Asp Ala Ile Ile Ala Ala Ala Asp
210 215 220

Val Leu Val Asn Arg Gly Ile Glu Gln Val Leu Val Thr Leu Gly Ala
225 230 235 240

Ala Gly Ala Val Leu Val Asn Ala Glu Gly Ala Trp Thr Ala Thr Ser
245 250 255

Pro Lys Ile Asp Val Val Ser Thr Val Gly Ala Gly Asp Cys Ala Leu
260 265 270

Ala Gly Phe Val Met Ala Arg Ser Gln Lys Lys Thr Leu Glu Glu Ser
275 280 285

Leu Leu Asn Ala Val Ser Tyr Gly Ser Thr Ala Ala Ser Leu Pro Gly
290 295 300

Thr Thr Ile Pro Arg Pro Asp Gln Leu Ala Thr Ala Gly Ala Thr Val
305 310 315 320

Thr Gln Val Lys Gly Leu Lys Glu Ser Ala
325 330

<210> 59

<211> 1155

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1132)

<223> RXA01702

<400> 59

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acatagttca gtgacagtca ccttttggag gagacacctt atg cct atc gca act 115
Met Pro Ile Ala Thr
1 5

ccc gag gtc tat aac gag atg ctc gat cgt gct aag gaa ggc gga ttc 163
Pro Glu Val Tyr Asn Glu Met Leu Asp Arg Ala Lys Glu Gly Gly Phe
10 15 20

gcc ttc cca gcc atc aac tgc acc tcc tcg gaa acc atc aac gca gct	211
Ala Phe Pro Ala Ile Asn Cys Thr Ser Ser Glu Thr Ile Asn Ala Ala	
25 30 35	
ctc aag ggc ttc gca gag gct gaa tct gac gga atc atc cag ttc tcc	259
Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly Ile Ile Gln Phe Ser	
40 45 50	
acc ggt ggt gca gag ttc ggt tcc ggc ctg gca gta aag aac aag gtc	307
Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala Val Lys Asn Lys Val	
55 60 65	
aag ggc gca gtt gcg ctt gca gcc ttc gcc cac gag gca gca aag agc	355
Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His Glu Ala Ala Lys Ser	
70 75 80 85	
tac ggc atc aac gtt gct ctg cac act gac cac tgc cag aag gaa gtc	403
Tyr Gly Ile Asn Val Ala Leu His Thr Asp His Cys Gln Lys Glu Val	
90 95 100	
ctg gac gag tac gtc cgc cca ctg ctg gct atc tcc cag gag cgc gtc	451
Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile Ser Gln Glu Arg Val	
105 110 115	
gac cgc ggc gag ctt cca ctg ttc cag tcc cac atg tgg gat ggt tcc	499
Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His Met Trp Asp Gly Ser	
120 125 130	
gct gtc cca atc gac gag aac ctc gaa atc gca cag gag ctg ctg gct	547
Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala Gln Glu Leu Leu Ala	
135 140 145	
aag gcc aag gca gcg aac atc atc ttg gaa gtt gag atc ggt gtt gtc	595
Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val Glu Ile Gly Val Val	
150 155 160 165	
ggt ggc gaa gaa gac ggc gtt gag gct aag gct ggc gca aac ctc tac	643
Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala Gly Ala Asn Leu Tyr	
170 175 180	
acc tcc cca gaa gac ttt gag aag acc atc gat gca atc ggc acc ggt	691
Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp Ala Ile Gly Thr Gly	
185 190 195	
gag aag ggc cgc tac ctg cta gca gct acc ttc ggt aac gtc cac ggc	739
Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe Gly Asn Val His Gly	
200 205 210	
ggt tac aag cca ggc aac gtc aag ctg cgc cca gag gtc ctc ctt gag	787
Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro Glu Val Leu Leu Glu	
215 220 225	
ggc cag cag gtt gca cgc aag aag ctt gga ctt gca gac gac gca ctt	835
Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu Ala Asp Asp Ala Leu	
230 235 240 245	
cca ttc gac ttc gtc ttc cac ggt ggc tca ggc tcc gag aag gaa aag	883
Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly Ser Glu Lys Glu Lys	
250 255 260	

atc gaa gag gcg ctg acc tac ggc gtc atc aag atg aac gtt gat act 931
 Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys Met Asn Val Asp Thr
 265 270 275
 gac acc cag tac gca ttc acc cgc cca atc gtc tcc cac atg ttt gag 979
 Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val Ser His Met Phe Glu
 280 285 290
 aac tac aac ggc gtt ctc aag atc gac ggc gag gtc gga aac aag aag 1027
 Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu Val Gly Asn Lys Lys
 295 300 305
 gct tac gac cca cgc tct tac atg aag aag gct gag cag agc atg tct 1075
 Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala Glu Gln Ser Met Ser
 310 315 320 325
 gag cgc att atc gag tct tgc cag gac ctc aag tct gtt gga aag acc 1123
 Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys Ser Val Gly Lys Thr
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 acc tct aag taatctcagc agttaaaaag ggc 1155
 Thr Ser Lys

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<211> 344

<212> PRT

<213> Corynebacterium glutamicum

<400> 60

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 20 25 30
 Thr Ile Asn Ala Ala Leu Lys Gly Phe Ala Glu Ala Glu Ser Asp Gly
 35 40 45
 Ile Ile Gln Phe Ser Thr Gly Gly Ala Glu Phe Gly Ser Gly Leu Ala
 50 55 60
 Val Lys Asn Lys Val Lys Gly Ala Val Ala Leu Ala Ala Phe Ala His
 65 70 75 80
 Glu Ala Ala Lys Ser Tyr Gly Ile Asn Val Ala Leu His Thr Asp His
 85 90 95
 Cys Gln Lys Glu Val Leu Asp Glu Tyr Val Arg Pro Leu Leu Ala Ile
 100 105 110
 Ser Gln Glu Arg Val Asp Arg Gly Glu Leu Pro Leu Phe Gln Ser His
 115 120 125
 Met Trp Asp Gly Ser Ala Val Pro Ile Asp Glu Asn Leu Glu Ile Ala
 130 135 140
 Gln Glu Leu Leu Ala Lys Ala Lys Ala Ala Asn Ile Ile Leu Glu Val
 145 150 155 160

Glu Ile Gly Val Val Gly Gly Glu Glu Asp Gly Val Glu Ala Lys Ala
 165 170 175
 Gly Ala Asn Leu Tyr Thr Ser Pro Glu Asp Phe Glu Lys Thr Ile Asp
 180 185 190
 Ala Ile Gly Thr Gly Glu Lys Gly Arg Tyr Leu Leu Ala Ala Thr Phe
 195 200 205
 Gly Asn Val His Gly Val Tyr Lys Pro Gly Asn Val Lys Leu Arg Pro
 210 215 220
 Glu Val Leu Leu Glu Gly Gln Gln Val Ala Arg Lys Lys Leu Gly Leu
 225 230 235 240
 Ala Asp Asp Ala Leu Pro Phe Asp Phe Val Phe His Gly Gly Ser Gly
 245 250 255
 Ser Glu Lys Glu Lys Ile Glu Glu Ala Leu Thr Tyr Gly Val Ile Lys
 260 265 270
 Met Asn Val Asp Thr Asp Thr Gln Tyr Ala Phe Thr Arg Pro Ile Val
 275 280 285
 Ser His Met Phe Glu Asn Tyr Asn Gly Val Leu Lys Ile Asp Gly Glu
 290 295 300
 Val Gly Asn Lys Lys Ala Tyr Asp Pro Arg Ser Tyr Met Lys Lys Ala
 305 310 315 320
 Glu Gln Ser Met Ser Glu Arg Ile Ile Glu Ser Cys Gln Asp Leu Lys
 325 330 335
 Ser Val Gly Lys Thr Thr Ser Lys
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<210> 61
 <211> 900
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(877)
 <223> RXA02258

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 Met Ala Arg Lys Pro
 1 5
 ctt atc gct ggt aac tgg aag atg aac ctg gat cac cag cag gca atc 163
 Leu Ile Ala Gly Asn Trp Lys Met Asn Leu Asp His Gln Gln Ala Ile
 10 15 20
 ggc act gtt cag aag ctt gca ttc gcc ctt cca aag gaa tac ttc gag 211
 Gly Thr Val Gln Lys Leu Ala Phe Ala Leu Pro Lys Glu Tyr Phe Glu
 25 30 35

aag gtt gac gtt gca gtc acc gtt cct ttc act gac atc cgc tcc gtc	259
Lys Val Asp Val Ala Val Thr Val Pro Phe Thr Asp Ile Arg Ser Val	
40 45 50	
cag act ctc gtt gag ggc gac aag ctt gag gtc act ttc ggt gct cag	307
Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val Thr Phe Gly Ala Gln	
55 60 65	
gac gtc tcc cag cac gag tcc ggt gcg tac acc ggt gaa gtt tct gca	355
Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr Gly Glu Val Ser Ala	
70 75 80 85	
agc atg ctg gca aag ttg aac tgc tct tgg gtt gtc gtt gga cac tcc	403
Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val Val Val Gly His Ser	
90 95 100	
gag cgc cgc gag tac cac aac gag tct gat gag ttg gtt gct gcg aag	451
Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu Leu Val Ala Ala Lys	
105 110 115	
gca aag gca gct ctg tcc aac ggc atc agc ccg atc gtc tgc gtt ggt	499
Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro Ile Val Cys Val Gly	
120 125 130	
gag cca ctg gaa atc cgt gaa gct ggc acc cac gtt gag tac gtc gtc	547
Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His Val Glu Tyr Val Val	
135 140 145	
gag cag acc cgt aag tcc ctt gct ggc ctg gat gct gct gag ctg gcc	595
Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp Ala Ala Glu Leu Ala	
150 155 160 165	
aac acc gtt atc gcg tat gag cca gtg tgg gct atc ggc acc ggt aag	643
Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala Ile Gly Thr Gly Lys	
170 175 180	
gtt gct tcc gca gct gac gct cag gaa gtg tgc aag gct atc cgc ggt	691
Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys Lys Ala Ile Arg Gly	
185 190 195	
ctg atc gtg gag ctt gca ggc gac gag gtc gct gag ggc ctg cgt att	739
Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala Glu Gly Leu Arg Ile	
200 205 210	
ctt tac ggt ggt tct gtt aag gca gaa acc gtc gct gag atc gtc ggt	787
Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val Ala Glu Ile Val Gly	
215 220 225	
cag cct gac gtc gac ggc gga ctt gtc ggt ggc gct tcc ctc gac ggt	835
Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly Ala Ser Leu Asp Gly	
230 235 240 245	
gaa gca ttc gcc aag ctg gct gcc aac gct gcg agc gtt gct	877
Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala Ser Val Ala	
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taaagtacag agctttaag cac	900

<211> 259

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 62

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 20 25 30

Lys Glu Tyr Phe Glu Lys Val Asp Val Ala Val Thr Val Pro Phe Thr
 35 40 45

Asp Ile Arg Ser Val Gln Thr Leu Val Glu Gly Asp Lys Leu Glu Val
 50 55 60

Thr Phe Gly Ala Gln Asp Val Ser Gln His Glu Ser Gly Ala Tyr Thr
 65 70 75 80

Gly Glu Val Ser Ala Ser Met Leu Ala Lys Leu Asn Cys Ser Trp Val
 85 90 95

Val Val Gly His Ser Glu Arg Arg Glu Tyr His Asn Glu Ser Asp Glu
 100 105 110

Leu Val Ala Ala Lys Ala Lys Ala Ala Leu Ser Asn Gly Ile Ser Pro
 115 120 125

Ile Val Cys Val Gly Glu Pro Leu Glu Ile Arg Glu Ala Gly Thr His
 130 135 140

Val Glu Tyr Val Val Glu Gln Thr Arg Lys Ser Leu Ala Gly Leu Asp
 145 150 155 160

Ala Ala Glu Leu Ala Asn Thr Val Ile Ala Tyr Glu Pro Val Trp Ala
 165 170 175

Ile Gly Thr Gly Lys Val Ala Ser Ala Ala Asp Ala Gln Glu Val Cys
 180 185 190

Lys Ala Ile Arg Gly Leu Ile Val Glu Leu Ala Gly Asp Glu Val Ala
 195 200 205

Glu Gly Leu Arg Ile Leu Tyr Gly Gly Ser Val Lys Ala Glu Thr Val
 210 215 220

Ala Glu Ile Val Gly Gln Pro Asp Val Asp Gly Gly Leu Val Gly Gly
 225 230 235 240

Ala Ser Leu Asp Gly Glu Ala Phe Ala Lys Leu Ala Ala Asn Ala Ala
 245 250 255

Ser Val Ala

<210> 63

<211> 1563

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1540)

<223> RXN01225

<400> 63

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cccgggttaa cccacgcct aagtcagtga aggacttttt atg acg cac aac cac 115
                                         Met Thr His Asn His
                                         1                               5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
                                         10                               15                               20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
                                         25                               30                               35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
                                         40                               45                               50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
                                         55                               60                               65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tgc atc 355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
                                         70                               75                               80                               85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                                         90                               95                               100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
                                         105                               110                               115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc 499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
                                         120                               125                               130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac 547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
                                         135                               140                               145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac 595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
                                         150                               155                               160                               165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga 643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                                         170                               175                               180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc 691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
                                         185                               190                               195

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aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile 200 205 210	739
gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr 215 220 225	787
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys 230 235 240 245	835
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys 250 255 260	883
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln 265 270 275	931
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu 280 285 290	979
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr 295 300 305	1027
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys 310 315 320 325	1075
ggt tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu 330 335 340	1123
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly 345 350 355	1171
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met 360 365 370	1219
gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val 375 380 385	1267
aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln 390 395 400 405	1315
atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly 410 415 420	1363
acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly 425 430 435	1411
cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc	1459

Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser
 440 445 450

aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc 1507
 Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480

cac 1563

<210> 64
 <211> 480
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 64
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 20 25 30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220

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Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
225                230                235                240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
                245                250                255

Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
                260                265                270

Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
                275                280                285

Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
                290                295                300

Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
305                310                315                320

Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
                325                330                335

Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
                340                345                350

Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
                355                360                365

Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
                370                375                380

Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
385                390                395                400

Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
                405                410                415

Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
                420                425                430

Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
                435                440                445

Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
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Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
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<210> 65

<211> 1563

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1540)

<223> FRXA01225

<400> 65

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                                         Met Thr His Asn His
                                         1 5

aag gac tgg aac gat cgc att gca gtt gcg gag gaa atg gtg ccg ttg 163
Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu Glu Met Val Pro Leu
                        10 15 20

atc ggg cgc ctg cac cgc aac aac aac gtg gtg gtt tcc gta ttc ggt 211
Ile Gly Arg Leu His Arg Asn Asn Asn Val Val Val Ser Val Phe Gly
                        25 30 35

cgt ctc ctt gtg aat gtc tca gac atc gat atc atc aag tct cac cgc 259
Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile Ile Lys Ser His Arg
                        40 45 50

tac gcc cgc cac atc ata tcc aag gaa ctt cca ctg gaa agc tcc ttg 307
Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro Leu Glu Ser Ser Leu
                        55 60 65

gat att ttg cgc gaa ctg gta gat atg aac ctt ggt acc gca tgc atc 355
Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu Gly Thr Ala Ser Ile
                        70 75 80 85

gac ctg gga cag ctg gcc tac agc ttc gaa gaa tcc gaa agc acc gac 403
Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu Ser Glu Ser Thr Asp
                        90 95 100

ctg cgt gcc ttc ctg gag gac gct ctc gcg ccg gtc att ggt gcg gaa 451
Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro Val Ile Gly Ala Glu
                        105 110 115

acc gac atc aac cca act gat atc gtg ctg tac ggt ttc ggc cgc atc 499
Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr Gly Phe Gly Arg Ile
                        120 125 130

ggt cgc ctg ctg gcc cgc atc ctg gtt tcc cgc gag gca ctg tat gac 547
Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg Glu Ala Leu Tyr Asp
                        135 140 145

ggt gct cgt ctg cgc gcc atc gtg gtc cgc aaa aat ggt gaa gaa gac 595
Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys Asn Gly Glu Glu Asp
                        150 155 160 165

ctg gtc aag cgc gca tcc ttg ctg cgt cgt gat tct gtc cac ggt gga 643
Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp Ser Val His Gly Gly
                        170 175 180

ttc gat ggc acc atc acc acc gat tat gac aac aac atc atc tgg gcc 691
Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn Asn Ile Ile Trp Ala
                        185 190 195

aac ggc acc cca atc aag gtc atc tac tcc aat gac cca gcc acc att 739
Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn Asp Pro Ala Thr Ile
                        200 205 210

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gat tac acc gaa tac ggc atc aat gac gcc gtc gtg gta gac aac acc Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val Val Val Asp Asn Thr 215 220 225	787
ggc cgc tgg cgt gac cgc gaa ggc ctg tcc cag cac ctc aag tcc aag Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln His Leu Lys Ser Lys 230 235 240 245	835
ggc gtt gcc aag gtt gta ctc acc gcg ccg ggc aag ggc gat ctg aag Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly Lys Gly Asp Leu Lys 250 255 260	883
aac atc gtg tac ggc atc aac cac acc gac atc acc gca gat gat cag Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile Thr Ala Asp Asp Gln 265 270 275	931
atc gtt tcc gca gca tca tgc acc acc aat gcc att acc cca gtg ctc Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala Ile Thr Pro Val Leu 280 285 290	979
aag gtg atc aat gat cgc tac ggc gtg gaa ttc ggc cac gta gaa acc Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe Gly His Val Glu Thr 295 300 305	1027
gtt cac tcc ttc acc aat gac cag aac ctg atc gac aac ttc cac aag Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile Asp Asn Phe His Lys 310 315 320 325	1075
ggc tct cgc cgt ggt cgc gca gca ggt ctg aat atg gtt ctc acc gaa Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn Met Val Leu Thr Glu 330 335 340	1123
acc ggc gct gca aag gct gta tcc aag gcg ctt cca gag ctg gaa ggc Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu Pro Glu Leu Glu Gly 345 350 355	1171
aag ctc acc ggc aat gcc atc cgc gtt cct acc cct gac gtg tcc atg Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr Pro Asp Val Ser Met 360 365 370	1219
gct gtg ctc aac ttg acc ctg aac acg gag gtg gac cgc gat gag gtc Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val Asp Arg Asp Glu Val 375 380 385	1267
aac gag ttc ctc cgc cgt gtg tcc ctg cac tct gac ttg cgc cag caa Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser Asp Leu Arg Gln Gln 390 395 400 405	1315
atc gac tgg atc cgt tcc cca gag gtt gtt tcc act gac ttc gtg ggc Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser Thr Asp Phe Val Gly 410 415 420	1363
acc acc cac gcg ggc atc gtt gat ggt cta gcc acc atc gca acc ggt Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala Thr Ile Ala Thr Gly 425 430 435	1411
cgc cac ctg gtg ctt tac gtg tgg tac gac aac gag ttc ggc tac tcc Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn Glu Phe Gly Tyr Ser 440 445 450	1459
aac cag gtc att cgc atc gtc gag gag atc gcc ggc gtg cgt cct cgc	1507

Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala Gly Val Arg Pro Arg
 455 460 465

gtg tac ccg gag cgc agg cag cca gcc gta cta taggttatcc aagcctaata 1560
 Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 470 475 480

cac 1563

<210> 66

<211> 480

<212> PRT

<213> Corynebacterium glutamicum

<400> 66

Met Thr His Asn His Lys Asp Trp Asn Asp Arg Ile Ala Val Ala Glu
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Glu Met Val Pro Leu Ile Gly Arg Leu His Arg Asn Asn Asn Val Val
 20 25 30

Val Ser Val Phe Gly Arg Leu Leu Val Asn Val Ser Asp Ile Asp Ile
 35 40 45

Ile Lys Ser His Arg Tyr Ala Arg His Ile Ile Ser Lys Glu Leu Pro
 50 55 60

Leu Glu Ser Ser Leu Asp Ile Leu Arg Glu Leu Val Asp Met Asn Leu
 65 70 75 80

Gly Thr Ala Ser Ile Asp Leu Gly Gln Leu Ala Tyr Ser Phe Glu Glu
 85 90 95

Ser Glu Ser Thr Asp Leu Arg Ala Phe Leu Glu Asp Ala Leu Ala Pro
 100 105 110

Val Ile Gly Ala Glu Thr Asp Ile Asn Pro Thr Asp Ile Val Leu Tyr
 115 120 125

Gly Phe Gly Arg Ile Gly Arg Leu Leu Ala Arg Ile Leu Val Ser Arg
 130 135 140

Glu Ala Leu Tyr Asp Gly Ala Arg Leu Arg Ala Ile Val Val Arg Lys
 145 150 155 160

Asn Gly Glu Glu Asp Leu Val Lys Arg Ala Ser Leu Leu Arg Arg Asp
 165 170 175

Ser Val His Gly Gly Phe Asp Gly Thr Ile Thr Thr Asp Tyr Asp Asn
 180 185 190

Asn Ile Ile Trp Ala Asn Gly Thr Pro Ile Lys Val Ile Tyr Ser Asn
 195 200 205

Asp Pro Ala Thr Ile Asp Tyr Thr Glu Tyr Gly Ile Asn Asp Ala Val
 210 215 220

Val Val Asp Asn Thr Gly Arg Trp Arg Asp Arg Glu Gly Leu Ser Gln
 225 230 235 240

His Leu Lys Ser Lys Gly Val Ala Lys Val Val Leu Thr Ala Pro Gly
 245 250 255
 Lys Gly Asp Leu Lys Asn Ile Val Tyr Gly Ile Asn His Thr Asp Ile
 260 265 270
 Thr Ala Asp Asp Gln Ile Val Ser Ala Ala Ser Cys Thr Thr Asn Ala
 275 280 285
 Ile Thr Pro Val Leu Lys Val Ile Asn Asp Arg Tyr Gly Val Glu Phe
 290 295 300
 Gly His Val Glu Thr Val His Ser Phe Thr Asn Asp Gln Asn Leu Ile
 305 310 315 320
 Asp Asn Phe His Lys Gly Ser Arg Arg Gly Arg Ala Ala Gly Leu Asn
 325 330 335
 Met Val Leu Thr Glu Thr Gly Ala Ala Lys Ala Val Ser Lys Ala Leu
 340 345 350
 Pro Glu Leu Glu Gly Lys Leu Thr Gly Asn Ala Ile Arg Val Pro Thr
 355 360 365
 Pro Asp Val Ser Met Ala Val Leu Asn Leu Thr Leu Asn Thr Glu Val
 370 375 380
 Asp Arg Asp Glu Val Asn Glu Phe Leu Arg Arg Val Ser Leu His Ser
 385 390 395 400
 Asp Leu Arg Gln Gln Ile Asp Trp Ile Arg Ser Pro Glu Val Val Ser
 405 410 415
 Thr Asp Phe Val Gly Thr Thr His Ala Gly Ile Val Asp Gly Leu Ala
 420 425 430
 Thr Ile Ala Thr Gly Arg His Leu Val Leu Tyr Val Trp Tyr Asp Asn
 435 440 445
 Glu Phe Gly Tyr Ser Asn Gln Val Ile Arg Ile Val Glu Glu Ile Ala
 450 455 460
 Gly Val Arg Pro Arg Val Tyr Pro Glu Arg Arg Gln Pro Ala Val Leu
 465 470 475 480

<210> 67

<211> 1125

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1102)

<223> RXA02256

<400> 67

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gacacattgc atttctctaca atcttttagag gagacacaac	atg acc att cgt gtt	115
	Met Thr Ile Arg Val	
	1 5	
ggt att aac gga ttt ggc cgt atc gga cgt aac ttc ttc cgc gca gtt	163	
Gly Ile Asn Gly Phe Gly Arg Ile Gly Arg Asn Phe Phe Arg Ala Val		
	10 15 20	
ctg gag cgc agc gac gat ctc gag gta gtt gca gtc aac gac ctc acc	211	
Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala Val Asn Asp Leu Thr		
	25 30 35	
gac aac aag acc ctt tcc acc ctt ctc aag ttc gac tcc atc atg ggc	259	
Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe Asp Ser Ile Met Gly		
	40 45 50	
cgc ctt ggc cag gaa gtt gaa tac gac gat gac tcc atc acc gtt ggt	307	
Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp Ser Ile Thr Val Gly		
	55 60 65	
ggc aag cgc atc gct gtt tac gca gag cgc gat cca aag aac ctg gac	355	
Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp Pro Lys Asn Leu Asp		
	70 75 80 85	
tgg gct gca cac aac gtt gac atc gtg atc gag tcc acc ggc ttc ttc	403	
Trp Ala Ala His Asn Val Asp Ile Val Ile Glu Ser Thr Gly Phe Phe		
	90 95 100	
acc gat gca aac gcg gct aag gct cac atc gaa gca ggt gcc aag aag	451	
Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu Ala Gly Ala Lys Lys		
	105 110 115	
gtc atc atc tcc gca cca gca agc aac gaa gac gca acc ttc gtt tac	499	
Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp Ala Thr Phe Val Tyr		
	120 125 130	
ggt gtg aac cac gag tcc tac gat cct gag aac cac aac gtg atc tcc	547	
Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn His Asn Val Ile Ser		
	135 140 145	
ggc gca tct tgc acc acc aac tgc ctc gca cca atg gca aag gtc cta	595	
Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro Met Ala Lys Val Leu		
	150 155 160 165	
aac gac aag ttc ggc atc gag aac ggc ctc atg acc acc gtt cac gca	643	
Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met Thr Thr Val His Ala		
	170 175 180	
tac act ggc gac cag cgc ctg cac gat gca cct cac cgc gac ctg cgt	691	
Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro His Arg Asp Leu Arg		
	185 190 195	
cgt gca cgt gca gca gca gtc aac atc gtt cct acc tcc acc ggt gca	739	
Arg Ala Arg Ala Ala Ala Val Asn Ile Val Pro Thr Ser Thr Gly Ala		
	200 205 210	
gct aag gct gtt gct ctg gtt ctc cca gag ctc aag ggc aag ctt gac	787	
Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu Lys Gly Lys Leu Asp		
	215 220 225	

ggc tac gca ctt cgc gtt cca gtt atc acc ggt tcc gca acc gac ctg 835
 Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly Ser Ala Thr Asp Leu
 230 235 240 245

 acc ttc aac acc aag tct gag gtc acc gtt gag tcc atc aac gct gca 883
 Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu Ser Ile Asn Ala Ala
 250 255 260

 atc aag gaa gct gca gtc ggc gag ttc ggc gag acc ctg gct tac tcc 931
 Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu Thr Leu Ala Tyr Ser
 265 270 275

 gaa gag cca ctg gtt tcc acc gac atc gtc cac gat tcc cac ggc tcc 979
 Glu Glu Pro Leu Val Ser Thr Asp Ile Val His Asp Ser His Gly Ser
 280 285 290

 atc ttc gac gct ggc ctg acc aag gtc tcc ggc aac acc gtc aag gtt 1027
 Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly Asn Thr Val Lys Val
 295 300 305

 gtt tcc tgg tac gac aac gag tgg ggc tac acc tgc cag ctc ctg cgt 1075
 Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr Cys Gln Leu Leu Arg
 310 315 320 325

 ctg acc gag ctc gta gct tcc aag ctc taattagttc acatcgctaa 1122
 Leu Thr Glu Leu Val Ala Ser Lys Leu
 330

 cgt 1125

<210> 68

<211> 334

<212> PRT

<213> Corynebacterium glutamicum

<400> 68

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 Phe Phe Arg Ala Val Leu Glu Arg Ser Asp Asp Leu Glu Val Val Ala
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 Val Asn Asp Leu Thr Asp Asn Lys Thr Leu Ser Thr Leu Leu Lys Phe
 35 40 45

 Asp Ser Ile Met Gly Arg Leu Gly Gln Glu Val Glu Tyr Asp Asp Asp
 50 55 60

 Ser Ile Thr Val Gly Gly Lys Arg Ile Ala Val Tyr Ala Glu Arg Asp
 65 70 75 80

 Pro Lys Asn Leu Asp Trp Ala Ala His Asn Val Asp Ile Val Ile Glu
 85 90 95

 Ser Thr Gly Phe Phe Thr Asp Ala Asn Ala Ala Lys Ala His Ile Glu
 100 105 110

 Ala Gly Ala Lys Lys Val Ile Ile Ser Ala Pro Ala Ser Asn Glu Asp
 115 120 125

Ala Thr Phe Val Tyr Gly Val Asn His Glu Ser Tyr Asp Pro Glu Asn
 130 135 140

His Asn Val Ile Ser Gly Ala Ser Cys Thr Thr Asn Cys Leu Ala Pro
 145 150 155 160

Met Ala Lys Val Leu Asn Asp Lys Phe Gly Ile Glu Asn Gly Leu Met
 165 170 175

Thr Thr Val His Ala Tyr Thr Gly Asp Gln Arg Leu His Asp Ala Pro
 180 185 190

His Arg Asp Leu Arg Arg Ala Arg Ala Ala Val Asn Ile Val Pro
 195 200 205

Thr Ser Thr Gly Ala Ala Lys Ala Val Ala Leu Val Leu Pro Glu Leu
 210 215 220

Lys Gly Lys Leu Asp Gly Tyr Ala Leu Arg Val Pro Val Ile Thr Gly
 225 230 235 240

Ser Ala Thr Asp Leu Thr Phe Asn Thr Lys Ser Glu Val Thr Val Glu
 245 250 255

Ser Ile Asn Ala Ala Ile Lys Glu Ala Ala Val Gly Glu Phe Gly Glu
 260 265 270

Thr Leu Ala Tyr Ser Glu Glu Pro Leu Val Ser Thr Asp Ile Val His
 275 280 285

Asp Ser His Gly Ser Ile Phe Asp Ala Gly Leu Thr Lys Val Ser Gly
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Asn Thr Val Lys Val Val Ser Trp Tyr Asp Asn Glu Trp Gly Tyr Thr
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Cys Gln Leu Leu Arg Leu Thr Glu Leu Val Ala Ser Lys Leu
 325 330

<210> 69
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1315)
 <223> RXA02257

<400> 69
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 Met Ala Val Lys Thr
 1 5

ctc aag gac ttg ctc gac gaa ggc gta gac gga cgc cac gtc atc gtt 163
 Leu Lys Asp Leu Leu Asp Glu Gly Val Asp Gly Arg His Val Ile Val
 10 15 20

cga tct gac ttc aat gtt ccc ctc aac gat gac cgc gag atc acc gat	211
Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp Arg Glu Ile Thr Asp	
25 30 35	
aag ggc cga atc att gcc tcc cta cca acc ctt aaa gca ctg agc gaa	259
Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu Lys Ala Leu Ser Glu	
40 45 50	
ggt ggc gca aag gtc atc gtc atg gct cac ctt ggc cgc cca aag ggc	307
Gly Gly Ala Lys Val Ile Val Met Ala His Leu Gly Arg Pro Lys Gly	
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gag gtc aac gag aag tac tcc ctc gca cct gtc gct gag gca ctc tcc	355
Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val Ala Glu Ala Leu Ser	
70 75 80 85	
gat gag ctt ggc cag tac gtt gca ctt gcc gca gac gtt gtt ggc gaa	403
Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala Asp Val Val Gly Glu	
90 95 100	
gac gca cac gag cgc gca aac ggc ctg acc gag ggc gac atc ctg ctc	451
Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu Gly Asp Ile Leu Leu	
105 110 115	
ctg gag aac gtg cgc ttc gac cca cgc gaa acc tcc aag gac gag gca	499
Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr Ser Lys Asp Glu Ala	
120 125 130	
gag cgc acc gct ttc gct cag gag ctc gca gct ctt gca gca gac aac	547
Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala Leu Ala Ala Asp Asn	
135 140 145	
ggc gca ttc gtt tct gac ggc ttc ggt gtt gtc cac cgc gca cag acc	595
Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val His Arg Ala Gln Thr	
150 155 160 165	
tcc gtc tac gac att gca aag ttg ctg cca cac tac gct ggc gga ctg	643
Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His Tyr Ala Gly Gly Leu	
170 175 180	
gta gag acc gag att tcc gtt ctg gaa aag atc gca gaa tca cca gag	691
Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile Ala Glu Ser Pro Glu	
185 190 195	
gca cca tac gta gtg gtt ctc ggt gga tcc aag gtc tct gac aag atc	739
Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys Val Ser Asp Lys Ile	
200 205 210	
ggt gtt att gag gcg ctg gct gcc aag gct gac aag atc atc gtc ggt	787
Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp Lys Ile Ile Val Gly	
215 220 225	
ggc ggc atg tgc tac acc ttc ctc gca gct cag gga cac aac gtt cag	835
Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln Gly His Asn Val Gln	
230 235 240 245	
cag tcc ctc ctg cag gaa gaa atg aag gct acc tgc acc gac ctg ctc	883
Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr Cys Thr Asp Leu Leu	
250 255 260	
gca cgc ttc ggt gac aag atc gtt ctc cca gtt gac ctg gtt gca gca	931

Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val Asp Leu Val Ala Ala
 265 270 275

tcc gaa ttt aac aag gac gca gag aag cag atc gtt gac ctg gac tcc 979
 Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile Val Asp Leu Asp Ser
 280 285 290

atc cca gaa ggc tgg atg tct ctt gac atc gga cca gag tcc gtc aag 1027
 Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly Pro Glu Ser Val Lys
 295 300 305

aac ttc ggt gag gtt ctc agc acc gct aag acc atc ttc tgg aac ggc 1075
 Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr Ile Phe Trp Asn Gly
 310 315 320 325

cca atg ggc gtg ttc gag ttc gca gca ttc tct gaa ggc acc cgc ggc 1123
 Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser Glu Gly Thr Arg Gly
 330 335 340

atc gcc cag gcc atc atc gat gca act gca ggc aac gac gca ttc tcc 1171
 Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly Asn Asp Ala Phe Ser
 345 350 355

gtt gtt ggc ggt ggc gac tcc gca gca tcc gtt cgc gtg ctc ggc ctg 1219
 Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val Arg Val Leu Gly Leu
 360 365 370

aac gaa gac ggc ttc tcc cac atc tcc acc ggt ggt ggc gca tcc ctc 1267
 Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly Gly Gly Ala Ser Leu
 375 380 385

gag tac ctt gaa ggc aag gaa ctc cca ggc gtt gca att ctc gct cag 1315
 Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val Ala Ile Leu Ala Gln
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taaatccgac acggcccttt gtt 1338

<210> 70

<211> 405

<212> PRT

<213> Corynebacterium glutamicum

<400> 70

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Arg His Val Ile Val Arg Ser Asp Phe Asn Val Pro Leu Asn Asp Asp
 20 25 30

Arg Glu Ile Thr Asp Lys Gly Arg Ile Ile Ala Ser Leu Pro Thr Leu
 35 40 45

Lys Ala Leu Ser Glu Gly Gly Ala Lys Val Ile Val Met Ala His Leu
 50 55 60

Gly Arg Pro Lys Gly Glu Val Asn Glu Lys Tyr Ser Leu Ala Pro Val
 65 70 75 80

Ala Glu Ala Leu Ser Asp Glu Leu Gly Gln Tyr Val Ala Leu Ala Ala
 85 90 95

Asp Val Val Gly Glu Asp Ala His Glu Arg Ala Asn Gly Leu Thr Glu
 100 105 110
 Gly Asp Ile Leu Leu Leu Glu Asn Val Arg Phe Asp Pro Arg Glu Thr
 115 120 125
 Ser Lys Asp Glu Ala Glu Arg Thr Ala Phe Ala Gln Glu Leu Ala Ala
 130 135 140
 Leu Ala Ala Asp Asn Gly Ala Phe Val Ser Asp Gly Phe Gly Val Val
 145 150 155 160
 His Arg Ala Gln Thr Ser Val Tyr Asp Ile Ala Lys Leu Leu Pro His
 165 170 175
 Tyr Ala Gly Gly Leu Val Glu Thr Glu Ile Ser Val Leu Glu Lys Ile
 180 185 190
 Ala Glu Ser Pro Glu Ala Pro Tyr Val Val Val Leu Gly Gly Ser Lys
 195 200 205
 Val Ser Asp Lys Ile Gly Val Ile Glu Ala Leu Ala Ala Lys Ala Asp
 210 215 220
 Lys Ile Ile Val Gly Gly Gly Met Cys Tyr Thr Phe Leu Ala Ala Gln
 225 230 235 240
 Gly His Asn Val Gln Gln Ser Leu Leu Gln Glu Glu Met Lys Ala Thr
 245 250 255
 Cys Thr Asp Leu Leu Ala Arg Phe Gly Asp Lys Ile Val Leu Pro Val
 260 265 270
 Asp Leu Val Ala Ala Ser Glu Phe Asn Lys Asp Ala Glu Lys Gln Ile
 275 280 285
 Val Asp Leu Asp Ser Ile Pro Glu Gly Trp Met Ser Leu Asp Ile Gly
 290 295 300
 Pro Glu Ser Val Lys Asn Phe Gly Glu Val Leu Ser Thr Ala Lys Thr
 305 310 315 320
 Ile Phe Trp Asn Gly Pro Met Gly Val Phe Glu Phe Ala Ala Phe Ser
 325 330 335
 Glu Gly Thr Arg Gly Ile Ala Gln Ala Ile Ile Asp Ala Thr Ala Gly
 340 345 350
 Asn Asp Ala Phe Ser Val Val Gly Gly Gly Asp Ser Ala Ala Ser Val
 355 360 365
 Arg Val Leu Gly Leu Asn Glu Asp Gly Phe Ser His Ile Ser Thr Gly
 370 375 380
 Gly Gly Ala Ser Leu Glu Tyr Leu Glu Gly Lys Glu Leu Pro Gly Val
 385 390 395 400
 Ala Ile Leu Ala Gln
 405

<400> 71																	
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												Val	Ala	Glu	Ile	Met	5
												1					
cac	gta	ttc	gct	cgc	gaa	att	ctc	gac	tcc	cgc	ggg	aac	cca	acc	gtc	163	
His	Val	Phe	Ala	Arg	Glu	Ile	Leu	Asp	Ser	Arg	Gly	Asn	Pro	Thr	Val		
				10					15					20			
gag	gca	gag	gtt	ttc	ctg	gat	gac	ggg	tcc	cac	ggg	gtc	gca	ggg	gtt	211	
Glu	Ala	Glu	Val	Phe	Leu	Asp	Asp	Gly	Ser	His	Gly	Val	Ala	Gly	Val		
				25					30					35			
cca	tcc	ggc	gca	tcc	acc	ggc	gtc	cac	gag	gct	cat	gag	ctg	cgt	gac	259	
Pro	Ser	Gly	Ala	Ser	Thr	Gly	Val	His	Glu	Ala	His	Glu	Leu	Arg	Asp		
				40					45					50			
ggg	ggc	gat	cgc	tac	ctg	ggc	aag	ggc	gtt	ttg	aag	gca	gtt	gaa	aac	307	
Gly	Gly	Asp	Arg	Tyr	Leu	Gly	Lys	Gly	Val	Leu	Lys	Ala	Val	Glu	Asn		
				55					60					65			
gtc	aac	gaa	gaa	atc	ggc	gac	gag	ctc	gct	ggc	cta	gag	gct	gac	gat	355	
Val	Asn	Glu	Glu	Ile	Gly	Asp	Glu	Leu	Ala	Gly	Leu	Glu	Ala	Asp	Asp		
70					75					80					85		
cag	cgc	ctc	atc	gac	gaa	gca	atg	atc	aag	ctt	gat	ggc	acc	gcc	aac	403	
Gln	Arg	Leu	Ile	Asp	Glu	Ala	Met	Ile	Lys	Leu	Asp	Gly	Thr	Ala	Asn		
				90					95					100			
aag	tcc	cgc	ctg	ggg	gca	aac	gca	atc	ctt	ggg	gtt	tcc	atg	gct	gtt	451	
Lys	Ser	Arg	Leu	Gly	Ala	Asn	Ala	Ile	Leu	Gly	Val	Ser	Met	Ala	Val		
				105					110					115			
gca	aag	gct	gct	gct	gat	tcc	gca	ggc	ctc	cca	ctg	ttc	cgc	tac	atc	499	
Ala	Lys	Ala	Ala	Ala	Asp	Ser	Ala	Gly	Leu	Pro	Leu	Phe	Arg	Tyr	Ile		
				120					125					130			
ggg	gga	cca	aac	gca	cac	gtt	ctt	cca	gtt	cca	atg	atg	aac	atc	atc	547	
Gly	Gly	Pro	Asn	Ala	His	Val	Leu	Pro	Val	Pro	Met	Met	Asn	Ile	Ile		
				135					140					145			
acc	ggg	ggc	gct	cac	gct	gac	tcc	ggg	gtt	gac	gtt	cag	gaa	ttc	atg	595	
Thr	Gly	Gly	Ala	His	Ala	Asp	Ser	Gly	Val	Asp	Val	Gln	Glu	Phe	Met		
150					155					160					165		
atc	gct	cca	atc	ggg	gca	gag	acc	ttc	tct	gag	gct	ctc	cgc	aac	ggc	643	
Ile	Ala	Pro	Ile	Gly	Ala	Glu	Thr	Phe	Ser	Glu	Ala	Leu	Arg	Asn	Gly		
				170					175					180			

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tcc acc gga ctt ggc gat gag ggc ggc ttc gct cct tcc gtc ggc tcc Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala Pro Ser Val Gly Ser 200 205 210	739
acc cgt gag gct ctt gac ctt atc gtt gag gca atc gag aag gct ggc Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala Ile Glu Lys Ala Gly 215 220 225	787
ttc acc cca ggc aag gac atc gct ctt gct ctg gac gtt gct tcc tct Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu Asp Val Ala Ser Ser 230 235 240 245	835
gag ttc ttc aag gac ggc acc tac cac ttc gaa ggt ggc cag cac tcc Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu Gly Gly Gln His Ser 250 255 260	883
gca gct gag atg gca aac gtt tac gct gag ctg gtt gac gcg tac cca Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu Val Asp Ala Tyr Pro 265 270 275	931
atc gtc tcc atc gag gac cca ctg cag gaa gat gac tgg gag ggt tac Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp Asp Trp Glu Gly Tyr 280 285 290	979
acc aac ctg acc gca acc atc ggc gac aag gtt cag atc gtt ggc gac Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val Gln Ile Val Gly Asp 295 300 305	1027
gac ttc ttc gtc acc aac cct gag cgc ctg aag gag ggc atc gct aag Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys Glu Gly Ile Ala Lys 310 315 320 325	1075
aag gct gcc aac tcc atc ctg gtt aag gtg aac cag atc ggt acc ctg Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn Gln Ile Gly Thr Leu 330 335 340	1123
acc gag acc ttc gac gct gtc gac atg gct cac cgc gca ggc tac acc Thr Glu Thr Phe Asp Ala Val Asp Met Ala His Arg Ala Gly Tyr Thr 345 350 355	1171
tcc atg atg tcc cac cgt tcc ggt gag acc gag gac acc acc att gct Ser Met Met Ser His Arg Ser Gly Glu Thr Glu Asp Thr Thr Ile Ala 360 365 370	1219
gac ctg gca gtt gca ctg aac tgt ggc cag atc aag act ggt gct cca Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile Lys Thr Gly Ala Pro 375 380 385	1267
gca cgt tcc gac cgt gtc gca aag tac aac cag ctt ctg cgc atc gag Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln Leu Leu Arg Ile Glu 390 395 400 405	1315
cag ctg ctt ggc gac gcc ggc gtc tac gca ggt cgc agc gca ttc cca Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly Arg Ser Ala Phe Pro 410 415 420	1363

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 Arg Phe Gln Gly
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1398

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<213> Corynebacterium glutamicum

<400> 72

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Gly Asn Pro Thr Val Glu Ala Glu Val Phe Leu Asp Asp Gly Ser His
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Gly Val Ala Gly Val Pro Ser Gly Ala Ser Thr Gly Val His Glu Ala
 35 40 45

His Glu Leu Arg Asp Gly Gly Asp Arg Tyr Leu Gly Lys Gly Val Leu
 50 55 60

Lys Ala Val Glu Asn Val Asn Glu Glu Ile Gly Asp Glu Leu Ala Gly
 65 70 75 80

Leu Glu Ala Asp Asp Gln Arg Leu Ile Asp Glu Ala Met Ile Lys Leu
 85 90 95

Asp Gly Thr Ala Asn Lys Ser Arg Leu Gly Ala Asn Ala Ile Leu Gly
 100 105 110

Val Ser Met Ala Val Ala Lys Ala Ala Ala Asp Ser Ala Gly Leu Pro
 115 120 125

Leu Phe Arg Tyr Ile Gly Gly Pro Asn Ala His Val Leu Pro Val Pro
 130 135 140

Met Met Asn Ile Ile Thr Gly Gly Ala His Ala Asp Ser Gly Val Asp
 145 150 155 160

Val Gln Glu Phe Met Ile Ala Pro Ile Gly Ala Glu Thr Phe Ser Glu
 165 170 175

Ala Leu Arg Asn Gly Ala Glu Val Tyr His Ala Leu Lys Ser Val Ile
 180 185 190

Lys Glu Lys Gly Leu Ser Thr Gly Leu Gly Asp Glu Gly Gly Phe Ala
 195 200 205

Pro Ser Val Gly Ser Thr Arg Glu Ala Leu Asp Leu Ile Val Glu Ala
 210 215 220

Ile Glu Lys Ala Gly Phe Thr Pro Gly Lys Asp Ile Ala Leu Ala Leu
 225 230 235 240

Asp Val Ala Ser Ser Glu Phe Phe Lys Asp Gly Thr Tyr His Phe Glu
 245 250 255

Gly Gly Gln His Ser Ala Ala Glu Met Ala Asn Val Tyr Ala Glu Leu
 260 265 270

Val Asp Ala Tyr Pro Ile Val Ser Ile Glu Asp Pro Leu Gln Glu Asp
 275 280 285

Asp Trp Glu Gly Tyr Thr Asn Leu Thr Ala Thr Ile Gly Asp Lys Val
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Gln Ile Val Gly Asp Asp Phe Phe Val Thr Asn Pro Glu Arg Leu Lys
 305 310 315 320

Glu Gly Ile Ala Lys Lys Ala Ala Asn Ser Ile Leu Val Lys Val Asn
 325 330 335

Gln Ile Gly Thr Leu Thr Glu Thr Phe Asp Ala Val Asp Met Ala His
 340 345 350

Arg Ala Gly Tyr Thr Ser Met Met Ser His Arg Ser Gly Glu Thr Glu
 355 360 365

Asp Thr Thr Ile Ala Asp Leu Ala Val Ala Leu Asn Cys Gly Gln Ile
 370 375 380

Lys Thr Gly Ala Pro Ala Arg Ser Asp Arg Val Ala Lys Tyr Asn Gln
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Leu Leu Arg Ile Glu Gln Leu Leu Gly Asp Ala Gly Val Tyr Ala Gly
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Arg Ser Ala Phe Pro Arg Phe Gln Gly
 420 425

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 <223> RXA01093

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 Met Gly Val Asp Arg
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cga act aag att gta tgt acc cta ggc cca gcg gtg gct agt gca gat 163
 Arg Thr Lys Ile Val Cys Thr Leu Gly Pro Ala Val Ala Ser Ala Asp
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gga att ctg cgt ttg gta gaa gac ggc atg gat gtt gct cgc ctc aac 211
 Gly Ile Leu Arg Leu Val Glu Asp Gly Met Asp Val Ala Arg Leu Asn
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ttc tcc cat ggt gac cac cca gat cat gag caa aac tac aag tgg gtc 259
 Phe Ser His Gly Asp His Pro Asp His Glu Gln Asn Tyr Lys Trp Val
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cgc gag gcg gcg gag aag act ggc cgt gca gtc ggt att ctc gca gac	307
Arg Glu Ala Ala Glu Lys Thr Gly Arg Ala Val Gly Ile Leu Ala Asp	
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Leu Gln Gly Pro Lys Ile Arg Leu Gly Arg Phe Thr Asp Gly Ala Thr	
70 75 80 85	
gtg tgg gaa aac ggc gag acc att cgg atc acc gtt gac gat gta gag	403
Val Trp Glu Asn Gly Glu Thr Ile Arg Ile Thr Val Asp Asp Val Glu	
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gga acg cac gat cgt gtg tcc acc acc tac aag aat ctg gca aaa gac	451
Gly Thr His Asp Arg Val Ser Thr Thr Tyr Lys Asn Leu Ala Lys Asp	
105 110 115	
gcg aag cca ggc gac cgc ctg ctc gtt gat gac ggc aag gtt ggc ctc	499
Ala Lys Pro Gly Asp Arg Leu Leu Val Asp Asp Gly Lys Val Gly Leu	
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gtc tgc gtt tcc gtc gaa ggt aac gac gtc atc tgt gag gtt gtt gag	547
Val Cys Val Ser Val Glu Gly Asn Asp Val Ile Cys Glu Val Val Glu	
135 140 145	
ggc gga cca gtc tcc aac aac aag ggt gtt tcc ctg cca ggt atg gat	595
Gly Gly Pro Val Ser Asn Asn Lys Gly Val Ser Leu Pro Gly Met Asp	
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Ile Ser Val Pro Ala Leu Ser Glu Lys Asp Ile Arg Asp Leu Arg Phe	
170 175 180	
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Ala Leu Lys Leu Gly Val Asp Phe Ile Ala Leu Ser Phe Val Arg Ser	
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Pro Ala Asp Ala Glu Leu Val His Lys Ile Met Asp Glu Glu Gly Arg	
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cgt gtt cct gtg atc gcc aag ctg gaa aag cca gag gct gtc acc tcc	787
Arg Val Pro Val Ile Ala Lys Leu Glu Lys Pro Glu Ala Val Thr Ser	
215 220 225	
ctc gag cca atc gtg ttg gca ttc gac gcc gtc atg gtt gct cgt ggt	835
Leu Glu Pro Ile Val Leu Ala Phe Asp Ala Val Met Val Ala Arg Gly	
230 235 240 245	
gac ctc ggc gtt gag gtt cct ctg gag gag gtt cca ctg gtt cag aag	883
Asp Leu Gly Val Glu Val Pro Leu Glu Glu Val Pro Leu Val Gln Lys	
250 255 260	
cgc gca atc cag att gcc cgt gag aac gca aag cca gtt atc gtg gca	931
Arg Ala Ile Gln Ile Ala Arg Glu Asn Ala Lys Pro Val Ile Val Ala	
265 270 275	
acc cag atg ctg gat tcc atg att gag aac tcc cgc cca acc cgt gcg	979
Thr Gln Met Leu Asp Ser Met Ile Glu Asn Ser Arg Pro Thr Arg Ala	
280 285 290	
gaa gct tct gac gtg gca aac gct gtg ctc gat ggc gca gat gct gtc	1027

Glu Ala Ser Asp Val Ala Asn Ala Val Leu Asp Gly Ala Asp Ala Val
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 atg ctt tct ggt gaa act tca gtg ggc aaa gat ccg cac aac gtt gtg 1075
 Met Leu Ser Gly Glu Thr Ser Val Gly Lys Asp Pro His Asn Val Val
 310 315 320 325
 cgc acc atg tct cgc att gtt cgc ttc gct gaa acc gac ggt cgc gtc 1123
 Arg Thr Met Ser Arg Ile Val Arg Phe Ala Glu Thr Asp Gly Arg Val
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 cca gac ctg acc cac atc cct cgc act aag cgt ggc gtt att tcc tac 1171
 Pro Asp Leu Thr His Ile Pro Arg Thr Lys Arg Gly Val Ile Ser Tyr
 345 350 355
 tct gca cgt gat atc gcc gag cgc ctc aac gct cgt gca ttg gtt gcg 1219
 Ser Ala Arg Asp Ile Ala Glu Arg Leu Asn Ala Arg Ala Leu Val Ala
 360 365 370
 ttc acc acc tct ggt gat acc gca aag cgt gtg gct cgt ctg cac agc 1267
 Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val Ala Arg Leu His Ser
 375 380 385
 cac ctg cca ctg ctc gtg ttc act cca aat gag gca gtt cgc tct gag 1315
 His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu Ala Val Arg Ser Glu
 390 395 400 405
 ctg gcg ctg acc tgg ggt gca acc acc ttc ctg tgt cca cct gtc agc 1363
 Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu Cys Pro Pro Val Ser
 410 415 420
 gat acc gat gac atg atg cgc gaa gtc gac cgt gct ctt tta gca atg 1411
 Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg Ala Leu Leu Ala Met
 425 430 435
 cct gag tac aac aag ggt gac atg atg gtt gtt gtt gca ggt tcc cct 1459
 Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val Val Ala Gly Ser Pro
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 cct ggt gtt acc ggt aac acc aac atg att cac gtc cac ctt ctt ggt 1507
 Pro Gly Val Thr Gly Asn Thr Asn Met Ile His Val His Leu Leu Gly
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<213> Corynebacterium glutamicum

<400> 74

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Val Ala Arg Leu Asn Phe Ser His Gly Asp His Pro Asp His Glu Gln

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Asn	Tyr	Lys	Trp	Val	Arg	Glu	Ala	Ala	Glu	Lys	Thr	Gly	Arg	Ala	Val	
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Gly	Ile	Leu	Ala	Asp	Leu	Gln	Gly	Pro	Lys	Ile	Arg	Leu	Gly	Arg	Phe	
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Thr	Asp	Gly	Ala	Thr	Val	Trp	Glu	Asn	Gly	Glu	Thr	Ile	Arg	Ile	Thr	
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Val	Asp	Asp	Val	Glu	Gly	Thr	His	Asp	Arg	Val	Ser	Thr	Thr	Tyr	Lys	
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Asn	Leu	Ala	Lys	Asp	Ala	Lys	Pro	Gly	Asp	Arg	Leu	Leu	Val	Asp	Asp	
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Cys	Glu	Val	Val	Glu	Gly	Gly	Pro	Val	Ser	Asn	Asn	Lys	Gly	Val	Ser	
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Leu	Pro	Gly	Met	Asp	Ile	Ser	Val	Pro	Ala	Leu	Ser	Glu	Lys	Asp	Ile	
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Arg	Asp	Leu	Arg	Phe	Ala	Leu	Lys	Leu	Gly	Val	Asp	Phe	Ile	Ala	Leu	
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Ser	Phe	Val	Arg	Ser	Pro	Ala	Asp	Ala	Glu	Leu	Val	His	Lys	Ile	Met	
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Asp	Glu	Glu	Gly	Arg	Arg	Val	Pro	Val	Ile	Ala	Lys	Leu	Glu	Lys	Pro	
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Glu	Ala	Val	Thr	Ser	Leu	Glu	Pro	Ile	Val	Leu	Ala	Phe	Asp	Ala	Val	
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Met	Val	Ala	Arg	Gly	Asp	Leu	Gly	Val	Glu	Val	Pro	Leu	Glu	Glu	Val	
					245					250					255	
Pro	Leu	Val	Gln	Lys	Arg	Ala	Ile	Gln	Ile	Ala	Arg	Glu	Asn	Ala	Lys	
260					265					270						
Pro	Val	Ile	Val	Ala	Thr	Gln	Met	Leu	Asp	Ser	Met	Ile	Glu	Asn	Ser	
275					280					285						
Arg	Pro	Thr	Arg	Ala	Glu	Ala	Ser	Asp	Val	Ala	Asn	Ala	Val	Leu	Asp	
290					295					300						
Gly	Ala	Asp	Ala	Val	Met	Leu	Ser	Gly	Glu	Thr	Ser	Val	Gly	Lys	Asp	
305					310					315					320	
Pro	His	Asn	Val	Val	Arg	Thr	Met	Ser	Arg	Ile	Val	Arg	Phe	Ala	Glu	
					325					330					335	
Thr	Asp	Gly	Arg	Val	Pro	Asp	Leu	Thr	His	Ile	Pro	Arg	Thr	Lys	Arg	
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Gly	Val	Ile	Ser	Tyr	Ser	Ala	Arg	Asp	Ile	Ala	Glu	Arg	Leu	Asn	Ala	
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Arg Ala Leu Val Ala Phe Thr Thr Ser Gly Asp Thr Ala Lys Arg Val
370 375 380

Ala Arg Leu His Ser His Leu Pro Leu Leu Val Phe Thr Pro Asn Glu
385 390 395 400

Ala Val Arg Ser Glu Leu Ala Leu Thr Trp Gly Ala Thr Thr Phe Leu
405 410 415

Cys Pro Pro Val Ser Asp Thr Asp Asp Met Met Arg Glu Val Asp Arg
420 425 430

Ala Leu Leu Ala Met Pro Glu Tyr Asn Lys Gly Asp Met Met Val Val
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Val Ala Gly Ser Pro Pro Gly Val Thr Gly Asn Thr Asn Met Ile His
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<211> 1980

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<213> Corynebacterium glutamicum

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<221> CDS

<222> (101)..(1957)

<223> RXN02675

<400> 75

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Met Asn Glu Phe Asp
1 5

cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta 163
Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
10 15 20

gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
25 30 35

tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
40 45 50

ctt cgc acc aaa gac ctc cgt ggc ctg cag caa cgc ctc tcc tct gtg 307
Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln Arg Leu Ser Ser Val
55 60 65

gga gct acc cgc ttg act acc acc gaa cca gca gtg cag gcc cgc ctc 355
Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala Val Gln Ala Arg Leu
70 75 80 85

aag gcc gcc cgc aat gtt atc gga gct ttc gca ggt gaa ggc cca ctt 403

Lys	Ala	Ala	Arg	Asn	Val	Ile	Gly	Ala	Phe	Ala	Gly	Glu	Gly	Pro	Leu		
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Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile		
			105					110					115				
ctc	gac	gag	cac	gcc	gaa	att	ctc	ctt	ggc	gaa	ccc	cta	ccg	gat	act	499	
Leu	Asp	Glu	His	Ala	Glu	Ile	Leu	Leu	Gly	Glu	Pro	Leu	Pro	Asp	Thr		
		120					125					130					
cca	tcc	tgc	atc	atg	gtc	acc	ctg	ccc	acc	gaa	gcc	gcc	acc	gac	att	547	
Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile		
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gaa	ctt	gtc	cgt	ggc	ttc	gcc	aaa	agc	ggc	atg	aat	cta	gct	cgc	atc	595	
Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met	Asn	Leu	Ala	Arg	Ile		
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Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	Ile	Arg	Val	Ser	Met		
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Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala		
		200					205					210					
gaa	gta	ggt	cgc	gca	cga	gta	acc	cgc	gac	gaa	acc	gga	aaa	gta	ctg	787	
Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu		
	215					220				225							
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Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro		
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Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	Pro	Ile	Glu	Val	Thr		
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cca	gaa	tgg	ttc	gac	aaa	cta	gaa	atc	ggc	agc	gtc	atc	aac	gtc	cca	931	
Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	Val	Ile	Asn	Val	Pro		
			265					270					275				
gac	acc	cgc	gga	tcc	cgc	cga	gca	ttc	acc	gtg	acc	agg	gtt	ttt	gat	979	
Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp		
			280				285					290					
ggc	gcg	gtc	ctc	gcc	gaa	ggc	cca	caa	aaa	gcc	tac	atc	tcc	aac	ggc	1027	
Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	Tyr	Ile	Ser	Asn	Gly		
	295					300					305						
acc	ctc	ctg	gaa	cac	aac	tac	gac	cgc	tcc	cgg	gtc	tac	ggc	atc	ccc	1075	
Thr	Leu	Leu	Glu	His	Asn	Tyr	Asp	Arg	Ser	Arg	Val	Tyr	Gly	Ile	Pro		
310					315				320						325		
gcc	gta	gtt	cag	cgc	atc	aac	ctc	aaa	gtc	ggc	gac	cgc	ctc	atc	ctt	1123	
Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	Asp	Arg	Leu	Ile	Leu		

330					335					340						
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Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr	
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cca	cgc	atc	agc	tgc	acc	ctt	cca	caa	gca	gtc	gat	gca	att	aaa	gtc	1219
Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val	
			360				365					370				
ggg	cac	cgc	gtg	ctt	ttc	gac	gac	gga	gcc	atc	gcc	gca	gtc	tgc	atc	1267
Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile	
			375			380					385					
gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val	
390					395					400					405	
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Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala	Ala	Tyr	Lys	Gly	Ile	
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Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp	
				425				430							435	
ctc	caa	cac	ctg	cgc	ttt	gtc	gtc	aaa	tac	gcc	gac	atc	gca	gcc	atc	1459
Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile	
			440				445						450			
tcc	ttc	atc	cga	aac	gtc	gcc	gac	gtg	gaa	tac	ctc	ctc	caa	gca	ctc	1507
Ser	Phe	Ile	Arg	Asn	Val	Ala	Asp	Val	Glu	Tyr	Leu	Leu	Gln	Ala	Leu	
			455				460					465				
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Ala	Asp	Ile	Gly	Asp	Pro	Val	Ala	Val	Glu	Arg	Leu	Gly	Leu	Val	Leu	
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aaa	atc	gag	acc	atc	cca	ggc	tac	gaa	ggc	ctc	gcc	caa	atc	ctc	ctg	1603
Lys	Ile	Glu	Thr	Ile	Pro	Gly	Tyr	Glu	Gly	Leu	Ala	Gln	Ile	Leu	Leu	
				490					495						500	
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Thr	Gly	Met	Arg	His	Glu	Asn	Phe	Gly	Ile	Met	Ile	Ala	Arg	Gly	Asp	
				505				510							515	
ctc	gcc	gtc	gaa	ctc	ggc	ttc	gac	cgc	atg	gca	gaa	gtc	ccc	caa	ctg	1699
Leu	Ala	Val	Glu	Leu	Gly	Phe	Asp	Arg	Met	Ala	Glu	Val	Pro	Gln	Leu	
			520				525						530			
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Ile	Met	Ala	Leu	Ala	Glu	Ala	Ala	His	Val	Pro	Thr	Ile	Leu	Ala	Thr	
			535				540					545				
caa	gtc	ctg	gaa	aac	atg	gcc	aaa	aac	gga	ctc	cca	tct	cgc	gca	gaa	1795
Gln	Val	Leu	Glu	Asn	Met	Ala	Lys	Asn	Gly	Leu	Pro	Ser	Arg	Ala	Glu	
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atc	acc	gac	gca	gca	atg	gca	ctt	cgc	gct	gaa	tgc	gtc	atg	ctg	aac	1843
Ile	Thr	Asp	Ala	Ala	Met	Ala	Leu	Arg	Ala	Glu	Cys	Val	Met	Leu	Asn	
				570					575						580	

aag gga cca cac atc aac gac gcc atc aag gtc ctc acc gaa atg agc 1891
 Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr Glu Met Ser
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cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg ctg cgc aag 1939
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<212> PRT

<213> Corynebacterium glutamicum

<400> 76

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Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu
 35 40 45

Met His Tyr Ala His Leu Arg Thr Lys Asp Leu Arg Gly Leu Gln Gln
 50 55 60

Arg Leu Ser Ser Val Gly Ala Thr Arg Leu Thr Thr Thr Glu Pro Ala
 65 70 75 80

Val Gln Ala Arg Leu Lys Ala Ala Arg Asn Val Ile Gly Ala Phe Ala
 85 90 95

Gly Glu Gly Pro Leu Tyr Pro Pro Ser Asp Val Val Asp Ala Phe Glu
 100 105 110

Asp Ala Asp Glu Ile Leu Asp Glu His Ala Glu Ile Leu Leu Gly Glu
 115 120 125

Pro Leu Pro Asp Thr Pro Ser Cys Ile Met Val Thr Leu Pro Thr Glu
 130 135 140

Ala Ala Thr Asp Ile Glu Leu Val Arg Gly Phe Ala Lys Ser Gly Met
 145 150 155 160

Asn Leu Ala Arg Ile Asn Cys Ala His Asp Asp Glu Thr Val Trp Lys
 165 170 175

Gln Met Ile Asp Asn Val His Thr Val Ala Glu Glu Val Gly Arg Glu
 180 185 190

Ile Arg Val Ser Met Asp Leu Ala Gly Pro Lys Val Arg Thr Gly Glu
 195 200 205

Ile Ala Pro Gly Ala Glu Val Gly Arg Ala Arg Val Thr Arg Asp Glu
 210 215 220

Thr Gly Lys Val Leu Thr Pro Ala Lys Leu Trp Ile Thr Ala His Gly
 225 230 235 240
 Ser Glu Pro Val Pro Ala Pro Glu Ser Leu Pro Gly Arg Pro Ala Leu
 245 250 255
 Pro Ile Glu Val Thr Pro Glu Trp Phe Asp Lys Leu Glu Ile Gly Ser
 260 265 270
 Val Ile Asn Val Pro Asp Thr Arg Gly Ser Arg Arg Ala Phe Thr Val
 275 280 285
 Thr Arg Val Phe Asp Gly Ala Val Leu Ala Glu Gly Pro Gln Lys Ala
 290 295 300
 Tyr Ile Ser Asn Gly Thr Leu Leu Glu His Asn Tyr Asp Arg Ser Arg
 305 310 315 320
 Val Tyr Gly Ile Pro Ala Val Val Gln Arg Ile Asn Leu Lys Val Gly
 325 330 335
 Asp Arg Leu Ile Leu Thr Asp Glu Glu Leu Thr Tyr Asp Pro Ser Leu
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 Gly Ser Gly Arg Thr Pro Arg Ile Ser Cys Thr Leu Pro Gln Ala Val
 355 360 365
 Asp Ala Ile Lys Val Gly His Arg Val Leu Phe Asp Asp Gly Ala Ile
 370 375 380
 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
 385 390 395 400
 Val Glu Leu Glu Val Thr His Ala Arg Pro Gln Gly Val Asn Leu Ala
 405 410 415
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 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
 435 440 445
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 465 470 475 480
 Leu Gly Leu Val Leu Lys Ile Glu Thr Ile Pro Gly Tyr Glu Gly Leu
 485 490 495
 Ala Gln Ile Leu Leu Thr Gly Met Arg His Glu Asn Phe Gly Ile Met
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 Ile Ala Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala
 515 520 525
 Glu Val Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro
 530 535 540

Thr Ile Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu
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Pro Ser Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu
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Cys Val Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val
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Arg Gly Asp Leu Ala Val Glu Leu Gly Phe Asp Arg Met Ala Glu Val
20 25 30

ccc caa ctg atc atg gcc ctt gca gaa gcc gcc cac gtc cca acc atc 144
Pro Gln Leu Ile Met Ala Leu Ala Glu Ala Ala His Val Pro Thr Ile
35 40 45

ttg gcc acc caa gtc ctg gaa aac atg gcc aaa aac gga ctc cca tct 192
Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
50 55 60

cgc gca gaa atc acc gac gca gca atg gca ctt cgc gct gaa tgc gtc 240
Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
65 70 75 80

atg ctg aac aag gga cca cac atc aac gac gcc atc aag gtc ctc acc 288
Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
85 90 95

gaa atg agc cgc aaa ctt ggt gca tcc caa cga aag agt agg ctg ctg 336
Glu Met Ser Arg Lys Leu Gly Ala Ser Gln Arg Lys Ser Arg Leu Leu
100 105 110

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Leu Arg Lys Val Lys Ser Trp Glu Glu
115 120

cgt 386

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 35 40 45
 Leu Ala Thr Gln Val Leu Glu Asn Met Ala Lys Asn Gly Leu Pro Ser
 50 55 60
 Arg Ala Glu Ile Thr Asp Ala Ala Met Ala Leu Arg Ala Glu Cys Val
 65 70 75 80
 Met Leu Asn Lys Gly Pro His Ile Asn Asp Ala Ile Lys Val Leu Thr
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 Met Asn Glu Phe Asp
 1 5
 cag gac att ctc cag gag atc aag act gaa ctc gac gag tta att cta 163
 Gln Asp Ile Leu Gln Glu Ile Lys Thr Glu Leu Asp Glu Leu Ile Leu
 10 15 20
 gaa ctt gat gag gtg aca caa act cac agc gag gcc atc ggg cag gtc 211
 Glu Leu Asp Glu Val Thr Gln Thr His Ser Glu Ala Ile Gly Gln Val
 25 30 35
 tcc cca acc cat tac gtt ggt gcc cgc aac ctc atg cat tac gcg cat 259
 Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu Met His Tyr Ala His
 40 45 50

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Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala	Val	Gln	Ala	Arg	Leu	
70					75					80					85	
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Lys	Ala	Ala	Arg	Asn	Val	Ile	Gly	Ala	Phe	Ala	Gly	Glu	Gly	Pro	Leu	
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Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	Asp	Ala	Asp	Glu	Ile	
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Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	Ala	Ala	Thr	Asp	Ile	
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Asn	Cys	Ala	His	Asp	Asp	Glu	Thr	Val	Trp	Lys	Gln	Met	Ile	Asp	Asn	
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Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	Ile	Arg	Val	Ser	Met	
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Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	Ile	Ala	Pro	Gly	Ala	
		200					205					210				
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Glu	Val	Gly	Arg	Ala	Arg	Val	Thr	Arg	Asp	Glu	Thr	Gly	Lys	Val	Leu	
	215					220					225					
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Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	Ser	Glu	Pro	Val	Pro	
230					235					240					245	
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Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	Pro	Ile	Glu	Val	Thr	
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Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	Val	Ile	Asn	Val	Pro	
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Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	Thr	Arg	Val	Phe	Asp	
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Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	Gly	Ser	Gly	Arg	Thr	
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Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	Asp	Ala	Ile	Lys	Val	
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ggg	cac	cgc	gtg	ctt	ttc	gac	gac	gga	gcc	atc	gcc	gca	gtc	tgc	atc	1267
Gly	His	Arg	Val	Leu	Phe	Asp	Asp	Gly	Ala	Ile	Ala	Ala	Val	Cys	Ile	
	375					380					385					
gac	aag	acc	tcc	act	gcc	gac	ggc	cac	aac	gac	gta	gaa	ttg	gaa	gtc	1315
Asp	Lys	Thr	Ser	Thr	Ala	Asp	Gly	His	Asn	Asp	Val	Glu	Leu	Glu	Val	
390					395					400					405	
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Thr	His	Ala	Arg	Pro	Gln	Gly	Val	Asn	Leu	Ala	Ala	Tyr	Lys	Gly	Ile	
				410				415						420		
aac	ctc	cca	gac	tcc	gaa	ctt	cca	ctc	cca	agc	ctc	act	gaa	gaa	gac	1411
Asn	Leu	Pro	Asp	Ser	Glu	Leu	Pro	Leu	Pro	Ser	Leu	Thr	Glu	Glu	Asp	
			425					430					435			
ctc	caa	cac	ctg	cgc	ttt	gtc	gtc	aaa	tac	gcc	gac	atc	gca	gcc	atc	1459
Leu	Gln	His	Leu	Arg	Phe	Val	Val	Lys	Tyr	Ala	Asp	Ile	Ala	Ala	Ile	
		440					445					450				
tcc	ttc	atc	cga	aac	gtc	gcc	gac	gtg	gaa	tac	ctc	ctc	caa	gca	ctc	1507
Ser	Phe	Ile	Arg	Asn	Val	Ala	Asp	Val	Glu	Tyr	Leu	Leu	Gln	Ala	Leu	
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<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 80

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Ala Ile Gly Gln Val Ser Pro Thr His Tyr Val Gly Ala Arg Asn Leu

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Arg	Leu	Ser	Ser	Val	Gly	Ala	Thr	Arg	Leu	Thr	Thr	Thr	Glu	Pro	Ala	
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Val	Gln	Ala	Arg	Leu	Lys	Ala	Ala	Arg	Asn	Val	Ile	Gly	Ala	Phe	Ala	
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Gly	Glu	Gly	Pro	Leu	Tyr	Pro	Pro	Ser	Asp	Val	Val	Asp	Ala	Phe	Glu	
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Asp	Ala	Asp	Glu	Ile	Leu	Asp	Glu	His	Ala	Glu	Ile	Leu	Leu	Gly	Glu	
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Pro	Leu	Pro	Asp	Thr	Pro	Ser	Cys	Ile	Met	Val	Thr	Leu	Pro	Thr	Glu	
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Ala	Ala	Thr	Asp	Ile	Glu	Leu	Val	Arg	Gly	Phe	Ala	Lys	Ser	Gly	Met	
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Gln	Met	Ile	Asp	Asn	Val	His	Thr	Val	Ala	Glu	Glu	Val	Gly	Arg	Glu	
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Ile	Arg	Val	Ser	Met	Asp	Leu	Ala	Gly	Pro	Lys	Val	Arg	Thr	Gly	Glu	
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210					215					220						
Thr	Gly	Lys	Val	Leu	Thr	Pro	Ala	Lys	Leu	Trp	Ile	Thr	Ala	His	Gly	
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Ser	Glu	Pro	Val	Pro	Ala	Pro	Glu	Ser	Leu	Pro	Gly	Arg	Pro	Ala	Leu	
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Pro	Ile	Glu	Val	Thr	Pro	Glu	Trp	Phe	Asp	Lys	Leu	Glu	Ile	Gly	Ser	
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Val	Ile	Asn	Val	Pro	Asp	Thr	Arg	Gly	Ser	Arg	Arg	Ala	Phe	Thr	Val	
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Thr	Arg	Val	Phe	Asp	Gly	Ala	Val	Leu	Ala	Glu	Gly	Pro	Gln	Lys	Ala	
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Val	Tyr	Gly	Ile	Pro	Ala	Val	Val	Gln	Arg	Ile	Asn	Leu	Lys	Val	Gly	
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Asp	Arg	Leu	Ile	Leu	Thr	Asp	Glu	Glu	Leu	Thr	Tyr	Asp	Pro	Ser	Leu	
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Gly	Ser	Gly	Arg	Thr	Pro	Arg	Ile	Ser	Cys	Thr	Leu	Pro	Gln	Ala	Val	
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 Ala Ala Val Cys Ile Asp Lys Thr Ser Thr Ala Asp Gly His Asn Asp
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 Ala Tyr Lys Gly Ile Asn Leu Pro Asp Ser Glu Leu Pro Leu Pro Ser
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 Leu Thr Glu Glu Asp Leu Gln His Leu Arg Phe Val Val Lys Tyr Ala
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 <223> RXA00682

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 Phe Pro Lys Pro Ser Asp Leu Pro Val Pro Lys Gly Ala Glu Gly Trp
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 Glu Asp Leu Tyr Pro Tyr Tyr Leu Val Phe Gln Asp Lys Leu Met Asp
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 caa gag aat gag aaa ttc tgg ttc tgc gat tca cag cac tgg cca act 259
 Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser Gln His Trp Pro Thr
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 gtg ttc aag cct ttt gaa act atc ggt ggt gaa ttc gct gta aag tgc 307
 Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu Phe Ala Val Lys Cys
 55 60 65
 ctc ggc caa tac aac gct cgg cat ttg atg atc ccg aat gcc aat ggc 355
 Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile Pro Asn Ala Asn Gly
 70 75 80 85
 atc gag ttc cgc gtg cat ctg gga tac ctc tat atg tcc cct att cca 403

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Ile	Thr	His	Tyr	Phe	Gln	Asn	Trp	Glu	Pro	Met	Leu	Ala	Asn	Trp	Lys		
			120				125					130					
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Glu	Arg	Val	Leu	Gly	Thr	Ile	Asn	Glu	Leu	Glu	Ser	Leu	Glu	Phe	Lys		
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Pro	Leu	Pro	Asp	Tyr	Val	Pro	Ile	Asp	Asp	Ile	Val	Ser	Gly	Lys	Ala		
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Lys	Asp	Gly	Thr	Glu	Val	Leu	Met	Glu	Asn	Phe	Asp	Arg	Leu	Ile	Gln		
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ctc	gcc	tac	caa	aac	tgg	caa	tac	cac	ttt	gag	ttc	ctc	aac	ttg	ggt	691	
Leu	Ala	Tyr	Gln	Asn	Trp	Gln	Tyr	His	Phe	Glu	Phe	Leu	Asn	Leu	Gly		
			185					190					195				
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Tyr	Ile	Ala	Tyr	Leu	Asp	Phe	Phe	Asn	Phe	Cys	Lys	Glu	Val	Phe	Pro		
		200					205					210					
gat	atc	cct	gat	caa	tca	att	tcg	atg	atg	gtt	cag	ggc	gtg	gat	atg	787	
Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val	Gln	Gly	Val	Asp	Met		
	215					220					225						
gag	ctg	ttc	cg	ccc	gat	gat	gaa	cta	aag	att	ctg	gca	cag	cta	cg	835	
Glu	Leu	Phe	Arg	Pro	Asp	Asp	Glu	Leu	Lys	Ile	Leu	Ala	Gln	Leu	Ala		
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gtc	gac	ctt	ggc	ctg	caa	act	cac	ttt	gcc	aac	ccg	gat	gat	ccg	caa	883	
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Ala	Arg	Trp	Glu	Glu	Ala	Gln	Asp	Pro	Trp	Phe	Asn	Phe	Thr	Val	Gly		
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Pro	Leu	Gly	Tyr	Ile	Ala	Asp	Tyr	Ile	Arg	Arg	Leu	Asp	Glu	Gly	Gln		
310					315				320						325		
acc	atc	tcc	cg	ccg	aaa	gat	gaa	ctc	atc	gca	gaa	aag	gaa	cg	gtg	1123	
Thr	Ile	Ser	Arg	Pro	Lys	Asp	Glu	Leu	Ile	Ala	Glu	Lys	Glu	Arg	Val		

330								335					340					
gtg	gaa	gaa	tac	cgc	gac	ctt	ttg	gat	gga	gaa	caa	ctc	gcg	cag	ttt	1171		
Val	Glu	Glu	Tyr	Arg	Asp	Leu	Leu	Asp	Gly	Glu	Gln	Leu	Ala	Gln	Phe			
			345					350					355					
gat	gct	aaa	tgc	ggc	ctc	gct	gct	act	gca	tac	ccc	tat	gtg	gaa	aac	1219		
Asp	Ala	Lys	Cys	Gly	Leu	Ala	Ala	Thr	Ala	Tyr	Pro	Tyr	Val	Glu	Asn			
		360					365					370						
cat	aac	ttc	tac	atc	gag	cac	tgg	acc	atg	tca	gta	ttt	tgg	cgc	aaa	1267		
His	Asn	Phe	Tyr	Ile	Glu	His	Trp	Thr	Met	Ser	Val	Phe	Trp	Arg	Lys			
		375				380					385							
gta	cgc	gaa	ctt	tcc	cgc	act	ctc	cag	ggc	tac	ggg	ttc	tgg	gag	aac	1315		
Val	Arg	Glu	Leu	Ser	Arg	Thr	Leu	Gln	Gly	Tyr	Gly	Phe	Trp	Glu	Asn			
					395					400					405			
gag	gat	gac	atg	ttg	tac	ctc	aac	cgc	act	gaa	gtc	cgc	gat	gtc	ctc	1363		
Glu	Asp	Asp	Met	Leu	Tyr	Leu	Asn	Arg	Thr	Glu	Val	Arg	Asp	Val	Leu			
				410					415					420				
ttc	gac	ctg	gct	act	gcg	tgg	ggg	gtc	ggc	gca	ccc	ggg	ggg	cca	att	1411		
Phe	Asp	Leu	Ala	Thr	Ala	Trp	Gly	Val	Gly	Ala	Pro	Gly	Gly	Pro	Ile			
			425				430						435					
ggc	acg	atc	att	tgg	ccg	gaa	gaa	att	gag	cga	aga	aaa	gca	att	gtc	1459		
Gly	Thr	Ile	Ile	Trp	Pro	Glu	Glu	Ile	Glu	Arg	Arg	Lys	Ala	Ile	Val			
		440					445					450						
acc	gct	ttg	aaa	act	gcc	cga	cca	gcg	cca	gct	ctt	aac	act	cct	cca	1507		
Thr	Ala	Leu	Lys	Thr	Ala	Arg	Pro	Ala	Pro	Ala	Leu	Asn	Thr	Pro	Pro			
		455				460					465							
gag	tcc	atc	acc	gaa	cct	ttc	acc	cgc	atg	ctc	tgg	gga	atc	acc	acc	1555		
Glu	Ser	Ile	Thr	Glu	Pro	Phe	Thr	Arg	Met	Leu	Trp	Gly	Ile	Thr	Thr			
					475					480					485			
gaa	cag	gtg	caa	tca	tgg	ttg	ggc	aat	gac	gag	gat	gcc	gaa	gaa	gga	1603		
Glu	Gln	Val	Gln	Ser	Trp	Leu	Gly	Asn	Asp	Glu	Asp	Ala	Glu	Glu	Gly			
				490				495						500				
acc	ctt	aaa	ggc	atg	gct	gca	tcc	cct	ggg	gtg	gtg	gaa	ggc	tac	gct	1651		
Thr	Leu	Lys	Gly	Met	Ala	Ala	Ser	Pro	Gly	Val	Val	Glu	Gly	Tyr	Ala			
			505					510					515					
cga	gta	att	ctc	agc	gca	gat	gac	ctt	tca	gaa	atc	cag	cag	gat	gaa	1699		
Arg	Val	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Ser	Glu	Ile	Gln	Gln	Asp	Glu			
			520				525					530						
atc	ctc	gtt	gcc	cct	gta	aca	gca	cct	tct	tgg	ggc	cca	atc	ttt	ggc	1747		
Ile	Leu	Val	Ala	Pro	Val	Thr	Ala	Pro	Ser	Trp	Gly	Pro	Ile	Phe	Gly			
			535			540					545							
aaa	atc	aag	gca	aca	gtc	act	gat	att	ggg	ggc	atg	atg	agc	cat	gct	1795		
Lys	Ile	Lys	Ala	Thr	Val	Thr	Asp	Ile	Gly	Gly	Met	Met	Ser	His	Ala			
					555				560						565			
gcg	atc	gtg	tgc	cgc	gaa	tac	ggc	ttg	ccg	gct	gtt	act	gga	act	ggc	1843		
Ala	Ile	Val	Cys	Arg	Glu	Tyr	Gly	Leu	Pro	Ala	Val	Thr	Gly	Thr	Gly			
				570				575						580				

gct gca tcc acc acc atc aaa acc ggc gat tac ctc aag gtc gat gga 1891
 Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr Leu Lys Val Asp Gly
 585 590 595

acc aag ggc aag gtt gtc att gtt gat cca gat gcg cca cgc atc gaa 1939
 Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp Ala Pro Arg Ile Glu
 600 605 610

gga ccc ggc gcg cac agc cat gcg cac tca gta gca gca cat ggg gtg 1987
 Gly Pro Gly Ala His Ser His Ala His Ser Val Ala Ala His Gly Val
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gat aca cat gcc tagtccacgc actgttctta tca 2022
 Asp Thr His Ala
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<213> Corynebacterium glutamicum

<400> 82

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Asp Lys Leu Met Asp Gln Glu Asn Glu Lys Phe Trp Phe Cys Asp Ser
 35 40 45

Gln His Trp Pro Thr Val Phe Lys Pro Phe Glu Thr Ile Gly Gly Glu
 50 55 60

Phe Ala Val Lys Cys Leu Gly Gln Tyr Asn Ala Arg His Leu Met Ile
 65 70 75 80

Pro Asn Ala Asn Gly Ile Glu Phe Arg Val His Leu Gly Tyr Leu Tyr
 85 90 95

Met Ser Pro Ile Pro Val Pro Glu Asp Gln Ile Ala Glu Arg Val Pro
 100 105 110

Met Phe Gln Glu Arg Ile Thr His Tyr Phe Gln Asn Trp Glu Pro Met
 115 120 125

Leu Ala Asn Trp Lys Glu Arg Val Leu Gly Thr Ile Asn Glu Leu Glu
 130 135 140

Ser Leu Glu Phe Lys Pro Leu Pro Asp Tyr Val Pro Ile Asp Asp Ile
 145 150 155 160

Val Ser Gly Lys Ala Lys Asp Gly Thr Glu Val Leu Met Glu Asn Phe
 165 170 175

Asp Arg Leu Ile Gln Leu Ala Tyr Gln Asn Trp Gln Tyr His Phe Glu
 180 185 190

Phe Leu Asn Leu Gly Tyr Ile Ala Tyr Leu Asp Phe Phe Asn Phe Cys

195					200					205					
Lys	Glu	Val	Phe	Pro	Asp	Ile	Pro	Asp	Gln	Ser	Ile	Ser	Met	Met	Val
210						215					220				
Gln	Gly	Val	Asp	Met	Glu	Leu	Phe	Arg	Pro	Asp	Asp	Glu	Leu	Lys	Ile
225					230					235					240
Leu	Ala	Gln	Leu	Ala	Val	Asp	Leu	Gly	Leu	Gln	Thr	His	Phe	Ala	Asn
				245					250					255	
Pro	Asp	Asp	Pro	Gln	Ala	Thr	Leu	Ala	Ala	Ile	Ala	Lys	Ala	Glu	Gly
			260					265					270		
Gly	Ala	Thr	Trp	Ile	Ala	Arg	Trp	Glu	Glu	Ala	Gln	Asp	Pro	Trp	Phe
		275					280					285			
Asn	Phe	Thr	Val	Gly	Asn	Gly	Phe	Tyr	Gly	His	Asp	Lys	Tyr	Trp	Ile
290						295					300				
Glu	His	Leu	Glu	Leu	Pro	Leu	Gly	Tyr	Ile	Ala	Asp	Tyr	Ile	Arg	Arg
305					310					315					320
Leu	Asp	Glu	Gly	Gln	Thr	Ile	Ser	Arg	Pro	Lys	Asp	Glu	Leu	Ile	Ala
				325					330					335	
Glu	Lys	Glu	Arg	Val	Val	Glu	Glu	Tyr	Arg	Asp	Leu	Leu	Asp	Gly	Glu
			340					345					350		
Gln	Leu	Ala	Gln	Phe	Asp	Ala	Lys	Cys	Gly	Leu	Ala	Ala	Thr	Ala	Tyr
		355					360					365			
Pro	Tyr	Val	Glu	Asn	His	Asn	Phe	Tyr	Ile	Glu	His	Trp	Thr	Met	Ser
		370				375					380				
Val	Phe	Trp	Arg	Lys	Val	Arg	Glu	Leu	Ser	Arg	Thr	Leu	Gln	Gly	Tyr
385					390					395					400
Gly	Phe	Trp	Glu	Asn	Glu	Asp	Asp	Met	Leu	Tyr	Leu	Asn	Arg	Thr	Glu
				405					410					415	
Val	Arg	Asp	Val	Leu	Phe	Asp	Leu	Ala	Thr	Ala	Trp	Gly	Val	Gly	Ala
			420					425					430		
Pro	Gly	Gly	Pro	Ile	Gly	Thr	Ile	Ile	Trp	Pro	Glu	Glu	Ile	Glu	Arg
		435					440					445			
Arg	Lys	Ala	Ile	Val	Thr	Ala	Leu	Lys	Thr	Ala	Arg	Pro	Ala	Pro	Ala
		450				455					460				
Leu	Asn	Thr	Pro	Pro	Glu	Ser	Ile	Thr	Glu	Pro	Phe	Thr	Arg	Met	Leu
465					470					475					480
Trp	Gly	Ile	Thr	Thr	Glu	Gln	Val	Gln	Ser	Trp	Leu	Gly	Asn	Asp	Glu
				485					490					495	
Asp	Ala	Glu	Glu	Gly	Thr	Leu	Lys	Gly	Met	Ala	Ala	Ser	Pro	Gly	Val
			500					505					510		
Val	Glu	Gly	Tyr	Ala	Arg	Val	Ile	Leu	Ser	Ala	Asp	Asp	Leu	Ser	Glu
		515					520					525			

Ile Gln Gln Asp Glu Ile Leu Val Ala Pro Val Thr Ala Pro Ser Trp
530 535 540

Gly Pro Ile Phe Gly Lys Ile Lys Ala Thr Val Thr Asp Ile Gly Gly
545 550 555 560

Met Met Ser His Ala Ala Ile Val Cys Arg Glu Tyr Gly Leu Pro Ala
565 570 575

Val Thr Gly Thr Gly Ala Ala Ser Thr Thr Ile Lys Thr Gly Asp Tyr
580 585 590

Leu Lys Val Asp Gly Thr Lys Gly Lys Val Val Ile Val Asp Pro Asp
595 600 605

Ala Pro Arg Ile Glu Gly Pro Gly Ala His Ser His Ala His Ser Val
610 615 620

Ala Ala His Gly Val Asp Thr His Ala
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<212> DNA

<213> Corynebacterium glutamicum

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<400> 83

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Met Thr Asn Ser Leu
1 5

aac atc ccg ttt gtc cag cgc ttc gat gaa ggc ctg gat cct gtt cta 163
Asn Ile Pro Phe Val Gln Arg Phe Asp Glu Gly Leu Asp Pro Val Leu
10 15 20

gaa gta ctc ggt ggc aag ggc gct tca cta gtc acc atg aca gat gct 211
Glu Val Leu Gly Gly Lys Gly Ala Ser Leu Val Thr Met Thr Asp Ala
25 30 35

gga atg ccc gtt cca cct gga ttt gtg gtc act act gcc agc ttt gat 259
Gly Met Pro Val Pro Pro Gly Phe Val Val Thr Thr Ala Ser Phe Asp
40 45 50

gaa ttc atc cgt gaa gca ggg gtt gct gaa cac atc gat aaa ttc cta 307
Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His Ile Asp Lys Phe Leu
55 60 65

aac gat ctc gat gca gaa gat gtt aag gaa gtg gat cga gtt tct gcg 355
Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val Asp Arg Val Ser Ala
70 75 80 85

atc atc cgc gat gag ctg tgc agt ctt gac gtt cca gag aat gct cgt 403

Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val Pro Glu Asn Ala Arg	
90 95 100	
ttc gca gtg cac cag gct tat cgc gat ctc atg gaa cga tgc ggt ggc	451
Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met Glu Arg Cys Gly Gly	
105 110 115	
gac gtc ccg gtt gct gtc cgg tca tcg gcc act gcc gaa gat ctg ccc	499
Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr Ala Glu Asp Leu Pro	
120 125 130	
gat gct tcc ttc gca ggg caa cag gac acc tat ctg tgg caa gtc ggt	547
Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr Leu Trp Gln Val Gly	
135 140 145	
ttg agc gct gtc act gaa cac atc cgt aaa tgc tgg gct tcg ctg ttc	595
Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys Trp Ala Ser Leu Phe	
150 155 160 165	
act tcc cgt gcc att atc tac cgt ctg aaa aac aac atc ccc aat gag	643
Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn Asn Ile Pro Asn Glu	
170 175 180	
ggc ctc tcc atg gcg gta gtt gtt caa aaa atg gtc aac tct cgt gtc	691
Gly Leu Ser Met Ala Val Val Val Gln Lys Met Val Asn Ser Arg Val	
185 190 195	
gca ggc gtg gca atc act atg aat cct tcc aac ggc gac cgc tcg aag	739
Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn Gly Asp Arg Ser Lys	
200 205 210	
atc acc atc gat tcc tca tgg ggt gtt ggt gaa atg gtg gtc tca ggt	787
Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu Met Val Val Ser Gly	
215 220 225	
gaa gtg aca cca gac aat atc ttg ctg gac aag atc acg ctg cag gtt	835
Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys Ile Thr Leu Gln Val	
230 235 240 245	
gtc tcc gaa cac att gga agc aaa cac gct gaa ctc atc ccc gat gcc	883
Val Ser Glu His Ile Gly Ser Lys His Ala Glu Leu Ile Pro Asp Ala	
250 255 260	
acc agt gga agc ctc gtg gaa aag ccc gtt gat gaa gaa cgc gca aac	931
Thr Ser Gly Ser Leu Val Glu Lys Pro Val Asp Glu Glu Arg Ala Asn	
265 270 275	
cgc cgc agt ctg act gat gag gaa atg ctc gct gtg gca caa atg gct	979
Arg Arg Ser Leu Thr Asp Glu Glu Met Leu Ala Val Ala Gln Met Ala	
280 285 290	
aag cgt gca gaa aaa cac tac aag tgc cca caa gat atc gaa tgg gcg	1027
Lys Arg Ala Glu Lys His Tyr Lys Cys Pro Gln Asp Ile Glu Trp Ala	
295 300 305	
ctg gac gct gat ctg cca gat gga gaa aac ctt ctg tta ttg caa tcc	1075
Leu Asp Ala Asp Leu Pro Asp Gly Glu Asn Leu Leu Leu Leu Gln Ser	
310 315 320 325	
cgc ccg gaa act atc cac tcc aac ggt gtg aag aag gaa acc cca act	1123
Arg Pro Glu Thr Ile His Ser Asn Gly Val Lys Lys Glu Thr Pro Thr	

330 335 340
 ccg cag gct gcc aaa acc ata ggc acc ttc gat ttc agc tca atc acc 1171
 Pro Gln Ala Ala Lys Thr Ile Gly Thr Phe Asp Phe Ser Ser Ile Thr
 345 350 355

gtc gca atg acc ggc acg aag taaaaccacc gcattttttc gtc 1215
 Val Ala Met Thr Gly Thr Lys
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<211> 364

<212> PRT

<213> Corynebacterium glutamicum

<400> 84

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 20 25 30

Thr Met Thr Asp Ala Gly Met Pro Val Pro Pro Gly Phe Val Val Thr
 35 40 45

Thr Ala Ser Phe Asp Glu Phe Ile Arg Glu Ala Gly Val Ala Glu His
 50 55 60

Ile Asp Lys Phe Leu Asn Asp Leu Asp Ala Glu Asp Val Lys Glu Val
 65 70 75 80

Asp Arg Val Ser Ala Ile Ile Arg Asp Glu Leu Cys Ser Leu Asp Val
 85 90 95

Pro Glu Asn Ala Arg Phe Ala Val His Gln Ala Tyr Arg Asp Leu Met
 100 105 110

Glu Arg Cys Gly Gly Asp Val Pro Val Ala Val Arg Ser Ser Ala Thr
 115 120 125

Ala Glu Asp Leu Pro Asp Ala Ser Phe Ala Gly Gln Gln Asp Thr Tyr
 130 135 140

Leu Trp Gln Val Gly Leu Ser Ala Val Thr Glu His Ile Arg Lys Cys
 145 150 155 160

Trp Ala Ser Leu Phe Thr Ser Arg Ala Ile Ile Tyr Arg Leu Lys Asn
 165 170 175

Asn Ile Pro Asn Glu Gly Leu Ser Met Ala Val Val Val Gln Lys Met
 180 185 190

Val Asn Ser Arg Val Ala Gly Val Ala Ile Thr Met Asn Pro Ser Asn
 195 200 205

Gly Asp Arg Ser Lys Ile Thr Ile Asp Ser Ser Trp Gly Val Gly Glu
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Met Val Val Ser Gly Glu Val Thr Pro Asp Asn Ile Leu Leu Asp Lys
 225 230 235 240

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				Met	Ala	His	Ser	Tyr								
				1				5								
gca	gaa	caa	tta	att	gac	act	ttg	gaa	gct	caa	ggg	gtg	aag	cga	att	163
Ala	Glu	Gln	Leu	Ile	Asp	Thr	Leu	Glu	Ala	Gln	Gly	Val	Lys	Arg	Ile	
			10					15						20		
tat	ggg	ttg	gtg	ggg	gac	agc	ctt	aat	ccg	atc	gtg	gat	gct	gtc	cgc	211
Tyr	Gly	Leu	Val	Gly	Asp	Ser	Leu	Asn	Pro	Ile	Val	Asp	Ala	Val	Arg	
		25						30					35			
caa	tca	gat	att	gag	tgg	gtg	cac	gtt	cga	aat	gag	gaa	gcg	gcg	gcg	259
Gln	Ser	Asp	Ile	Glu	Trp	Val	His	Val	Arg	Asn	Glu	Glu	Ala	Ala	Ala	
		40					45					50				
ttt	gca	gcc	ggg	gcg	gaa	tcg	ttg	atc	act	ggg	gag	ctg	gca	gta	tgt	307
Phe	Ala	Ala	Gly	Ala	Glu	Ser	Leu	Ile	Thr	Gly	Glu	Leu	Ala	Val	Cys	
	55					60					65					
gct	gct	tct	tgt	ggg	cct	gga	aac	aca	cac	ctg	att	cag	ggg	ctt	tat	355
Ala	Ala	Ser	Cys	Gly	Pro	Gly	Asn	Thr	His	Leu	Ile	Gln	Gly	Leu	Tyr	

70	75	80	85	
gat tcg cat cga aat ggt gcg aag gtg ttg gcc atc gct agc cat att				403
Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala Ile Ala Ser His Ile	90	95	100	
ccg agt gcc cag att ggt tcg acg ttc ttc cag gaa acg cat ccg gag				451
Pro Ser Ala Gln Ile Gly Ser Thr Phe Phe Gln Glu Thr His Pro Glu	105	110	115	
att ttg ttt aag gaa tgc tct ggt tac tgc gag atg gtg aat ggt ggt				499
Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu Met Val Asn Gly Gly	120	125	130	
gag cag ggt gaa cgc att ttg cat cac gcg att cag tcc acc atg gcg				547
Glu Gln Gly Glu Arg Ile Leu His His Ala Ile Gln Ser Thr Met Ala	135	140	145	
ggt aaa ggt gtg tcg gtg gta gtg att cct ggt gat atc gct aag gaa				595
Gly Lys Gly Val Ser Val Val Val Ile Pro Gly Asp Ile Ala Lys Glu	150	155	160	165
gac gca ggt gac ggt act tat tcc aat tcc act att tct tct ggc act				643
Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr Ile Ser Ser Gly Thr	170	175	180	
cct gtg gtg ttc ccg gat cct act gag gct gca gcg ctg gtg gag gcg				691
Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala Ala Leu Val Glu Ala	185	190	195	
att aac aac gct aag tct gtc act ttg ttc tgc ggt gcg ggc gtg aag				739
Ile Asn Asn Ala Lys Ser Val Thr Leu Phe Cys Gly Ala Gly Val Lys	200	205	210	
aat gct cgc gcg cag gtg ttg gag ttg gcg gag aag att aaa tca ccg				787
Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu Lys Ile Lys Ser Pro	215	220	225	
atc ggg cat gcg ctg ggt ggt aag cag tac atc cag cat gag aat ccg				835
Ile Gly His Ala Leu Gly Gly Lys Gln Tyr Ile Gln His Glu Asn Pro	230	235	240	245
ttt gag gtc ggc atg tct ggc ctg ctt ggt tac ggc gcc tgc gtg gat				883
Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr Gly Ala Cys Val Asp	250	255	260	
gcg tcc aat gag gcg gat ctg ctg att cta ttg ggt acg gat ttc cct				931
Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu Gly Thr Asp Phe Pro	265	270	275	
tat tct gat ttc ctt cct aaa gac aac gtt gcc cag gtg gat atc aac				979
Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala Gln Val Asp Ile Asn	280	285	290	
ggt gcg cac att ggt cga cgt acc acg gtg aag tat ccg gtg acc ggt				1027
Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys Tyr Pro Val Thr Gly	295	300	305	
gat gtt gct gca aca atc gaa aat att ttg cct cat gtg aag gaa aaa				1075
Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro His Val Lys Glu Lys	310	315	320	325

aca gat cgt tcc ttc ctt gat cgg atg ctc aag gca cac gag cgt aag	1123
Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys Ala His Glu Arg Lys	
330 335 340	
ttg agc tcg gtg gta gag acg tac aca cat aac gtc gag aag cat gtg	1171
Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn Val Glu Lys His Val	
345 350 355	
cct att cac cct gaa tac gtt gcc tct att ttg aac gag ctg gcg gat	1219
Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu Asn Glu Leu Ala Asp	
360 365 370	
aag gat gcg gtg ttt act gtg gat acc ggc atg tgc aat gtg tgg cat	1267
Lys Asp Ala Val Phe Thr Val Asp Thr Gly Met Cys Asn Val Trp His	
375 380 385	
gcg agg tac atc gag aat ccg gag gga acg cgc gac ttt gtg ggt tca	1315
Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg Asp Phe Val Gly Ser	
390 395 400 405	
ttc cgc cac ggc acg atg gct aat gcg ttg cct cat gcg att ggt gcg	1363
Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro His Ala Ile Gly Ala	
410 415 420	
caa agt gtt gat cga aac cgc cag gtg atc gcg atg tgt ggc gat ggt	1411
Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala Met Cys Gly Asp Gly	
425 430 435	
ggt ttg ggc atg ctg ctg ggt gag ctt ctg acc gtt aag ctg cac caa	1459
Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr Val Lys Leu His Gln	
440 445 450	
ctt ccg ctg aag gct gtg gtg ttt aac aac agt tct ttg ggc atg gtg	1507
Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser Ser Leu Gly Met Val	
455 460 465	
aag ttg gag atg ctc gtg gag gga cag cca gaa ttt ggt act gac cat	1555
Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu Phe Gly Thr Asp His	
470 475 480 485	
gag gaa gtg aat ttc gca gag att gcg gcg gct gcg ggt atc aaa tcg	1603
Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala Gly Ile Lys Ser	
490 495 500	
gta cgc atc acc gat ccg aag aaa gtt cgc gag cag cta gct gag gca	1651
Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu Gln Leu Ala Glu Ala	
505 510 515	
ttg gca tat cct gga cct gta ctg atc gat atc gtc acg gat cct aat	1699
Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile Val Thr Asp Pro Asn	
520 525 530	
gcg ctg tcg atc cca cca acc atc acg tgg gaa cag gtc atg gga ttc	1747
Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu Gln Val Met Gly Phe	
535 540 545	
agc aag gcg gcc acc cga acc gtc ttt ggt gga gga gta gga gcg atg	1795
Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly Gly Val Gly Ala Met	
550 555 560 565	

atc gat ctg gcc cgt tgc aac ata agg aat att cct act cca 1837
 Ile Asp Leu Ala Arg Ser Asn Ile Arg Asn Ile Pro Thr Pro
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<211> 579

<212> PRT

<213> Corynebacterium glutamicum

<400> 86

Met Ala His Ser Tyr Ala Glu Gln Leu Ile Asp Thr Leu Glu Ala Gln
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Gly Val Lys Arg Ile Tyr Gly Leu Val Gly Asp Ser Leu Asn Pro Ile
 20 25 30

Val Asp Ala Val Arg Gln Ser Asp Ile Glu Trp Val His Val Arg Asn
 35 40 45

Glu Glu Ala Ala Ala Phe Ala Ala Gly Ala Glu Ser Leu Ile Thr Gly
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Ile Gln Gly Leu Tyr Asp Ser His Arg Asn Gly Ala Lys Val Leu Ala
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Glu Thr His Pro Glu Ile Leu Phe Lys Glu Cys Ser Gly Tyr Cys Glu
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Gln Ser Thr Met Ala Gly Lys Gly Val Ser Val Val Val Ile Pro Gly
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Asp Ile Ala Lys Glu Asp Ala Gly Asp Gly Thr Tyr Ser Asn Ser Thr
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Ile Ser Ser Gly Thr Pro Val Val Phe Pro Asp Pro Thr Glu Ala Ala
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Gly Ala Gly Val Lys Asn Ala Arg Ala Gln Val Leu Glu Leu Ala Glu
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Gln His Glu Asn Pro Phe Glu Val Gly Met Ser Gly Leu Leu Gly Tyr
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Gly Ala Cys Val Asp Ala Ser Asn Glu Ala Asp Leu Leu Ile Leu Leu
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 Gly Thr Asp Phe Pro Tyr Ser Asp Phe Leu Pro Lys Asp Asn Val Ala
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 Gln Val Asp Ile Asn Gly Ala His Ile Gly Arg Arg Thr Thr Val Lys
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 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
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 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
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 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
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 His Ala Ile Gly Ala Gln Ser Val Asp Arg Asn Arg Gln Val Ile Ala
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 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
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 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
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 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
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 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
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 Gln Val Met Gly Phe Ser Lys Ala Ala Thr Arg Thr Val Phe Gly Gly
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 Tyr Pro Val Thr Gly Asp Val Ala Ala Thr Ile Glu Asn Ile Leu Pro
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 His Val Lys Glu Lys Thr Asp Arg Ser Phe Leu Asp Arg Met Leu Lys
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 Ala His Glu Arg Lys Leu Ser Ser Val Val Glu Thr Tyr Thr His Asn
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 Val Glu Lys His Val Pro Ile His Pro Glu Tyr Val Ala Ser Ile Leu
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 Cys Asn Val Trp His Ala Arg Tyr Ile Glu Asn Pro Glu Gly Thr Arg
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 Asp Phe Val Gly Ser Phe Arg His Gly Thr Met Ala Asn Ala Leu Pro
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 Met Cys Gly Asp Gly Gly Leu Gly Met Leu Leu Gly Glu Leu Leu Thr
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 Val Lys Leu His Gln Leu Pro Leu Lys Ala Val Val Phe Asn Asn Ser
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 Ser Leu Gly Met Val Lys Leu Glu Met Leu Val Glu Gly Gln Pro Glu
 195 200 205
 Phe Gly Thr Asp His Glu Glu Val Asn Phe Ala Glu Ile Ala Ala Ala
 210 215 220
 Ala Gly Ile Lys Ser Val Arg Ile Thr Asp Pro Lys Lys Val Arg Glu
 225 230 235 240
 Gln Leu Ala Glu Ala Leu Ala Tyr Pro Gly Pro Val Leu Ile Asp Ile
 245 250 255

Val Thr Asp Pro Asn Ala Leu Ser Ile Pro Pro Thr Ile Thr Trp Glu
 260 265 270

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gtc gag acc tac gac cca tcc ttt gcg tac gag atc gca cac ctg gtt 259
 Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu Ile Ala His Leu Val
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cac cgt ggc atc gac cgc atg tac ggc cca ggc aag ggt gaa gat gtt 307
 His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly Lys Gly Glu Asp Val
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 Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile
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 Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys
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Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
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Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
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Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
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 Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
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 Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
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 Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
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 Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
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 Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
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 Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
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 Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
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 Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
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 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu

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Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
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cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct 289
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Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
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Gly	Pro	Tyr	Val	Ala	Val	Ser	Asp	Phe	Ser	Thr	Asp	Leu	Pro	Asn	Gln	
185				190				195								
atc	cgt	gaa	tgg	gtc	cca	ggc	gac	tac	acc	gtt	ctc	ggt	gca	gat	ggc	739
Ile	Arg	Glu	Trp	Val	Pro	Gly	Asp	Tyr	Thr	Val	Leu	Gly	Ala	Asp	Gly	
200				205				210								
ttc	ggt	ttc	tct	gat	acc	cgc	cca	gct	gct	cgt	cgc	ttc	ttc	aac	atc	787
Phe	Gly	Phe	Ser	Asp	Thr	Arg	Pro	Ala	Ala	Arg	Arg	Phe	Phe	Asn	Ile	
215				220				225								
gac	gct	gag	tcc	att	gtt	gtt	gca	gtg	ctg	aac	tcc	ctg	gca	cgc	gaa	835
Asp	Ala	Glu	Ser	Ile	Val	Val	Ala	Val	Leu	Asn	Ser	Leu	Ala	Arg	Glu	
230				235				240				245				
ggc	aag	atc	gac	gtc	tcc	gtt	gct	g								

ttg gat gat cct acg agt gtt tcc gta gat cca aac gct cct gag gaa 931
 Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
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taaatcacct caagggacag ata 954

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Ser Thr Asn Glu Gly Val Glu Thr Tyr Asp Pro Ser Phe Ala Tyr Glu
 35 40 45

Ile Ala His Leu Val His Arg Gly Ile Asp Arg Met Tyr Gly Pro Gly
 50 55 60

Lys Gly Glu Asp Val Ile Tyr Tyr Ile Thr Ile Tyr Asn Glu Pro Thr
 65 70 75 80

Pro Gln Pro Ala Glu Pro Glu Gly Leu Asp Val Glu Gly Leu His Lys
 85 90 95

Gly Ile Tyr Leu Tyr Ser Arg Gly Glu Gly Thr Gly His Glu Ala Asn
 100 105 110

Ile Leu Ala Ser Gly Val Gly Met Gln Trp Ala Leu Lys Ala Ala Ser
 115 120 125

Ile Leu Glu Ala Asp Tyr Gly Val Arg Ala Asn Ile Tyr Ser Ala Thr
 130 135 140

Ser Trp Val Asn Leu Ala Arg Asp Gly Ala Ala Arg Asn Lys Ala Gln
 145 150 155 160

Leu Arg Asn Pro Gly Ala Asp Ala Gly Glu Ala Phe Val Thr Thr Gln
 165 170 175

Leu Lys Gln Thr Ser Gly Pro Tyr Val Ala Val Ser Asp Phe Ser Thr
 180 185 190

Asp Leu Pro Asn Gln Ile Arg Glu Trp Val Pro Gly Asp Tyr Thr Val
 195 200 205

Leu Gly Ala Asp Gly Phe Gly Phe Ser Asp Thr Arg Pro Ala Ala Arg
 210 215 220

Arg Phe Phe Asn Ile Asp Ala Glu Ser Ile Val Val Ala Val Leu Asn
 225 230 235 240

Ser Leu Ala Arg Glu Gly Lys Ile Asp Val Ser Val Ala Ala Gln Ala
 245 250 255

Ala Glu Lys Phe Lys Leu Asp Asp Pro Thr Ser Val Ser Val Asp Pro
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Asn Ala Pro Glu Glu
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<222> (101)..(508)

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 Met Ala Asp Gln Ala
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aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65

cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85

cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100

cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115

gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
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ggc gca gcc 508
 Gly Ala Ala
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 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
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 Met Ala Asp Gln Ala
 1 5
 aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20
 gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35
 gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259

Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50
 cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65
 cgc gta tct ctt ccc cca atg acg tca acc gac tac gtc aac acc att 355
 Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp Tyr Val Asn Thr Ile
 70 75 80 85
 cca acc tct atg gaa cct gaa ttc cca ggc gat gag gaa atg gag aag 403
 Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp Glu Glu Met Glu Lys
 90 95 100
 cgt tac cgt cgt tgg att cgc tgg aac gca gcc atc atg gtt cac cgc 451
 Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala Ile Met Val His Arg
 105 110 115
 gct cag cga cca ggc atc ggc gtc ggc gga cac att tcc act tac gca 499
 Ala Gln Arg Pro Gly Ile Gly Val Gly Gly His Ile Ser Thr Tyr Ala
 120 125 130
 ggc gca gcc 508
 Gly Ala Ala
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<210> 100

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<213> Corynebacterium glutamicum

<400> 100

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 Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45
 Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60
 Arg Ala Ser Ala Lys Arg Val Ser Leu Pro Pro Met Thr Ser Thr Asp
 65 70 75 80
 Tyr Val Asn Thr Ile Pro Thr Ser Met Glu Pro Glu Phe Pro Gly Asp
 85 90 95
 Glu Glu Met Glu Lys Arg Tyr Arg Arg Trp Ile Arg Trp Asn Ala Ala
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 Ile Ser Thr Tyr Ala Gly Ala Ala
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 Pro Ser Tyr Pro His Pro His Gly Met Lys Asp Phe Trp Glu Phe Pro
 20 25 30
 act gtg tcc atg ggt ctt ggc cca atg gat gcc att tac cag gca cgt 144
 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 ttc aac cgc tac ctc gaa aac cgt ggc atc aag gac acc tct gac cag 192
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca 240
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc 288
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt 336
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110
 aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc 384
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125
 tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg 432
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc 480
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt 528
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac 576
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac 624

Met	Thr	Asp	Glu	Glu	Ile	Trp	Lys	Leu	Pro	Arg	Gly	Gly	His	Asp	Tyr	
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cgc	aag	gtt	tac	gca	gcc	tac	aag	cga	gct	ctt	gag	acc	aag	gat	cgc	672
Arg	Lys	Val	Tyr	Ala	Ala	Tyr	Lys	Arg	Ala	Leu	Glu	Thr	Lys	Asp	Arg	
	210					215					220					
cca	acc	gtc	atc	ctt	gct	cac	acc	att	aag	ggc	tac	gga	ctc	ggc	cac	720
Pro	Thr	Val	Ile	Leu	Ala	His	Thr	Ile	Lys	Gly	Tyr	Gly	Leu	Gly	His	
225					230					235					240	
aac	ttc	gaa	ggc	cgt	aac	gca	acc	cac	cag	atg	aag	aag	ctg	acg	ctt	768
Asn	Phe	Glu	Gly	Arg	Asn	Ala	Thr	His	Gln	Met	Lys	Lys	Leu	Thr	Leu	
				245					250					255		
gat	gat	ctg	aag	ttg	ttc	cgc	gac	aag	cag	ggc	atc	cca	atc	acc	gat	816
Asp	Asp	Leu	Lys	Leu	Phe	Arg	Asp	Lys	Gln	Gly	Ile	Pro	Ile	Thr	Asp	
		260						265					270			
gag	cag	ctg	gag	aag	gat	cct	tac	ctt	cct	cct	tac	tac	cac	cca	ggt	864
Glu	Gln	Leu	Glu	Lys	Asp	Pro	Tyr	Leu	Pro	Pro	Tyr	Tyr	His	Pro	Gly	
		275					280					285				
gaa	gac	gct	cct	gaa	atc	aag	tac	atg	aag	gaa	cgt	cgc	gca	gcg	ctc	912
Glu	Asp	Ala	Pro	Glu	Ile	Lys	Tyr	Met	Lys	Glu	Arg	Arg	Ala	Ala	Leu	
	290					295					300					
ggt	ggc	tac	ctg	cca	gag	cgt	cgt	gag	aac	tac	gat	cca	att	cag	gtt	960
Gly	Gly	Tyr	Leu	Pro	Glu	Arg	Arg	Glu	Asn	Tyr	Asp	Pro	Ile	Gln	Val	
305					310					315					320	
cca	cca	ctg	gat	aag	ctt	cgc	tct	gtc	cgt	aag	ggc	tcc	ggc	aag	cag	1008
Pro	Pro	Leu	Asp	Lys	Leu	Arg	Ser	Val	Arg	Lys	Gly	Ser	Gly	Lys	Gln	
				325					330					335		
cag	atc	gct	acc	acc	atg	gcg	act	gtt	cgt	acc	ttc	aag	gaa	ctg	atg	1056
Gln	Ile	Ala	Thr	Thr	Met	Ala	Thr	Val	Arg	Thr	Phe	Lys	Glu	Leu	Met	
			340					345					350			
cgc	gat	aag	ggc	ttg	gct	gat	cgc	ctt	gtc	cca	atc	att	cct	gat	gag	1104
Arg	Asp	Lys	Gly	Leu	Ala	Asp	Arg	Leu	Val	Pro	Ile	Ile	Pro	Asp	Glu	
		355					360					365				
gca	cgt	acc	ttc	ggt	ctt	gac	tct	tgg	ttc	cca	acc	ttg	aag	atc	tac	1152
Ala	Arg	Thr	Phe	Gly	Leu	Asp	Ser	Trp	Phe	Pro	Thr	Leu	Lys	Ile	Tyr	
	370					375					380					
aac	ccg	cac	ggt	cag	aac	tac	gtg	cct	gtt	gac	cac	gac	ctg	atg	ctc	1200
Asn	Pro	His	Gly	Gln	Asn	Tyr	Val	Pro	Val	Asp	His	Asp	Leu	Met	Leu	
385					390					395					400	
tcc	tac	cgt	gag	gca	cct	gaa	gga	cag	atc	ctg	cac	gaa	ggc	atc	aac	1248
Ser	Tyr	Arg	Glu	Ala	Pro	Glu	Gly	Gln	Ile	Leu	His	Glu	Gly	Ile	Asn	
				405					410					415		
gag	gct	ggt	tcc	gtg	gca	tcg	ttc	atc	gct	gcg	ggt	acc	tcc	tac	gcc	1296
Glu	Ala	Gly	Ser	Val	Ala	Ser	Phe	Ile	Ala	Ala	Gly	Thr	Ser	Tyr	Ala	
			420					425					430			
acc	cac	ggc	aag	gcc	atg	att	ccg	ctg	tac	atc	ttc	tac	tcg	atg	ttc	1344
Thr	His	Gly	Lys	Ala	Met	Ile	Pro	Leu	Tyr	Ile	Phe	Tyr	Ser	Met	Phe	

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 Gly Ile Pro Ala His Arg
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<210> 102
 <211> 454
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 102
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 Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45
 Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60
 His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80
 Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95
 Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
 100 105 110
 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255

Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415
 Glu Ala Gly Ser Val Ala Ser Phe Ile Ala Ala Gly Thr Ser Tyr Ala
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 Thr His Gly Lys Ala Met Ile Pro Leu Tyr Ile Phe Tyr Ser Met Phe
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 Gly Ile Pro Ala His Arg
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<210> 103

<211> 1287

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1287)

<223> FRXA02897

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ccg	tcc	tac	cct	cac	cca	cac	ggt	atg	aag	gac	ttc	tgg	gag	ttc	cca	96
Pro	Ser	Tyr	Pro	His	Pro	His	Gly	Met	Lys	Asp	Phe	Trp	Glu	Phe	Pro	
			20					25					30			
act	gtg	tcc	atg	ggt	ctt	ggc	cca	atg	gat	gcc	att	tac	cag	gca	cgt	144
Thr	Val	Ser	Met	Gly	Leu	Gly	Pro	Met	Asp	Ala	Ile	Tyr	Gln	Ala	Arg	

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Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln			
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cac gtc tgg gcc ttc ctt ggc gac ggc gaa atg gac gag cca gaa tca			240
His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser			
65	70	75	80
cgt ggt ctc atc cag cag gct gca ctg aac aac ctg gac aac ctg acc			288
Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr			
	85	90	95
ttc gtg gtt aac tgc aac ctg cag cgt ctc gac gga cct gtc cgc ggt			336
Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly			
	100	105	110
aac acc aag atc atc cag gaa ctc gag tcc ttc ttc cgt ggc gca ggc			384
Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly			
	115	120	125
tgg tct gtg atc aag gtt gtt tgg ggt cgc gag tgg gat gaa ctt ctg			432
Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu			
	130	135	140
gag aag gac cag gat ggt gca ctt gtt gag atc atg aac aac acc tcc			480
Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser			
145	150	155	160
gat ggt gac tac cag acc ttc aag gct aac gac ggc gca tat gtt cgt			528
Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg			
	165	170	175
gag cac ttc ttc gga cgt gac cca cgc acc gca aag ctc gtt gag aac			576
Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn			
	180	185	190
atg acc gac gaa gaa atc tgg aag ctt cca cgt ggc ggc cac gat tac			624
Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr			
	195	200	205
cgc aag gtt tac gca gcc tac aag cga gct ctt gag acc aag gat cgc			672
Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg			
	210	215	220
cca acc gtc atc ctt gct cac acc att aag ggc tac gga ctc ggc cac			720
Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His			
225	230	235	240
aac ttc gaa ggc cgt aac gca acc cac cag atg aag aag ctg acg ctt			768
Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu			
	245	250	255
gat gat ctg aag ttg ttc cgc gac aag cag ggc atc cca atc acc gat			816
Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp			
	260	265	270
gag cag ctg gag aag gat cct tac ctt cct cct tac tac cac cca ggt			864
Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly			
	275	280	285

gaa gac gct cct gaa atc aag tac atg aag gaa cgt cgc gca gcg ctc 912
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300

ggt ggc tac ctg cca gag cgt cgt gag aac tac gat cca att cag gtt 960
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320

cca cca ctg gat aag ctt cgc tct gtc cgt aag ggc tcc ggc aag cag 1008
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335

cag atc gct acc acc atg gcg act gtt cgt acc ttc aag gaa ctg atg 1056
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350

cgc gat aag ggc ttg gct gat cgc ctt gtc cca atc att cct gat gag 1104
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365

gca cgt acc ttc ggt ctt gac tct tgg ttc cca acc ttg aag atc tac 1152
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380

aac ccg cac ggt cag aac tac gtg cct gtt gac cac gac ctg atg ctc 1200
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
 385 390 395 400

tcc tac cgt gag gca cct gaa gga cag atc ctg cac gaa ggc atc aac 1248
 Ser Tyr Arg Glu Ala Pro Glu Gly Gln Ile Leu His Glu Gly Ile Asn
 405 410 415

gag gct ggt tcc gtg gca tcg ttc atc gct gcg ggt acc 1287
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<210> 104

<211> 429

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 104

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 20 25 30

Thr Val Ser Met Gly Leu Gly Pro Met Asp Ala Ile Tyr Gln Ala Arg
 35 40 45

Phe Asn Arg Tyr Leu Glu Asn Arg Gly Ile Lys Asp Thr Ser Asp Gln
 50 55 60

His Val Trp Ala Phe Leu Gly Asp Gly Glu Met Asp Glu Pro Glu Ser
 65 70 75 80

Arg Gly Leu Ile Gln Gln Ala Ala Leu Asn Asn Leu Asp Asn Leu Thr
 85 90 95

Phe Val Val Asn Cys Asn Leu Gln Arg Leu Asp Gly Pro Val Arg Gly
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 Asn Thr Lys Ile Ile Gln Glu Leu Glu Ser Phe Phe Arg Gly Ala Gly
 115 120 125
 Trp Ser Val Ile Lys Val Val Trp Gly Arg Glu Trp Asp Glu Leu Leu
 130 135 140
 Glu Lys Asp Gln Asp Gly Ala Leu Val Glu Ile Met Asn Asn Thr Ser
 145 150 155 160
 Asp Gly Asp Tyr Gln Thr Phe Lys Ala Asn Asp Gly Ala Tyr Val Arg
 165 170 175
 Glu His Phe Phe Gly Arg Asp Pro Arg Thr Ala Lys Leu Val Glu Asn
 180 185 190
 Met Thr Asp Glu Glu Ile Trp Lys Leu Pro Arg Gly Gly His Asp Tyr
 195 200 205
 Arg Lys Val Tyr Ala Ala Tyr Lys Arg Ala Leu Glu Thr Lys Asp Arg
 210 215 220
 Pro Thr Val Ile Leu Ala His Thr Ile Lys Gly Tyr Gly Leu Gly His
 225 230 235 240
 Asn Phe Glu Gly Arg Asn Ala Thr His Gln Met Lys Lys Leu Thr Leu
 245 250 255
 Asp Asp Leu Lys Leu Phe Arg Asp Lys Gln Gly Ile Pro Ile Thr Asp
 260 265 270
 Glu Gln Leu Glu Lys Asp Pro Tyr Leu Pro Pro Tyr Tyr His Pro Gly
 275 280 285
 Glu Asp Ala Pro Glu Ile Lys Tyr Met Lys Glu Arg Arg Ala Ala Leu
 290 295 300
 Gly Gly Tyr Leu Pro Glu Arg Arg Glu Asn Tyr Asp Pro Ile Gln Val
 305 310 315 320
 Pro Pro Leu Asp Lys Leu Arg Ser Val Arg Lys Gly Ser Gly Lys Gln
 325 330 335
 Gln Ile Ala Thr Thr Met Ala Thr Val Arg Thr Phe Lys Glu Leu Met
 340 345 350
 Arg Asp Lys Gly Leu Ala Asp Arg Leu Val Pro Ile Ile Pro Asp Glu
 355 360 365
 Ala Arg Thr Phe Gly Leu Asp Ser Trp Phe Pro Thr Leu Lys Ile Tyr
 370 375 380
 Asn Pro His Gly Gln Asn Tyr Val Pro Val Asp His Asp Leu Met Leu
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 <222> (88)..(1110)
 <223> RXN03083

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 Met Ala Lys Arg Ile Val Ile Ile Gly
 1 5
 ggt gga cct gca ggc tat gaa gcc gca ctc gca ggc gct aaa tac ggt 162
 Gly Gly Pro Ala Gly Tyr Glu Ala Ala Leu Ala Gly Ala Lys Tyr Gly
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 gca gaa gtt acc gtt att gaa gat gtc gga gtt ggc gga tcc gca gtc 210
 Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
 30 35 40
 acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 258
 Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
 45 50 55
 aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 306
 Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
 60 65 70
 gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 354
 Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
 75 80 85
 ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 402
 Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser
 90 95 100 105
 gat gtc cgc atg att aac ggt gtg ggc cgc ttt gat gat tac aac acc 450
 Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr
 110 115 120
 aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa 498
 Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu
 125 130 135
 gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc 546
 Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro
 140 145 150
 cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg 594
 Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp
 155 160 165


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cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt 642
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val
170 175 180 185

ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc 690
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu
190 195 200

ggc gtc aaa gtc acc atg gtg gca tcc cgt gac cgc att ttg cct cac 738
Gly Val Lys Val Thr Met Val Ala Ser Arg Asp Arg Ile Leu Pro His
205 210 215

gat gac gca gat gcc gca gac gtg ctg gaa acc gtt ctg gct gag cgc 786
Asp Asp Ala Asp Ala Ala Asp Val Leu Glu Thr Val Leu Ala Glu Arg
220 225 230

gga gta tcc ctg gaa aag cat gcc cgc gtg gag tct gtc acc cgc acc 834
Gly Val Ser Leu Glu Lys His Ala Arg Val Glu Ser Val Thr Arg Thr
235 240 245

gaa gac ggt ggc gtg tgt gtt cgc act gct gac gga cga gaa atc tac 882
Glu Asp Gly Gly Val Cys Val Arg Thr Ala Asp Gly Arg Glu Ile Tyr
250 255 260 265

ggt tct cac gcg ttg atg act gtt ggt tcc att cca aac acg gca gat 930
Gly Ser His Ala Leu Met Thr Val Gly Ser Ile Pro Asn Thr Ala Asp
270 275 280

ctt ggc ctg gag aac atc ggt gtt gag ctg gca cca tcc ggc cat atc 978
Leu Gly Leu Glu Asn Ile Gly Val Glu Leu Ala Pro Ser Gly His Ile
285 290 295

aag gtt gac cgg tct ccc gca cca aca tcc ccg gtg tgt acg cag cag 1026
Lys Val Asp Arg Ser Pro Ala Pro Thr Ser Pro Val Cys Thr Gln Gln
300 305 310

gtg act gta ctg acc tat tcc cac tgg cgt ccg ttg cag cga tgc agg 1074
Val Thr Val Leu Thr Tyr Ser His Trp Arg Pro Leu Gln Arg Cys Arg
315 320 325

gcc gta tgc cca tgt atc acg cac tgc gtg aag gcg tgagccccat 1120
Ala Val Ser Pro Cys Ile Thr His Ser Val Lys Ala
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<210> 106

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 106

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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
35 40 45

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Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
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 Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80
 Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95
 Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110
 Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
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 Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140
 Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160
 Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175
 Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190
 Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205
 Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220
 Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His
 225 230 235 240
 Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
 245 250 255
 Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
 260 265 270
 Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
 275 280 285
 Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Ser Pro Ala
 290 295 300
 Pro Thr Ser Pro Val Cys Thr Gln Gln Val Thr Val Leu Thr Tyr Ser
 305 310 315 320
 His Trp Arg Pro Leu Gln Arg Cys Arg Ala Val Ser Pro Cys Ile Thr
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 His Ser Val Lys Ala
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<210> 107

<211> 1518

<212> DNA

<213> Corynebacterium glutamicum

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<222> (89)..(1495)

<223> FRXA02853

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Met Ala Lys Arg Ile Val Ile Ile Gly

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Ala Glu Val Thr Val Ile Glu Asp Val Gly Val Gly Gly Ser Ala Val
30 35 40acc atg gac tgt gta cct tca aag tcc ttc atc gct ggt acc ggt atc 259
Thr Met Asp Cys Val Pro Ser Lys Ser Phe Ile Ala Gly Thr Gly Ile
45 50 55aaa acc gac ctc cga cgt gct gat gac atg gga ctt aac cgt ggg ctt 307
Lys Thr Asp Leu Arg Arg Ala Asp Asp Met Gly Leu Asn Arg Gly Leu
60 65 70gga aaa gca cac cta gaa atc gat gca ctg aac atc cgt gtg aag gac 355
Gly Lys Ala His Leu Glu Ile Asp Ala Leu Asn Ile Arg Val Lys Asp
75 80 85ctt gcg aaa gca cag tcc gaa gat atc ttg ggc cag ctg cag cgc tca 403
Leu Ala Lys Ala Gln Ser Glu Asp Ile Leu Gly Gln Leu Gln Arg Ser
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Asp Val Arg Met Ile Asn Gly Val Gly Arg Phe Asp Asp Tyr Asn Thr
110 115 120aag caa acc acc cac tac att aaa gtc acc cac agc gat ggc tcc gaa 499
Lys Gln Thr Thr His Tyr Ile Lys Val Thr His Ser Asp Gly Ser Glu
125 130 135gaa acc gtt gag tgc gat ctg gtg ctg gtt gca act ggt gca acc ccc 547
Glu Thr Val Glu Cys Asp Leu Val Leu Val Ala Thr Gly Ala Thr Pro
140 145 150cgc att ctt aaa ggt gca gag cca gac ggc gag cgc atc ttg acc tgg 595
Arg Ile Leu Lys Gly Ala Glu Pro Asp Gly Glu Arg Ile Leu Thr Trp
155 160 165cgt cag gtc tac gac att gaa gaa ctc ccc acc cac ctt atc gtg gtt 643
Arg Gln Val Tyr Asp Ile Glu Glu Leu Pro Thr His Leu Ile Val Val
170 175 180 185ggt tcc ggt gtg acc ggt gcg gaa ttt gtc tct gcg ttt gct gaa ctc 691
Gly Ser Gly Val Thr Gly Ala Glu Phe Val Ser Ala Phe Ala Glu Leu

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Gly	Val	Lys	Val	Thr	Met	Val	Ala	Ser	Arg	Asp	Arg	Ile	Leu	Pro	His						
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gat	gac	gca	gat	gcc	gca	gac	gtg	ctg	gaa	acc	gtt	ctg	gct	gag	cgc	787					
Asp	Asp	Ala	Asp	Ala	Ala	Asp	Val	Leu	Glu	Thr	Val	Leu	Ala	Glu	Arg						
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Gly	Val	Ser	Leu	Glu	Lys	His	Ala	Arg	Val	Glu	Ser	Val	Thr	Arg	Thr						
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Glu	Asp	Gly	Gly	Val	Cys	Val	Arg	Thr	Ala	Asp	Gly	Arg	Glu	Ile	Tyr						
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ggt	tct	cac	gcg	ttg	atg	act	gtt	ggt	tcc	att	cca	aac	acg	gca	gat	931					
Gly	Ser	His	Ala	Leu	Met	Thr	Val	Gly	Ser	Ile	Pro	Asn	Thr	Ala	Asp						
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ctt	ggc	ctg	gag	aac	atc	ggt	gtt	gag	ctg	gca	cca	tcc	ggc	cat	atc	979					
Leu	Gly	Leu	Glu	Asn	Ile	Gly	Val	Glu	Leu	Ala	Pro	Ser	Gly	His	Ile						
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Lys	Val	Asp	Arg	Val	Ser	Arg	Thr	Asn	Ile	Pro	Gly	Val	Tyr	Ala	Ala						
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ggt	gac	tgt	act	gac	cta	ttc	cca	ctg	gcg	tcc	gtt	gca	gcg	atg	cag	1075					
Gly	Asp	Cys	Thr	Asp	Leu	Phe	Pro	Leu	Ala	Ser	Val	Ala	Ala	Met	Gln						
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ggc	cgt	atc	gcc	atg	tat	cac	gca	ctc	ggt	gaa	ggc	gtg	agc	ccc	atc	1123					
Gly	Arg	Ile	Ala	Met	Tyr	His	Ala	Leu	Gly	Glu	Gly	Val	Ser	Pro	Ile						
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cgt	ttg	aag	act	gtt	gcc	acc	gca	gtg	ttt	acc	cgc	cca	gag	atc	gca	1171					
Arg	Leu	Lys	Thr	Val	Ala	Thr	Ala	Val	Phe	Thr	Arg	Pro	Glu	Ile	Ala						
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Ala	Val	Gly	Ile	Thr	His	Ala	Gln	Val	Asp	Ser	Gly	Glu	Val	Ser	Ala						
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cgc	gtg	att	gtg	ctt	cct	ttg	gct	act	aac	cca	cgc	gcc	aag	atg	cgt	1267					
Arg	Val	Ile	Val	Leu	Pro	Leu	Ala	Thr	Asn	Pro	Arg	Ala	Lys	Met	Arg						
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tcc	ctg	cgc	cac	ggt	ttt	gtg	aag	ctg	ttc	tgc	cgc	cgt	aac	tct	ggc	1315					
Ser	Leu	Arg	His	Gly	Phe	Val	Lys	Leu	Phe	Cys	Arg	Arg	Asn	Ser	Gly						
			395				400						405								
ctg	atc	atc	ggt	ggt	gtc	gtg	gtg	gca	ccg	acc	gcg	tct	gag	ctg	atc	1363					
Leu	Ile	Ile	Gly	Gly	Val	Val	Val	Ala	Pro	Thr	Ala	Ser	Glu	Leu	Ile						
			410				415						425								
cta	ccg	atc	gct	gtg	gca	gtg	acc	aac	cgt	ctg	aca	gtt	gct	gat	ctg	1411					
Leu	Pro	Ile	Ala	Val	Ala	Val	Thr	Asn	Arg	Leu	Thr	Val	Ala	Asp	Leu						
			430				435						440								

gct gat acc ttc gcg gtg tac cca tca ttg tca ggt tcg att act gaa 1459
 Ala Asp Thr Phe Ala Val Tyr Pro Ser Leu Ser Gly Ser Ile Thr Glu
 445 450 455

gca gca cgt cag ctg gtt caa cat gat gat cta ggc taatttttct 1505
 Ala Ala Arg Gln Leu Val Gln His Asp Asp Leu Gly
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<210> 108

<211> 469

<212> PRT

<213> Corynebacterium glutamicum

<400> 108

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Asp Val Gly Val Gly Gly Ser Ala Val Thr Met Asp Cys Val Pro Ser
 35 40 45

Lys Ser Phe Ile Ala Gly Thr Gly Ile Lys Thr Asp Leu Arg Arg Ala
 50 55 60

Asp Asp Met Gly Leu Asn Arg Gly Leu Gly Lys Ala His Leu Glu Ile
 65 70 75 80

Asp Ala Leu Asn Ile Arg Val Lys Asp Leu Ala Lys Ala Gln Ser Glu
 85 90 95

Asp Ile Leu Gly Gln Leu Gln Arg Ser Asp Val Arg Met Ile Asn Gly
 100 105 110

Val Gly Arg Phe Asp Asp Tyr Asn Thr Lys Gln Thr Thr His Tyr Ile
 115 120 125

Lys Val Thr His Ser Asp Gly Ser Glu Glu Thr Val Glu Cys Asp Leu
 130 135 140

Val Leu Val Ala Thr Gly Ala Thr Pro Arg Ile Leu Lys Gly Ala Glu
 145 150 155 160

Pro Asp Gly Glu Arg Ile Leu Thr Trp Arg Gln Val Tyr Asp Ile Glu
 165 170 175

Glu Leu Pro Thr His Leu Ile Val Val Gly Ser Gly Val Thr Gly Ala
 180 185 190

Glu Phe Val Ser Ala Phe Ala Glu Leu Gly Val Lys Val Thr Met Val
 195 200 205

Ala Ser Arg Asp Arg Ile Leu Pro His Asp Asp Ala Asp Ala Ala Asp
 210 215 220

Val Leu Glu Thr Val Leu Ala Glu Arg Gly Val Ser Leu Glu Lys His

225 230 235 240
 Ala Arg Val Glu Ser Val Thr Arg Thr Glu Asp Gly Gly Val Cys Val
 245 250 255
 Arg Thr Ala Asp Gly Arg Glu Ile Tyr Gly Ser His Ala Leu Met Thr
 260 265 270
 Val Gly Ser Ile Pro Asn Thr Ala Asp Leu Gly Leu Glu Asn Ile Gly
 275 280 285
 Val Glu Leu Ala Pro Ser Gly His Ile Lys Val Asp Arg Val Ser Arg
 290 295 300
 Thr Asn Ile Pro Gly Val Tyr Ala Ala Gly Asp Cys Thr Asp Leu Phe
 305 310 315 320
 Pro Leu Ala Ser Val Ala Ala Met Gln Gly Arg Ile Ala Met Tyr His
 325 330 335
 Ala Leu Gly Glu Gly Val Ser Pro Ile Arg Leu Lys Thr Val Ala Thr
 340 345 350
 Ala Val Phe Thr Arg Pro Glu Ile Ala Ala Val Gly Ile Thr His Ala
 355 360 365
 Gln Val Asp Ser Gly Glu Val Ser Ala Arg Val Ile Val Leu Pro Leu
 370 375 380
 Ala Thr Asn Pro Arg Ala Lys Met Arg Ser Leu Arg His Gly Phe Val
 385 390 395 400
 Lys Leu Phe Cys Arg Arg Asn Ser Gly Leu Ile Ile Gly Gly Val Val
 405 410 415
 Val Ala Pro Thr Ala Ser Glu Leu Ile Leu Pro Ile Ala Val Ala Val
 420 425 430
 Thr Asn Arg Leu Thr Val Ala Asp Leu Ala Asp Thr Phe Ala Val Tyr
 435 440 445
 Pro Ser Leu Ser Gly Ser Ile Thr Glu Ala Ala Arg Gln Leu Val Gln
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 His Asp Asp Leu Gly
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<210> 109

<211> 2895

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(2872)

<223> RXA02259

<400> 109

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	Val Phe Lys Val Val	
	1 5	
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Gly Glu Val Ile Ala Glu Gln Glu Gly Gln Glu Val Tyr Glu Leu Val		
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Glu Gln Ala Arg Leu Thr Ser Phe Asp Ile Ala Lys Gly Asn Ala Glu		
40 45 50		
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Met Asp Ser Leu Val Gln Val Phe Asp Gly Ile Thr Pro Ala Lys Ala		
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Thr Pro Ile Ala Arg Ala Phe Ser His Phe Ala Leu Leu Ala Asn Leu		
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gcg gaa gac ctc tac gat gaa gag ctt cgt gaa cag gct ctc gat gca	403	
Ala Glu Asp Leu Tyr Asp Glu Glu Leu Arg Glu Gln Ala Leu Asp Ala		
90 95 100		
ggc gac acc cct ccg gac agc act ctt gat gcc acc tgg ctg aaa ctc	451	
Gly Asp Thr Pro Pro Asp Ser Thr Leu Asp Ala Thr Trp Leu Lys Leu		
105 110 115		
aat gag ggc aat gtt ggc gca gaa gct gtg gcc gat gtg ctg cgc aat	499	
Asn Glu Gly Asn Val Gly Ala Glu Ala Val Ala Asp Val Leu Arg Asn		
120 125 130		
gct gag gtg gcg ccg gtt ctg act gcg cac cca act gag act cgc cgc	547	
Ala Glu Val Ala Pro Val Leu Thr Ala His Pro Thr Glu Thr Arg Arg		
135 140 145		
cgc act gtt ttt gat gcg caa aag tgg atc acc acc cac atg cgt gaa	595	
Arg Thr Val Phe Asp Ala Gln Lys Trp Ile Thr Thr His Met Arg Glu		
150 155 160 165		
cgc cac gct ttg cag tct gcg gag cct acc gct cgt acg caa agc aag	643	
Arg His Ala Leu Gln Ser Ala Glu Pro Thr Ala Arg Thr Gln Ser Lys		
170 175 180		
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Leu Asp Glu Ile Glu Lys Asn Ile Arg Arg Arg Ile Thr Ile Leu Trp		
185 190 195		
cag acc gcg ttg att cgt gtg gcc cgc cca cgt atc gag gac gag atc	739	
Gln Thr Ala Leu Ile Arg Val Ala Arg Pro Arg Ile Glu Asp Glu Ile		
200 205 210		
gaa gta ggg ctg cgc tac tac aag ctg agc ctt ttg gaa gag att cca	787	
Glu Val Gly Leu Arg Tyr Tyr Lys Leu Ser Leu Leu Glu Glu Ile Pro		
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cgt atc aac cgt gat gtg gct gtt gag ctt cgt gag cgt ttc ggc gag	835	

Arg 230	Ile	Asn	Arg	Asp	Val 235	Ala	Val	Glu	Leu	Arg 240	Glu	Arg	Phe	Gly	Glu 245	
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Gly	Val	Pro	Leu	Lys 250	Pro	Val	Val	Lys	Pro 255	Gly	Ser	Trp	Ile	Gly	Gly	
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Thr	His	Arg	Ala 280	Ala	Glu	Thr	Val	Leu 285	Lys	Tyr	Tyr	Ala	Arg	Gln	Leu	
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His	Ser	Leu	Glu	His	Glu	Ser	Leu	Ser	Asp	Arg	Met	Asn	Lys	Val		
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Thr	Pro	Gln	Leu	Leu	Ala	Leu	Ala	Asp	Ala	Gly	His	Asn	Asp	Val	Pro	
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Ser	Arg	Val	Asp	Glu	Pro	Tyr	Arg	Arg	Ala	Val	His	Gly	Val	Arg	Gly	
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cgt	atc	ctc	gcg	acg	acg	gcc	gag	ctg	atc	ggc	gag	gac	gcc	gtt	gag	1171
Arg	Ile	Leu	Ala	Thr	Thr	Ala	Glu	Leu	Ile	Gly	Glu	Asp	Ala	Val	Glu	
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Gly	Val	Trp	Phe	Lys	Val	Phe	Thr	Pro	Tyr	Ala	Ser	Pro	Glu	Glu	Phe	
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Val	Leu	Ile	Ala	Asp	Asp	Arg	Leu	Ser	Val	Leu	Ile	Ser	Ala	Ile	Glu	
390					395				400						405	
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Ser	Phe	Gly	Phe	Asn	Leu	Tyr	Ala	Leu	Asp	Leu	Arg	Gln	Asn	Ser	Glu	
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Ser	Tyr	Glu	Asp	Val	Leu	Thr	Glu	Leu	Phe	Glu	Arg	Ala	Gln	Val	Thr	
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gca	aac	tac	cg	gag	ctg	tct	gaa	gca	gag	aag	ctt	gag	gtg	ctg	ctg	1459
Ala	Asn	Tyr	Arg	Glu	Leu	Ser	Glu	Ala	Glu	Lys	Leu	Glu	Val	Leu	Leu	
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aag	gaa	ctg	cg	agc	cct	cgt	ccg	ctg	atc	ccg	cac	ggc	tca	gat	gaa	1507
Lys	Glu	Leu	Arg	Ser	Pro	Arg	Pro	Leu	Ile	Pro	His	Gly	Ser	Asp	Glu	
	455					460					465					
tac	agc	gag	gtc	acc	gac	cg	gag	ctc	ggc	atc	ttc	cg	acc	gcg	tcg	1555
Tyr	Ser	Glu	Val	Thr	Asp	Arg	Glu	Leu	Gly	Ile	Phe	Arg	Thr	Ala	Ser	

470	475	480	485	
gag gct gtt aag aaa ttc ggg cca cgg atg gtg cct cac tgc atc atc				1603
Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val Pro His Cys Ile Ile				
	490	495	500	
tcc atg gca tca tgc gtc acc gat gtg ctc gag ccg atg gtg ttg ctc				1651
Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu Pro Met Val Leu Leu				
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aag gaa ttc gga ctc atc gca gcc aac ggc gac aac cca cgc ggc acc				1699
Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp Asn Pro Arg Gly Thr				
	520	525	530	
gtc gat gtc atc cca ctg ttc gaa acc atc gaa gat ctc cag gcc ggc				1747
Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu Asp Leu Gln Ala Gly				
	535	540	545	
gcc gga atc ctc gac gaa ctg tgg aaa att gat ctc tac cgc aac tac				1795
Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp Leu Tyr Arg Asn Tyr				
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ctc ctg cag cgc gac aac gtc cag gaa gtc atg ctc ggt tac tcc gat				1843
Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met Leu Gly Tyr Ser Asp				
	570	575	580	
tcc aac aag gat ggc gga tat ttc tcc gca aac tgg gcg ctt tac gac				1891
Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn Trp Ala Leu Tyr Asp				
	585	590	595	
gcg gaa ctg cag ctc gtc gaa cta tgc cga tca gcc ggg gtc aag ctt				1939
Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser Ala Gly Val Lys Leu				
	600	605	610	
cgc ctg ttc cac ggc cgt ggt ggc acc gtc ggc cgc ggt ggc gga cct				1987
Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly Arg Gly Gly Gly Pro				
	615	620	625	
tcc tac gac gcg att ctt gcc cag ccc agg ggg gct gtc caa ggt tcc				2035
Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly Ala Val Gln Gly Ser				
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gtg cgc atc acc gag cag ggc gag atc atc tcc gct aag tac ggc aac				2083
Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser Ala Lys Tyr Gly Asn				
	650	655	660	
ccc gaa acc gcg cgc cga aac ctc gaa gcc ctg gtc tca gcc acg ctt				2131
Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu Val Ser Ala Thr Leu				
	665	670	675	
gag gca tgc ctt ctc gac gtc tcc gaa ctc acc gat cac caa cgc gcg				2179
Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr Asp His Gln Arg Ala				
	680	685	690	
tac gac atc atg agt gag atc tct gag ctc agc ttg aag aag tac gcc				2227
Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser Leu Lys Lys Tyr Ala				
	695	700	705	
tcc ttg gtg cac gag gat caa ggc ttc atc gat tac ttc acc cag tcc				2275
Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp Tyr Phe Thr Gln Ser				
	710	715	720	725

acg ccg ctg cag gag att gga tcc ctc aac atc gga tcc agg cct tcc	2323
Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile Gly Ser Arg Pro Ser	
730 735 740	
tca cgc aag cag acc tcc tcg gtg gaa gat ttg cga gcc atc cca tgg	2371
Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu Arg Ala Ile Pro Trp	
745 750 755	
gtg ctc agc tgg tca cag tct cgt gtc atg ctg cca ggc tgg ttt ggt	2419
Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu Pro Gly Trp Phe Gly	
760 765 770	
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Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu Ser Gly Glu Gln Ala Thr	
775 780 785	
caa cgc att gcc gag ctg caa aca ctc aat gag tcc tgg cca ttt ttc	2515
Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu Ser Trp Pro Phe Phe	
790 795 800 805	
acc tca gtg ttg gat aac atg gct cag gtg atg tcc aag gca gag ctg	2563
Thr Ser Val Leu Asp Asn Met Ala Gln Val Met Ser Lys Ala Glu Leu	
810 815 820	
cgt ttg gca aag ctc tac gca gac ctg atc cca gat acg gaa gta gcc	2611
Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro Asp Thr Glu Val Ala	
825 830 835	
gag cga gtc tat tcc gtc atc cgc gag gag tac ttc ctg acc aag aag	2659
Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr Phe Leu Thr Lys Lys	
840 845 850	
atg ttc tgc gta atc acc ggc tct gat gat ctg ctt gat gac aac cca	2707
Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu Leu Asp Asp Asn Pro	
855 860 865	
ctt etc gca cgc tct gtc cag cgc cga tac ccc tac ctg ctt cca ctc	2755
Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro Tyr Leu Leu Pro Leu	
870 875 880 885	
aac gtg atc cag gta gag atg atg cga cgc tac cga aaa ggc gac caa	2803
Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr Arg Lys Gly Asp Gln	
890 895 900	
agc gag caa gtg tcc cgc aac att cag ctg acc atg aac ggt ctt tcc	2851
Ser Glu Gln Val Ser Arg Asn Ile Gln Leu Thr Met Asn Gly Leu Ser	
905 910 915	
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Thr Ala Leu Arg Asn Ser Gly	
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<211> 924

<212> PRT

<213> Corynebacterium glutamicum

<400> 110

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Val Tyr Glu Leu	Val Glu Gln Ala	Arg Leu Thr Ser	Phe Asp Ile Ala
35	40	45	
Lys Gly Asn Ala	Glu Met Asp Ser	Leu Val Gln Val	Phe Asp Gly Ile
50	55	60	
Thr Pro Ala Lys	Ala Thr Pro Ile	Ala Arg Ala Phe	Ser His Phe Ala
65	70	75	80
Leu Leu Ala Asn	Leu Ala Glu Asp	Leu Tyr Asp Glu	Glu Leu Arg Glu
85	90	95	
Gln Ala Leu Asp	Ala Gly Asp Thr	Pro Pro Asp Ser	Thr Leu Asp Ala
100	105	110	
Thr Trp Leu Lys	Leu Asn Glu Gly	Asn Val Gly Ala	Glu Ala Val Ala
115	120	125	
Asp Val Leu Arg	Asn Ala Glu Val	Ala Pro Val Leu	Thr Ala His Pro
130	135	140	
Thr Glu Thr Arg	Arg Arg Thr Val	Phe Asp Ala Gln	Lys Trp Ile Thr
145	150	155	160
Thr His Met Arg	Glu Arg His Ala	Leu Gln Ser Ala	Glu Pro Thr Ala
165	170	175	
Arg Thr Gln Ser	Lys Leu Asp Glu	Ile Glu Lys Asn	Ile Arg Arg Arg
180	185	190	
Ile Thr Ile Leu	Trp Gln Thr Ala	Leu Ile Arg Val	Ala Arg Pro Arg
195	200	205	
Ile Glu Asp Glu	Ile Glu Val Gly	Leu Arg Tyr Tyr	Lys Leu Ser Leu
210	215	220	
Leu Glu Glu Ile	Pro Arg Ile Asn	Arg Asp Val Ala	Val Glu Leu Arg
225	230	235	240
Glu Arg Phe Gly	Glu Gly Val Pro	Leu Lys Pro Val	Val Lys Pro Gly
245	250	255	
Ser Trp Ile Gly	Gly Asp His Asp	Gly Asn Pro Tyr	Val Thr Ala Glu
260	265	270	
Thr Val Glu Tyr	Ser Thr His Arg	Ala Ala Glu Thr	Val Leu Lys Tyr
275	280	285	
Tyr Ala Arg Gln	Leu His Ser Leu	Glu His Glu Leu	Ser Leu Ser Asp
290	295	300	
Arg Met Asn Lys	Val Thr Pro Gln	Leu Leu Ala Leu	Ala Asp Ala Gly
305	310	315	320
His Asn Asp Val	Pro Ser Arg Val	Asp Glu Pro Tyr	Arg Arg Ala Val
325	330	335	

His Gly Val Arg Gly Arg Ile Leu Ala Thr Thr Ala Glu Leu Ile Gly
 340 345 350
 Glu Asp Ala Val Glu Gly Val Trp Phe Lys Val Phe Thr Pro Tyr Ala
 355 360 365
 Ser Pro Glu Glu Phe Leu Asn Asp Ala Leu Thr Ile Asp His Ser Leu
 370 375 380
 Arg Glu Ser Lys Asp Val Leu Ile Ala Asp Asp Arg Leu Ser Val Leu
 385 390 395 400
 Ile Ser Ala Ile Glu Ser Phe Gly Phe Asn Leu Tyr Ala Leu Asp Leu
 405 410 415
 Arg Gln Asn Ser Glu Ser Tyr Glu Asp Val Leu Thr Glu Leu Phe Glu
 420 425 430
 Arg Ala Gln Val Thr Ala Asn Tyr Arg Glu Leu Ser Glu Ala Glu Lys
 435 440 445
 Leu Glu Val Leu Leu Lys Glu Leu Arg Ser Pro Arg Pro Leu Ile Pro
 450 455 460
 His Gly Ser Asp Glu Tyr Ser Glu Val Thr Asp Arg Glu Leu Gly Ile
 465 470 475 480
 Phe Arg Thr Ala Ser Glu Ala Val Lys Lys Phe Gly Pro Arg Met Val
 485 490 495
 Pro His Cys Ile Ile Ser Met Ala Ser Ser Val Thr Asp Val Leu Glu
 500 505 510
 Pro Met Val Leu Leu Lys Glu Phe Gly Leu Ile Ala Ala Asn Gly Asp
 515 520 525
 Asn Pro Arg Gly Thr Val Asp Val Ile Pro Leu Phe Glu Thr Ile Glu
 530 535 540
 Asp Leu Gln Ala Gly Ala Gly Ile Leu Asp Glu Leu Trp Lys Ile Asp
 545 550 555 560
 Leu Tyr Arg Asn Tyr Leu Leu Gln Arg Asp Asn Val Gln Glu Val Met
 565 570 575
 Leu Gly Tyr Ser Asp Ser Asn Lys Asp Gly Gly Tyr Phe Ser Ala Asn
 580 585 590
 Trp Ala Leu Tyr Asp Ala Glu Leu Gln Leu Val Glu Leu Cys Arg Ser
 595 600 605
 Ala Gly Val Lys Leu Arg Leu Phe His Gly Arg Gly Gly Thr Val Gly
 610 615 620
 Arg Gly Gly Gly Pro Ser Tyr Asp Ala Ile Leu Ala Gln Pro Arg Gly
 625 630 635 640
 Ala Val Gln Gly Ser Val Arg Ile Thr Glu Gln Gly Glu Ile Ile Ser
 645 650 655

Ala Lys Tyr Gly Asn Pro Glu Thr Ala Arg Arg Asn Leu Glu Ala Leu
 660 665 670
 Val Ser Ala Thr Leu Glu Ala Ser Leu Leu Asp Val Ser Glu Leu Thr
 675 680 685
 Asp His Gln Arg Ala Tyr Asp Ile Met Ser Glu Ile Ser Glu Leu Ser
 690 695 700
 Leu Lys Lys Tyr Ala Ser Leu Val His Glu Asp Gln Gly Phe Ile Asp
 705 710 715 720
 Tyr Phe Thr Gln Ser Thr Pro Leu Gln Glu Ile Gly Ser Leu Asn Ile
 725 730 735
 Gly Ser Arg Pro Ser Ser Arg Lys Gln Thr Ser Ser Val Glu Asp Leu
 740 745 750
 Arg Ala Ile Pro Trp Val Leu Ser Trp Ser Gln Ser Arg Val Met Leu
 755 760 765
 Pro Gly Trp Phe Gly Val Gly Thr Ala Leu Glu Gln Trp Ile Gly Glu
 770 775 780
 Gly Glu Gln Ala Thr Gln Arg Ile Ala Glu Leu Gln Thr Leu Asn Glu
 785 790 795 800
 Ser Trp Pro Phe Phe Thr Ser Val Leu Asp Asn Met Ala Gln Val Met
 805 810 815
 Ser Lys Ala Glu Leu Arg Leu Ala Lys Leu Tyr Ala Asp Leu Ile Pro
 820 825 830
 Asp Thr Glu Val Ala Glu Arg Val Tyr Ser Val Ile Arg Glu Glu Tyr
 835 840 845
 Phe Leu Thr Lys Lys Met Phe Cys Val Ile Thr Gly Ser Asp Asp Leu
 850 855 860
 Leu Asp Asp Asn Pro Leu Leu Ala Arg Ser Val Gln Arg Arg Tyr Pro
 865 870 875 880
 Tyr Leu Leu Pro Leu Asn Val Ile Gln Val Glu Met Met Arg Arg Tyr
 885 890 895
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<210> 111

<211> 939

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(916)

<223> RXN02326

<400> 111

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                                         Met Leu Gly Arg Pro
                                         1           5

acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac 163
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His
                        10                        15                        20

ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa 211
Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln
                        25                        30                        35

aag tac gac atc cca gac tct gtc atc gcg ttc ctg cgc ggc gag ctt 259
Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu
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ggt aac cct cca ggt ggc tgg cca gag cca ctg cgc acc cgc gca ctg 307
Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu Arg Thr Arg Ala Leu
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gaa ggc cgc tcc gaa ggc aag gca cct ctg acg gaa gtt cct gag gaa 355
Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr Glu Val Pro Glu Glu
                        70                        75                        80                        85

gag cag gcg cac ctc gac gct gat gat tcc aag gaa cgt cgc aat agc 403
Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser
                        90                        95                        100

ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac 451
Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His
                        105                        110                        115

cgt cgc cgc ttc ggc aac acc tct gcg ctg gat gat cgt gaa ttc ttc 499
Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp Asp Arg Glu Phe Phe
                        120                        125                        130

tac ggc ctg gtc gaa ggc cgc gag act ttg atc cgc ctg cca gat gtg 547
Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile Arg Leu Pro Asp Val
                        135                        140                        145

cgc acc cca ctg ctt gtt cgc ctg gat gcg atc tct gag cca gac gat 595
Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile Ser Glu Pro Asp Asp
                        150                        155                        160                        165

aag ggt atg cgc aat gtt gtg gcc aac gtc aac ggc cag atc cgc cca 643
Lys Gly Met Arg Asn Val Val Ala Asn Val Asn Gly Gln Ile Arg Pro
                        170                        175                        180

atg cgt gtg cgt gac cgc tcc gtt gag tct gtc acc gca acc gca gaa 691
Met Arg Val Arg Asp Arg Ser Val Glu Ser Val Thr Ala Thr Ala Glu
                        185                        190                        195

aag gca gat tcc tcc aac aag ggc cat gtt gct gca cca ttc gct ggt 739
Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala Ala Pro Phe Ala Gly
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gtt gtc acc gtg act gtt gct gaa ggt gat gag gtc aag gct gga gat 787

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Val Val Thr Val Thr Val Ala Glu Gly Asp Glu Val Lys Ala Gly Asp
 215 220 225

gca gtc gca atc atc gag gct atg aag atg gaa gca aca atc act gct 835
 Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu Ala Thr Ile Thr Ala
 230 235 240 245

tct gtt gac ggc aaa atc gat cgc gtt gtg gtt cct gct gca acg aag 883
 Ser Val Asp Gly Lys Ile Asp Arg Val Val Val Pro Ala Ala Thr Lys
 250 255 260

gtg gaa ggt ggc gac ttg atc gtc gtc gtt tcc taaacctttc tgtaaaaagc 936
 Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
 265 270

ccc 939

<210> 112
 <211> 272
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 112
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Asp Leu Ala Leu His Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe
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Ala Ala Asp Pro Gln Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe
 35 40 45

Leu Arg Gly Glu Leu Gly Asn Pro Pro Gly Gly Trp Pro Glu Pro Leu
 50 55 60

Arg Thr Arg Ala Leu Glu Gly Arg Ser Glu Gly Lys Ala Pro Leu Thr
 65 70 75 80

Glu Val Pro Glu Glu Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys
 85 90 95

Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
 100 105 110

Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
 115 120 125

Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
 130 135 140

Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
 145 150 155 160

Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
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Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
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				1				5								
acc aag gtc acc cca tcc tcc aag gtt gtt ggc gac ctc gca ctc cac	163															
Thr Lys Val Thr Pro Ser Ser Lys Val Val Gly Asp Leu Ala Leu His																
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ctc gtt ggt gcg ggt gtg gat cca gca gac ttt gct gcc gat cca caa	211															
Leu Val Gly Ala Gly Val Asp Pro Ala Asp Phe Ala Ala Asp Pro Gln																
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Lys Tyr Asp Ile Pro Asp Ser Val Ile Ala Phe Leu Arg Gly Glu Leu																
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Glu Gln Ala His Leu Asp Ala Asp Asp Ser Lys Glu Arg Arg Asn Ser																
	90							95					100			
ctc aac cgc ctg ctg ttc ccg aag cca acc gaa gag ttc ctc gag cac	451															
Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu Glu Phe Leu Glu His																

105										110					115					
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120						125						130								
tac	ggc	ctg	gtc	gaa	ggc	cgc	gag	act	ttg	atc	cgc	ctg	cca	gat	gtg	547				
Tyr	Gly	Leu	Val	Glu	Gly	Arg	Glu	Thr	Leu	Ile	Arg	Leu	Pro	Asp	Val					
135						140						145								
cgc	acc	cca	ctg	ctt	gtt	cgc	ctg	gat	gcg	atc	tct	gag	cca	gac	gat	595				
Arg	Thr	Pro	Leu	Leu	Val	Arg	Leu	Asp	Ala	Ile	Ser	Glu	Pro	Asp	Asp					
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Lys	Gly	Met	Arg	Asn	Val	Val	Ala	Asn	Val	Asn	Gly	Gln	Ile	Arg	Pro					
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Met	Arg	Val	Arg	Asp	Arg	Ser	Val	Glu	Ser	Val	Thr	Ala	Thr	Ala	Glu					
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Lys	Ala	Asp	Ser	Ser	Asn	Lys	Gly	His	Val	Ala	Ala	Pro	Phe	Ala	Gly					
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Val	Val	Thr	Val	Thr	Val	Ala	Glu	Gly	Asp	Glu	Val	Lys	Ala	Gly	Asp					
215						220						225								
gca	gtc	gca	atc	atc	gag	gct	atg	aag	atg	gaa	gca	aca	atc	act	gct	835				
Ala	Val	Ala	Ile	Ile	Glu	Ala	Met	Lys	Met	Glu	Ala	Thr	Ile	Thr	Ala					
230			235						240			245								
tct	gtt	gac	ggc	aaa	atc	gat	cgc	gtt	gtg	gtt	cct	gct	gca	acg	aag	883				
Ser	Val	Asp	Gly	Lys	Ile	Asp	Arg	Val	Val	Val	Pro	Ala	Ala	Thr	Lys					
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gtg	gaa	ggt	ggc	gac	ttg	atc	gtc	gtc	gtt	tcc	taa	ac	ctt	ttc	tg	936				
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ccc															939					

<210> 114

<211> 272

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 114

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		20						25					30		

Ala	Ala	Asp	Pro	Gln	Lys	Tyr	Asp	Ile	Pro	Asp	Ser	Val	Ile	Ala	Phe
		35					40					45			

Leu	Arg	Gly	Glu	Leu	Gly	Asn	Pro	Pro	Gly	Gly	Trp	Pro	Glu	Pro	Leu
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      85              90              95
Glu Arg Arg Asn Ser Leu Asn Arg Leu Leu Phe Pro Lys Pro Thr Glu
      100              105              110
Glu Phe Leu Glu His Arg Arg Arg Phe Gly Asn Thr Ser Ala Leu Asp
      115              120              125
Asp Arg Glu Phe Phe Tyr Gly Leu Val Glu Gly Arg Glu Thr Leu Ile
      130              135              140
Arg Leu Pro Asp Val Arg Thr Pro Leu Leu Val Arg Leu Asp Ala Ile
      145              150              155              160
Ser Glu Pro Asp Asp Lys Gly Met Arg Asn Val Val Ala Asn Val Asn
      165              170              175
Gly Gln Ile Arg Pro Met Arg Val Arg Asp Arg Ser Val Glu Ser Val
      180              185              190
Thr Ala Thr Ala Glu Lys Ala Asp Ser Ser Asn Lys Gly His Val Ala
      195              200              205
Ala Pro Phe Ala Gly Val Val Thr Val Thr Val Ala Glu Gly Asp Glu
      210              215              220
Val Lys Ala Gly Asp Ala Val Ala Ile Ile Glu Ala Met Lys Met Glu
      225              230              235              240
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Pro Ala Ala Thr Lys Val Glu Gly Gly Asp Leu Ile Val Val Val Ser
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<210> 115

<211> 1083

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1060)

<223> RXN02327

<400> 115

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 Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln
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 Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
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 Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
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 Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
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Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
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His Val His Thr His Asp Thr Ala Gly Gly Gln Leu Ala Thr Tyr Phe
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Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
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Ala Phe Ala His Thr Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val
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Ser Asp Leu Glu Pro Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro
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Phe Glu Ser Gly Thr Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu
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 Val Ala Met Arg Phe Leu Phe Glu Asp Pro Trp Asp Arg Leu Asp Glu
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Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp Ile Phe Arg Ile Phe	
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Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro Ala Ile Asp Ala Val	
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Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr Leu Asp Tyr Tyr Leu	
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Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala His Ile Leu Ala Ile	
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Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala Val Thr Lys Leu Val	
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Gly Ala Asp Ala Val Asp Gly Ala Ser Gly Thr Val Trp His His	
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Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala Ala Phe Ala His Thr	
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Arg Arg Asp Thr Gly Leu Ser Leu Glu Ala Val Ser Asp Leu Glu Pro	
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Tyr Trp Glu Ala Val Arg Gly Leu Tyr Leu Pro Phe Glu Ser Gly Thr	
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Pro Gly Pro Thr Gly Arg Val Tyr Arg His Glu Ile Pro Gly Gly Gln	
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Asp Arg Leu Asp Glu Leu Arg Glu Ala Met Pro Asn Val Asn Ile Gln
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Met Leu Leu Arg Gly Arg Asn Thr Val Gly Tyr Thr Pro Tyr Pro Asp
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Ser Val Cys Arg Ala Phe Val Lys Glu Ala Ala Ser Ser Gly Val Asp
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Ile Phe Arg Ile Phe Asp Ala Leu Asn Asp Val Ser Gln Met Arg Pro
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Ala Ile Asp Ala Val Leu Glu Thr Asn Thr Ala Val Ala Glu Val Ala
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Met Ala Tyr Ser Gly Asp Leu Ser Asp Pro Asn Glu Lys Leu Tyr Thr
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Leu Asp Tyr Tyr Leu Lys Met Ala Glu Glu Ile Val Lys Ser Gly Ala
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His Ile Leu Ala Ile Lys Asp Met Ala Gly Leu Leu Arg Pro Ala Ala
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Val Thr Lys Leu Val Thr Ala Leu Arg Arg Glu Phe Asp Leu Pro Val
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Thr Val Trp His His Leu Pro Ser His Pro Leu Ser Ala Ile Val Ala
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 Val Thr Ala Ile Thr 5
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ctt ggc ggt ctc ttg ttg aaa gga ata att act cta gtg tcg act cac 163
 Leu Gly Gly Leu Leu Leu Lys Gly Ile Ile Thr Leu Val Ser Thr His 20
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 Thr Ser Ser Thr Leu Pro Ala Phe Lys Lys Ile Leu Val Ala Asn Arg 35
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ggc gaa atc gcg gtc cgt gct ttc cgt gca gca ctc gaa acc ggt gca 259
 Gly Glu Ile Ala Val Arg Ala Phe Arg Ala Ala Leu Glu Thr Gly Ala 50
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 Ala Thr Val Ala Ile Tyr Pro Arg Glu Asp Arg Gly Ser Phe His Arg 65
 55 60

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 Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val 85
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 Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val 100
 90 95

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Pro	His	Gly	Val	Arg	Pro	Lys	Asp	Val	Ala	Ala	Pro	Ile	Asp	Lys	Leu					
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Pro	Asn	Ile	Lys	Asp	Leu	Pro	Leu	Pro	Arg	Gly	Ser	Arg	Asp	Arg						
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 Gly Ser Phe His Arg Ser Phe Ala Ser Glu Ala Val Arg Ile Gly Thr
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 Glu Gly Ser Pro Val Lys Ala Tyr Leu Asp Ile Asp Glu Ile Ile Gly
 85 90 95
 Ala Ala Lys Lys Val Lys Ala Asp Ala Ile Tyr Pro Gly Tyr Gly Phe
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 Leu Ser Glu Asn Ala Gln Leu Ala Arg Glu Cys Ala Glu Asn Gly Ile
 115 120 125
 Thr Phe Ile Gly Pro Thr Pro Glu Val Leu Asp Leu Thr Gly Asp Lys
 130 135 140
 Ser Arg Ala Val Thr Ala Ala Lys Lys Ala Gly Leu Pro Val Leu Ala
 145 150 155 160
 Glu Ser Thr Pro Ser Lys Asn Ile Asp Glu Ile Val Lys Ser Ala Glu
 165 170 175
 Gly Gln Thr Tyr Pro Ile Phe Val Lys Ala Val Ala Gly Gly Gly Gly
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 Arg Gly Met Arg Phe Val Ala Ser Pro Asp Glu Leu Arg Lys Leu Ala
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 Thr Glu Ala Ser Arg Glu Ala Glu Ala Ala Phe Gly Asp Gly Ala Val
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 Tyr Val Glu Arg Ala Val Ile Asn Pro Gln His Ile Glu Val Gln Ile
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 Leu Gly Asp His Thr Gly Glu Val Val His Leu Tyr Glu Arg Asp Cys
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 Ser Leu Gln Arg Arg His Gln Lys Val Val Glu Ile Ala Pro Ala Gln
 260 265 270
 His Leu Asp Pro Glu Leu Arg Asp Arg Ile Cys Ala Asp Ala Val Lys
 275 280 285
 Phe Cys Arg Ser Ile Gly Tyr Gln Gly Ala Gly Thr Val Glu Phe Leu
 290 295 300
 Val Asp Glu Lys Gly Asn His Val Phe Ile Glu Met Asn Pro Arg Ile
 305 310 315 320
 Gln Val Glu His Thr Val Thr Glu Glu Val Thr Glu Val Asp Leu Val
 325 330 335
 Lys Ala Gln Met Arg Leu Ala Ala Gly Ala Thr Leu Lys Glu Leu Gly
 340 345 350
 Leu Thr Gln Asp Lys Ile Lys Thr His Gly Ala Ala Leu Gln Cys Arg

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          355              360              365
Ile Thr Thr Glu Asp Pro Asn Asn Gly Phe Arg Pro Asp Thr Gly Thr
 370              375              380

Ile Thr Ala Tyr Arg Ser Pro Gly Gly Ala Gly Val Arg Leu Asp Gly
385              390              395              400

Ala Ala Gln Leu Gly Gly Glu Ile Thr Ala His Phe Asp Ser Met Leu
          405              410              415

Val Lys Met Thr Cys Arg Gly Ser Asp Phe Glu Thr Ala Val Ala Arg
          420              425              430

Ala Gln Arg Ala Leu Ala Glu Phe Thr Val Ser Gly Val Ala Thr Asn
          435              440              445

Ile Gly Phe Leu Arg Ala Leu Leu Arg Glu Glu Asp Phe Thr Ser Lys
 450              455              460

Arg Ile Ala Thr Gly Phe Ile Ala Asp His Pro His Leu Leu Gln Ala
465              470              475              480

Pro Pro Ala Asp Asp Glu Gln Gly Arg Ile Leu Asp Tyr Leu Ala Asp
          485              490              495

Val Thr Val Asn Lys Pro His Gly Val Arg Pro Lys Asp Val Ala Ala
          500              505              510

Pro Ile Asp Lys Leu Pro Asn Ile Lys Asp Leu Pro Leu Pro Arg Gly
 515              520              525

Ser Arg Asp Arg
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<210> 121
<211> 1406
<212> DNA
<213> Corynebacterium glutamicum

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<220>
<221> CDS
<222> (1)..(1383)
<223> FRXA02328

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<400> 121
gct tct gaa gct gtc cgc att ggt acc gaa ggc tca cca gtc aag gcg      48
Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
  1              5              10              15

tac ctg gac atc gat gaa att atc ggt gca gct aaa aaa gtt aaa gca      96
Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
          20              25              30

gat gcc att tac ccg gga tac ggc ttc ctg tct gaa aat gcc cag ctt      144
Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
          35              40              45

gcc cgc gag tgt gcg gaa aac ggc att act ttt att ggc cca acc cca      192
Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro

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50	55	60	
gag gtt ctt gat ctc acc ggt gat aag tct cgc gcg gta acc gcc gcg Glu Val Leu Asp Leu Thr Gly Asp Lys Ser Arg Ala Val Thr Ala Ala 65 70 75 80			240
aag aag gct ggt ctg cca gtt ttg gcg gaa tcc acc ccg agc aaa aac Lys Lys Ala Gly Leu Pro Val Leu Ala Glu Ser Thr Pro Ser Lys Asn 85 90 95			288
atc gat gag atc gtt aaa agc gct gaa ggc cag act tac ccc atc ttt Ile Asp Glu Ile Val Lys Ser Ala Glu Gly Gln Thr Tyr Pro Ile Phe 100 105 110			336
gtg aag gca gtt gcc ggt ggt ggc gga cgc ggt atg cgt ttt gtt gct Val Lys Ala Val Ala Gly Gly Gly Arg Gly Met Arg Phe Val Ala 115 120 125			384
tca cct gat gag ctt cgc aaa tta gca aca gaa gca tct cgt gaa gct Ser Pro Asp Glu Leu Arg Lys Leu Ala Thr Glu Ala Ser Arg Glu Ala 130 135 140			432
gaa gcg gct ttc ggc gat ggc gcg gta tat gtc gaa cgt gct gtg att Glu Ala Ala Phe Gly Asp Gly Ala Val Tyr Val Glu Arg Ala Val Ile 145 150 155 160			480
aac cct cag cat att gaa gtg cag atc ctt ggc gat cac act gga gaa Asn Pro Gln His Ile Glu Val Gln Ile Leu Gly Asp His Thr Gly Glu 165 170 175			528
gtt gta cac ctt tat gaa cgt gac tgc tca ctg cag cgt cgt cac caa Val Val His Leu Tyr Glu Arg Asp Cys Ser Leu Gln Arg Arg His Gln 180 185 190			576
aaa gtt gtc gaa att gcg cca gca cag cat ttg gat cca gaa ctg cgt Lys Val Val Glu Ile Ala Pro Ala Gln His Leu Asp Pro Glu Leu Arg 195 200 205			624
gat cgc att tgt gcg gat gca gta aag ttc tgc cgc tcc att ggt tac Asp Arg Ile Cys Ala Asp Ala Val Lys Phe Cys Arg Ser Ile Gly Tyr 210 215 220			672
cag ggc gcg gga acc gtg gaa ttc ttg gtc gat gaa aag ggc aac cac Gln Gly Ala Gly Thr Val Glu Phe Leu Val Asp Glu Lys Gly Asn His 225 230 235 240			720
gtc ttc atc gaa atg aac cca cgt atc cag gtt gag cac acc gtg act Val Phe Ile Glu Met Asn Pro Arg Ile Gln Val Glu His Thr Val Thr 245 250 255			768
gaa gaa gtc acc gag gtg gac ctg gtg aag gcg cag atg cgc ttg gct Glu Glu Val Thr Glu Val Asp Leu Val Lys Ala Gln Met Arg Leu Ala 260 265 270			816
gct ggt gca acc ttg aag gaa ttg ggt ctg acc caa gat aag atc aag Ala Gly Ala Thr Leu Lys Glu Leu Gly Leu Thr Gln Asp Lys Ile Lys 275 280 285			864
acc cac ggt gca gca ctg cag tgc cgc atc acc acg gaa gat cca aac Thr His Gly Ala Ala Leu Gln Cys Arg Ile Thr Thr Glu Asp Pro Asn 290 295 300			912

aac ggc ttc cgc cca gat acc gga act atc acc gcg tac cgc tca cca 960
 Asn Gly Phe Arg Pro Asp Thr Gly Thr Ile Thr Ala Tyr Arg Ser Pro
 305 310 315 320

 ggc gga gct ggc gtt cgt ctt gac ggt gca gct cag ctc ggt ggc gaa 1008
 Gly Gly Ala Gly Val Arg Leu Asp Gly Ala Ala Gln Leu Gly Gly Glu
 325 330 335

 atc acc gca cac ttt gac tcc atg ctg gtg aaa atg acc tgc cgt ggt 1056
 Ile Thr Ala His Phe Asp Ser Met Leu Val Lys Met Thr Cys Arg Gly
 340 345 350

 tcc gac ttt gaa act gct gtt gct cgt gca cag cgc gcg ttg gct gag 1104
 Ser Asp Phe Glu Thr Ala Val Ala Arg Ala Gln Arg Ala Leu Ala Glu
 355 360 365

 ttc acc gtg tct ggt gtt gca acc aac att ggt ttc ttg cgt gcg ttg 1152
 Phe Thr Val Ser Gly Val Ala Thr Asn Ile Gly Phe Leu Arg Ala Leu
 370 375 380

 ctg cgg gaa gag gac ttc act tcc aag cgc atc gcc acc gga ttc att 1200
 Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
 385 390 395 400

 gcc gat cac ccg cac ctc ctt cag gct cca cct gct gat gat gag cag 1248
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
 405 410 415

 gga cgc atc ctg gat tac ttg gca gat gtc acc gtg aac aag cct cat 1296
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
 420 425 430

 ggt gtg cgt cca aag gat gtt gca gct cct atc gat aag ctg cct aac 1344
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
 435 440 445

 atc aag gat ctg cca ctg cca cgc ggt tcc cgt gac cgc tgaagcagct 1393
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

 tggcccagcc gcg 1406

<210> 122

<211> 461

<212> PRT

<213> Corynebacterium glutamicum

<400> 122

Ala Ser Glu Ala Val Arg Ile Gly Thr Glu Gly Ser Pro Val Lys Ala
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Tyr Leu Asp Ile Asp Glu Ile Ile Gly Ala Ala Lys Lys Val Lys Ala
 20 25 30

Asp Ala Ile Tyr Pro Gly Tyr Gly Phe Leu Ser Glu Asn Ala Gln Leu
 35 40 45

Ala Arg Glu Cys Ala Glu Asn Gly Ile Thr Phe Ile Gly Pro Thr Pro
 50 55 60

Glu	Val	Leu	Asp	Leu	Thr	Gly	Asp	Lys	Ser	Arg	Ala	Val	Thr	Ala	Ala		
65					70					75					80		
Lys	Lys	Ala	Gly	Leu	Pro	Val	Leu	Ala	Glu	Ser	Thr	Pro	Ser	Lys	Asn		
				85					90					95			
Ile	Asp	Glu	Ile	Val	Lys	Ser	Ala	Glu	Gly	Gln	Thr	Tyr	Pro	Ile	Phe		
			100					105					110				
Val	Lys	Ala	Val	Ala	Gly	Gly	Gly	Gly	Arg	Gly	Met	Arg	Phe	Val	Ala		
		115					120					125					
Ser	Pro	Asp	Glu	Leu	Arg	Lys	Leu	Ala	Thr	Glu	Ala	Ser	Arg	Glu	Ala		
	130					135					140						
Glu	Ala	Ala	Phe	Gly	Asp	Gly	Ala	Val	Tyr	Val	Glu	Arg	Ala	Val	Ile		
145					150					155					160		
Asn	Pro	Gln	His	Ile	Glu	Val	Gln	Ile	Leu	Gly	Asp	His	Thr	Gly	Glu		
				165					170					175			
Val	Val	His	Leu	Tyr	Glu	Arg	Asp	Cys	Ser	Leu	Gln	Arg	Arg	His	Gln		
			180					185					190				
Lys	Val	Val	Glu	Ile	Ala	Pro	Ala	Gln	His	Leu	Asp	Pro	Glu	Leu	Arg		
		195					200					205					
Asp	Arg	Ile	Cys	Ala	Asp	Ala	Val	Lys	Phe	Cys	Arg	Ser	Ile	Gly	Tyr		
	210					215					220						
Gln	Gly	Ala	Gly	Thr	Val	Glu	Phe	Leu	Val	Asp	Glu	Lys	Gly	Asn	His		
225					230					235					240		
Val	Phe	Ile	Glu	Met	Asn	Pro	Arg	Ile	Gln	Val	Glu	His	Thr	Val	Thr		
				245					250					255			
Glu	Glu	Val	Thr	Glu	Val	Asp	Leu	Val	Lys	Ala	Gln	Met	Arg	Leu	Ala		
			260					265					270				
Ala	Gly	Ala	Thr	Leu	Lys	Glu	Leu	Gly	Leu	Thr	Gln	Asp	Lys	Ile	Lys		
		275					280					285					
Thr	His	Gly	Ala	Ala	Leu	Gln	Cys	Arg	Ile	Thr	Thr	Glu	Asp	Pro	Asn		
	290					295					300						
Asn	Gly	Phe	Arg	Pro	Asp	Thr	Gly	Thr	Ile	Thr	Ala	Tyr	Arg	Ser	Pro		
305					310					315					320		
Gly	Gly	Ala	Gly	Val	Arg	Leu	Asp	Gly	Ala	Ala	Gln	Leu	Gly	Gly	Glu		
				325					330					335			
Ile	Thr	Ala	His	Phe	Asp	Ser	Met	Leu	Val	Lys	Met	Thr	Cys	Arg	Gly		
			340					345					350				
Ser	Asp	Phe	Glu	Thr	Ala	Val	Ala	Arg	Ala	Gln	Arg	Ala	Leu	Ala	Glu		
		355					360					365					
Phe	Thr	Val	Ser	Gly	Val	Ala	Thr	Asn	Ile	Gly	Phe	Leu	Arg	Ala	Leu		
	370					375					380						

Leu Arg Glu Glu Asp Phe Thr Ser Lys Arg Ile Ala Thr Gly Phe Ile
 385 390 395 400
 Ala Asp His Pro His Leu Leu Gln Ala Pro Pro Ala Asp Asp Glu Gln
 405 410 415
 Gly Arg Ile Leu Asp Tyr Leu Ala Asp Val Thr Val Asn Lys Pro His
 420 425 430
 Gly Val Arg Pro Lys Asp Val Ala Ala Pro Ile Asp Lys Leu Pro Asn
 435 440 445
 Ile Lys Asp Leu Pro Leu Pro Arg Gly Ser Arg Asp Arg
 450 455 460

<210> 123
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXN01048

<400> 123
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 gagcttccccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
 55 60 65
 aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
 70 75 80 85
 gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
 90 95 100
 ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
 105 110 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	
acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc	883
Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly	
250 255 260	
gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct	931
Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala	
265 270 275	
ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca	979
Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro	
280 285 290	
acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc	1027
Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val	
295 300 305	
gcg acc ggg cgc tct gac ctg cct aac cag atc aac aac gtg ctg gcg	1075
Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala	
310 315 320 325	
ttc cca gga att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc	1123
Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile	
330 335 340	
acc ccc gag atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag	1171
Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln	
345 350 355	
ctg agg acc tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc	1219

Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro
 360 365 370
 gcg ttg ccc caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc 1267
 Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg
 375 380 385
 aaa acg ctt aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg 1315
 Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala
 390 395 400 405
 cca ata ttt taagagcaaa cttgaggccc aca 1347
 Pro Ile Phe

<210> 124
 <211> 408
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 124
 Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
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 Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30
 Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45
 Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60
 His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80
 Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205

Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255
 Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
 305 310 315 320
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
 325 330 335
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
 340 345 350
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
 355 360 365
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
 370 375 380
 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
 385 390 395 400
 Leu Pro Val Glu Ala Pro Ile Phe
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<210> 125

<211> 311

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(288)

<223> FRXA01048

<400> 125

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 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
 1 5 10 15

att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30

atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr

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          35          40          45
tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
      50          55          60

caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
      65          70          75          80

aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
          85          90          95

taagagcaaa cttgaggccc aca 311

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<210> 126
 <211> 96
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 126
Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
      1          5          10          15

Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
          20          25          30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
          35          40          45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
          50          55          60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
      65          70          75          80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
          85          90          95

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<210> 127
 <211> 1063
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1063)
 <223> FRXA00290

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<400> 127
agctacagat ttagctagtg tttttgttcc agaaccctaa atgaggttct acccttaaca 60

gagcttcccc caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
          Met Thr Ile Asp Leu
          1          5

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cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac	163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His	
10 15 20	
gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg	211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met	
25 30 35	
cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa	259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu	
40 45 50	
gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga	307
Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly	
55 60 65	
aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc	355
Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly	
70 75 80 85	
gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag	403
Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln	
90 95 100	
ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac	451
Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp	
105 110 115	
gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct	499
Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro	
120 125 130	
tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc	547
Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe	
135 140 145	
gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac	595
Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His	
150 155 160 165	
gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac	643
Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn	
170 175 180	
tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att	691
Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile	
185 190 195	
tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac	739
Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn	
200 205 210	
gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac	787
Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His	
215 220 225	
gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag	835
Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys	
230 235 240 245	

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

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<212> PRT

<213> Corynebacterium glutamicum

<400> 128

Met Thr Ile Asp Leu Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu
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Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
 20 25 30

Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45

Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60

His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80

Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95

Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110

Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125

Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140

Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160

Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175

Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp

	180		185		190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val	195		200		205
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser	210		215		220
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala	225		230		235
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn	245		250		255
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn	260		265		270
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe	275		280		285
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys	290		295		300
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg	305		310		315
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Ser

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<220>
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 <223> RXA02694

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 tgggttggtcc ggtaggggaa atcaggaagt gggatcgaaa atg aaa gaa acc gtc 115
 Met Lys Glu Thr Val
 1 5
 ggt aac aag att gtc ctc att ggc gca gga gat gtt gga gtt gca tac 163
 Gly Asn Lys Ile Val Leu Ile Gly Ala Gly Asp Val Gly Val Ala Tyr
 10 15 20
 gca tac gca ctg atc aac cag ggc atg gca gat cac ctt gcg atc atc 211
 Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp His Leu Ala Ile Ile
 25 30 35
 gac atc gat gaa aag aaa ctc gaa ggc aac gtc atg gac tta aac cat 259
 Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val Met Asp Leu Asn His
 40 45 50
 ggt gtt gtg tgg gcc gat tcc cgc acc cgc gtc acc aag ggc acc tac 307
 Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val Thr Lys Gly Thr Tyr

55	60	65	
gct gac tgc gaa gac gca gcc atg gtt gtc att tgt gcc ggc gca gcc Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile Cys Ala Gly Ala Ala 70 75 80 85			355
caa aag cca ggc gag acc cgc ctc cag ctg gtg gac aaa aac gtc aag Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val Asp Lys Asn Val Lys 90 95 100			403
att atg aaa tcc atc gtc ggc gat gtc atg gac agc gga ttc gac ggc Ile Met Lys Ser Ile Val Gly Asp Val Met Asp Ser Gly Phe Asp Gly 105 110 115			451
atc ttc ctc gtg gcg tcc aac cca gtg gat atc ctg acc tac gca gtg Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile Leu Thr Tyr Ala Val 120 125 130			499
tgg aaa ttc tcc ggc ttg gaa tgg aac cgc gtg atc ggc tcc gga act Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val Ile Gly Ser Gly Thr 135 140 145			547
gtc ctg gac tcc gct cga ttc cgc tac atg ctg ggc gaa ctc tac gaa Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu Gly Glu Leu Tyr Glu 150 155 160 165			595
gtg gca cca agc tcc gtc cac gcc tac atc atc ggc gaa cac ggc gac Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile Gly Glu His Gly Asp 170 175 180			643
act gaa ctt cca gtc ctg tcc tcc gcg acc atc gca ggc gta tcg ctt Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile Ala Gly Val Ser Leu 185 190 195			691
agc cga atg ctg gac aaa gac cca gag ctt gag ggc cgt cta gag aaa Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu Gly Arg Leu Glu Lys 200 205 210			739
att ttc gaa gac acc cgc gac gct gcc tat cac att atc gac gcc aag Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His Ile Ile Asp Ala Lys 215 220 225			787
ggc tcc act tcc tac ggc atc ggc atg ggt ctt gct cgc atc acc cgc Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu Ala Arg Ile Thr Arg 230 235 240 245			835
gca atc cta cag aac caa gac gtt gca gtc cca gtc tct gca ctg ctc Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro Val Ser Ala Leu Leu 250 255 260			883
cac ggt gaa tac ggt gag gaa gac atc tac atc ggc acc cca gct gtg His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile Gly Thr Pro Ala Val 265 270 275			931
gtg aac cgc cga ggc atc cgc cgc gtt gtc gaa cta gaa atc acc gac Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu Leu Glu Ile Thr Asp 280 285 290			979
cac gag atg gaa cgc ttc aag cat tcc gca aat acc ctg cgc gaa att His Glu Met Glu Arg Phe Lys His Ser Ala Asn Thr Leu Arg Glu Ile 295 300 305			1027

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 Gln Lys Gln Phe Phe
 310

1065

<210> 130

<211> 314

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<213> Corynebacterium glutamicum

<400> 130

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Val Gly Val Ala Tyr Ala Tyr Ala Leu Ile Asn Gln Gly Met Ala Asp
 20 25 30

His Leu Ala Ile Ile Asp Ile Asp Glu Lys Lys Leu Glu Gly Asn Val
 35 40 45

Met Asp Leu Asn His Gly Val Val Trp Ala Asp Ser Arg Thr Arg Val
 50 55 60

Thr Lys Gly Thr Tyr Ala Asp Cys Glu Asp Ala Ala Met Val Val Ile
 65 70 75 80

Cys Ala Gly Ala Ala Gln Lys Pro Gly Glu Thr Arg Leu Gln Leu Val
 85 90 95

Asp Lys Asn Val Lys Ile Met Lys Ser Ile Val Gly Asp Val Met Asp
 100 105 110

Ser Gly Phe Asp Gly Ile Phe Leu Val Ala Ser Asn Pro Val Asp Ile
 115 120 125

Leu Thr Tyr Ala Val Trp Lys Phe Ser Gly Leu Glu Trp Asn Arg Val
 130 135 140

Ile Gly Ser Gly Thr Val Leu Asp Ser Ala Arg Phe Arg Tyr Met Leu
 145 150 155 160

Gly Glu Leu Tyr Glu Val Ala Pro Ser Ser Val His Ala Tyr Ile Ile
 165 170 175

Gly Glu His Gly Asp Thr Glu Leu Pro Val Leu Ser Ser Ala Thr Ile
 180 185 190

Ala Gly Val Ser Leu Ser Arg Met Leu Asp Lys Asp Pro Glu Leu Glu
 195 200 205

Gly Arg Leu Glu Lys Ile Phe Glu Asp Thr Arg Asp Ala Ala Tyr His
 210 215 220

Ile Ile Asp Ala Lys Gly Ser Thr Ser Tyr Gly Ile Gly Met Gly Leu
 225 230 235 240

Ala Arg Ile Thr Arg Ala Ile Leu Gln Asn Gln Asp Val Ala Val Pro
 245 250 255

Val Ser Ala Leu Leu His Gly Glu Tyr Gly Glu Glu Asp Ile Tyr Ile

	260		265		270
Gly Thr Pro Ala Val Val Asn Arg Arg Gly Ile Arg Arg Val Val Glu					
275		280		285	
Leu Glu Ile Thr Asp His Glu Met Glu Arg Phe Lys His Ser Ala Asn					
290	295	300			
Thr Leu Arg Glu Ile Gln Lys Gln Phe Phe					
305	310				

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2944)
 <223> RXN00296

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 Met Thr His Thr Ile 5
 1
 aaa ttc aac aga ctc gac cca gaa gta ttt agc cag cat tct cgc gcg 163
 Lys Phe Asn Arg Leu Asp Pro Glu Val Phe Ser Gln His Ser Arg Ala 20
 10 15
 aag ctg cgc acg gat atg aca acc cgt gca gca tat tct tct gat gca 211
 Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala Tyr Ser Ser Asp Ala 35
 25 30
 gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa aat gtg 259
 Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu Asn Val 50
 40 45
 gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg tgg tct 307
 Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly Trp Ser 65
 55 60
 gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg atc ggt 355
 Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala Ile Gly 85
 70 75 80
 gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att tta gat 403
 Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile Leu Asp 100
 90 95
 att gat cca gtt gca caa act gca gtt gtg gaa ccc ggt gtg gtg tgt 451
 Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu Pro Gly Val Val Cys 115
 105 110
 gat gcc ttg cgc gat gca gcc gca gaa ttc gga tta act tac ggc ccg 499
 Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly Leu Thr Tyr Gly Pro 130
 120 125

gat cct tcc acg cat tcc cgg tgc acg atc ggt ggc atg gtt gcc aac	547
Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly Gly Met Val Ala Asn	
135 140 145	
aat gcg tgt ggt tca cac tcg gtt gca ttc ggt aca gct gcg gaa aat	595
Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly Thr Ala Ala Glu Asn	
150 155 160 165	
ctc gtg gat gtc acg ctc atg ctc agc gat ggc cga gaa gtc act gtg	643
Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly Arg Glu Val Thr Val	
170 175 180	
aca aaa gat ggc tgc gat gat gct gag atc aat cag aag ctc acc gac	691
Thr Lys Asp Gly Cys Asp Asp Ala Glu Ile Asn Gln Lys Leu Thr Asp	
185 190 195	
tta gcg tcc aag aat cag gac ctt att agt aaa gaa ctg ggt cgt ttc	739
Leu Ala Ser Lys Asn Gln Asp Leu Ile Ser Lys Glu Leu Gly Arg Phe	
200 205 210	
cct cgc caa gtg tcg ggc tac ggt ttg cat tat ctt gcc cac gac atg	787
Pro Arg Gln Val Ser Gly Tyr Gly Leu His Tyr Leu Ala His Asp Met	
215 220 225	
gcc aaa gca atg gcg ggc acc gag gga acc att gga atc att act cgg	835
Ala Lys Ala Met Ala Gly Thr Glu Gly Thr Ile Gly Ile Ile Thr Arg	
230 235 240 245	
ttg acg gtg aag ttg gtt cca aca ccc aaa gtg aaa gcg ctt gct gtc	883
Leu Thr Val Lys Leu Val Pro Thr Pro Lys Val Lys Ala Leu Ala Val	
250 255 260	
ctg gct ttc gac acg gtt ttt gac gcc gcc cga gca gcc gcc aaa ttg	931
Leu Ala Phe Asp Thr Val Phe Asp Ala Ala Arg Ala Ala Lys Leu	
265 270 275	
cga ctg cct ggg gta gca acc att gaa ggc atg ggc gga gat ctc ctc	979
Arg Leu Pro Gly Val Ala Thr Ile Glu Gly Met Gly Gly Asp Leu Leu	
280 285 290	
gct gcg ctg cgc agt aaa cag gga caa tca gaa gct ggg cag aat ctt	1027
Ala Ala Leu Arg Ser Lys Gln Gly Gln Ser Glu Ala Gly Gln Asn Leu	
295 300 305	
cca gga aac cgc atc ggc att gaa gcc ggc gga tgg ttg tac tgc gag	1075
Pro Gly Asn Arg Ile Gly Ile Glu Ala Gly Gly Trp Leu Tyr Cys Glu	
310 315 320 325	
aca gga agt gac acc ctg cag gcc gcg gta caa gcc gcc gag gaa gtc	1123
Thr Gly Ser Asp Thr Leu Gln Ala Ala Val Gln Ala Ala Glu Glu Val	
330 335 340	
gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag cct tct	1171
Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu Pro Ser	
345 350 355	
gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc att gtc	1219
Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly Ile Val	
360 365 370	
acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa gac tcg	1267

Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro	Asn	Trp	Glu	Asp	Ser	
	375					380					385					
gcg	gtg	cct	cca	gag	aat	tta	gct	gat	tat	ctc	cgc	gat	ctt	tat	gcg	1315
Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu	Arg	Asp	Leu	Tyr	Ala	
390					395					400					405	
ctg	atg	gat	aag	ttc	gat	tac	cag	ggt	att	cca	ttt	gga	cac	ttt	gga	1363
Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His	Phe	Gly	
				410					415					420		
gaa	ggc	tgc	gtc	cac	gtt	cgc	atc	agt	ttt	gat	ttc	tct	acc	aag	gaa	1411
Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp	Phe	Ser	Thr	Lys	Glu	
			425					430					435			
ggc	ctg	aag	aaa	ttc	gag	gcg	ttc	atg	aat	gaa	gcc	tcc	acc	ttg	gtg	1459
Gly	Leu	Lys	Lys	Phe	Glu	Ala	Phe	Met	Asn	Glu	Ala	Ser	Thr	Leu	Val	
		440					445					450				
gcg	tct	tat	ggt	ggc	agc	ctc	tcg	ggc	gag	cat	gga	gac	ggt	cgc	gcc	1507
Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His	Gly	Asp	Gly	Arg	Ala	
	455					460					465					
cgc	tca	tcc	ttc	ctt	gac	cgc	atg	tat	tca	gca	gaa	atg	cgt	gca	ctc	1555
Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala	Glu	Met	Arg	Ala	Leu	
470					475					480					485	
ttc	gaa	gaa	ttc	aag	ctg	att	ttc	gat	ccc	cag	cgc	atc	ttc	aat	ccg	1603
Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln	Arg	Ile	Phe	Asn	Pro	
				490					495					500		
gga	gtg	ttg	gtc	tgg	gca	gat	cct	gtc	atg	caa	gga	ctt	cgc	atg	gac	1651
Gly	Val	Leu	Val	Trp	Ala	Asp	Pro	Val	Met	Gln	Gly	Leu	Arg	Met	Asp	
			505					510					515			
ccg	ggc	cag	cgc	gcc	ctc	gac	atc	acg	ccc	gta	cac	aaa	ttc	tct	aaa	1699
Pro	Gly	Gln	Arg	Ala	Leu	Asp	Ile	Thr	Pro	Val	His	Lys	Phe	Ser	Lys	
		520					525					530				
gac	aaa	ggt	tcc	atg	atc	aac	gcg	gtg	aat	cgc	tgc	gtg	ggt	gta	tcc	1747
Asp	Lys	Gly	Ser	Met	Ile	Asn	Ala	Val	Asn	Arg	Cys	Val	Gly	Val	Ser	
	535					540					545					
gca	tgc	cgc	tca	gaa	tcc	gac	gcg	atg	tgc	ccg	tcc	ttc	caa	atc	acc	1795
Ala	Cys	Arg	Ser	Glu	Ser	Asp	Ala	Met	Cys	Pro	Ser	Phe	Gln	Ile	Thr	
550					555					560					565	
ggc	gac	gaa	gta	cat	tcc	acc	aga	ggc	cgc	gcc	cgc	ttg	ctc	tct	gag	1843
Gly	Asp	Glu	Val	His	Ser	Thr	Arg	Gly	Arg	Ala	Arg	Leu	Leu	Ser	Glu	
				570					575					580		
atg	ttc	cgc	ggt	gaa	tcc	atc	gcc	gac	ggc	tac	cgc	agc	gaa	gaa	gtc	1891
Met	Phe	Arg	Gly	Glu	Ser	Ile	Ala	Asp	Gly	Tyr	Arg	Ser	Glu	Glu	Val	
			585					590					595			
aat	gaa	gcc	ctt	gac	ctg	tgc	ctt	tcc	tgc	aaa	gca	tgc	gca	tcg	gaa	1939
Asn	Glu	Ala	Leu	Asp	Leu	Cys	Leu	Ser	Cys	Lys	Ala	Cys	Ala	Ser	Glu	
		600					605					610				
tgt	cca	gtc	aac	gtc	gac	atg	tcc	acc	tac	aaa	gcc	gaa	ttc	ctg	gac	1987
Cys	Pro	Val	Asn	Val	Asp	Met	Ser	Thr	Tyr	Lys	Ala	Glu	Phe	Leu	Asp	

615	620	625	
aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc atg ggc Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val Met Gly 630 635 640 645			2035
tgg ctg ccg ctt ctg gga cac gtt gcc cat aaa ata ccg ctt ctt cct Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu Leu Pro 650 655 660			2083
acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca gtg gtg Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro Val Val 665 670 675			2131
cgc aag gtc ggc ggg ctc gct gat cgc ccg ttg att tcc ttc gcc cac Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe Ala His 680 685 690			2179
cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa acg gtg Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu Thr Val 695 700 705			2227
gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga cca gct Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly Pro Ala 710 715 720 725			2275
cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg gtc atc His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val Val Ile 730 735 740			2323
cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc ggc caa Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr Gly Gln 745 750 755			2371
ttg agc atg aca aag aaa gtc cta gaa caa acg gcg aaa gtg atg aaa Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val Met Lys 760 765 770			2419
ccc tac ctg gac caa ggt cta aca gtc gtt ggt ttg gaa cct tcg tgc Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro Ser Cys 775 780 785			2467
acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac cct gat Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn Pro Asp 790 795 800 805			2515
ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc atc gca Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val Ile Ala 810 815 820			2563
cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta aca gaa Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu Thr Glu 825 830 835			2611
tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta ggc gac Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu Gly Asp 840 845 850			2659
cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa gat gaa Pro Gln Gln Ser Ala Leu Leu Leu Glu Ala Leu Gly Val Lys Asp Glu 855 860 865			2707

caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc ttt gaa 2755
 Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly Phe Glu
 870 875 880 885

aaa gac cac gct gaa atg tcc ttc gca ctt ggt gaa cga gag ctg ttc 2803
 Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu Leu Phe
 890 895 900

ccc aag gtc aga aaa gca gaa gga cat gtg att gct gac ggt ttc tcc 2851
 Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly Phe Ser
 905 910 915

tgc cgc acc cag atc gaa caa ggc acc gga aaa caa gca acg cac ctt 2899
 Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr His Leu
 920 925 930

gca gag gtg gtc tta agc atc ttg gag caa aac aac atg gca caa 2944
 Ala Glu Val Val Leu Ser Ile Leu Glu Gln Asn Asn Met Ala Gln
 935 940 945

taacgatcat gcaacaggtg ctg 2967

<210> 132

<211> 948

<212> PRT

<213> Corynebacterium glutamicum

<400> 132

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Gln His Ser Arg Ala Lys Leu Arg Thr Asp Met Thr Thr Arg Ala Ala
 20 25 30

Tyr Ser Ser Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala
 35 40 45

Glu Pro Glu Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val
 50 55 60

Ala Arg Gly Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala
 65 70 75 80

Gly Asn Ala Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe
 85 90 95

Asn Arg Ile Leu Asp Ile Asp Pro Val Ala Gln Thr Ala Val Val Glu
 100 105 110

Pro Gly Val Val Cys Asp Ala Leu Arg Asp Ala Ala Ala Glu Phe Gly
 115 120 125

Leu Thr Tyr Gly Pro Asp Pro Ser Thr His Ser Arg Cys Thr Ile Gly
 130 135 140

Gly Met Val Ala Asn Asn Ala Cys Gly Ser His Ser Val Ala Phe Gly
 145 150 155 160

Thr Ala Ala Glu Asn Leu Val Asp Val Thr Leu Met Leu Ser Asp Gly

165										170					175				
Arg	Glu	Val	Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn				
			180					185					190						
Gln	Lys	Leu	Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys				
		195					200					205							
Glu	Leu	Gly	Arg	Phe	Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr				
	210					215					220								
Leu	Ala	His	Asp	Met	Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile				
225					230					235					240				
Gly	Ile	Ile	Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val				
			245						250					255					
Lys	Ala	Leu	Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg				
			260					265					270						
Ala	Ala	Ala	Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met				
		275					280					285							
Gly	Gly	Asp	Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu				
	290					295					300								
Ala	Gly	Gln	Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly				
305					310					315					320				
Trp	Leu	Tyr	Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln				
			325					330						335					
Ala	Ala	Glu	Glu	Val	Ala	Thr	Ala	Val	Asp	Thr	Ile	Asp	Tyr	Val	Val				
		340						345					350						
Val	Ser	Glu	Pro	Ser	Glu	Met	Arg	Glu	Leu	Trp	Arg	Ile	Arg	Glu	Ser				
		355					360					365							
Ser	Ala	Gly	Ile	Val	Thr	Arg	Leu	Ala	Asp	Gly	Gly	Glu	Ala	Trp	Pro				
	370					375					380								
Asn	Trp	Glu	Asp	Ser	Ala	Val	Pro	Pro	Glu	Asn	Leu	Ala	Asp	Tyr	Leu				
385					390					395					400				
Arg	Asp	Leu	Tyr	Ala	Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro				
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Phe	Gly	His	Phe	Gly	Glu	Gly	Cys	Val	His	Val	Arg	Ile	Ser	Phe	Asp				
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Ala	Ser	Thr	Leu	Val	Ala	Ser	Tyr	Gly	Gly	Ser	Leu	Ser	Gly	Glu	His				
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Gly	Asp	Gly	Arg	Ala	Arg	Ser	Ser	Phe	Leu	Asp	Arg	Met	Tyr	Ser	Ala				
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Glu	Met	Arg	Ala	Leu	Phe	Glu	Glu	Phe	Lys	Leu	Ile	Phe	Asp	Pro	Gln				
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Arg Ile Phe Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln
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 Gly Leu Arg Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val
 515 520 525
 His Lys Phe Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg
 530 535 540
 Cys Val Gly Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro
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 Ser Phe Gln Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala
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 Arg Leu Leu Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr
 580 585 590
 Arg Ser Glu Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys
 595 600 605
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 Ala Glu Phe Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala
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 His Tyr Val Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys
 645 650 655
 Ile Pro Leu Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu
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 Ile Ser Phe Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn
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 Ser Gly Glu Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu
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 Asp Thr Gly Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly
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 Tyr Asn Val Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp
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 His Ser Thr Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr
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 Ala Lys Val Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly
 770 775 780
 Leu Glu Pro Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu
 785 790 795 800
 Ser Asp Asn Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe
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Ala Glu Val Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser
 820 825 830

Leu Gln Leu Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu
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Arg Ser Leu Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu
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Gly Val Lys Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly
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Asn Trp Gly Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly
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Glu Arg Glu Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile
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Ala Asp Gly Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys
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gat gca gga att ttt aga cgc gtc cct gca gct gta gct gaa cca gaa 144
 Asp Ala Gly Ile Phe Arg Arg Val Pro Ala Ala Val Ala Glu Pro Glu
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aat gtg gaa caa att cgt gat gcc att gct gtt gcg gtg gca cga ggg 192
 Asn Val Glu Gln Ile Arg Asp Ala Ile Ala Val Ala Val Ala Arg Gly
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tgg tct gtt gtt ggg cgc ggt gga gga agc tcg gtt gct gga aat gcg 240
 Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
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atc ggt gaa ggt ttg atc atc gat acg tca cgc tat ttc aac cgc att 288
 Ile Gly Glu Gly Leu Ile Ile Asp Thr Ser Arg Tyr Phe Asn Arg Ile

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Leu	Asp	Ile	Asp	Pro	Val	Ala	Gln	Thr	Ala	Val	Val	Glu	Pro	Gly	Val		
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gtg	tgt	gat	gcc	ttg	cgc	gat	gca	gcc	gca	gaa	ttc	gga	tta	act	tac	384	
Val	Cys	Asp	Ala	Leu	Arg	Asp	Ala	Ala	Glu	Phe		Gly	Leu	Thr	Tyr		
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Gly	Pro	Asp	Pro	Ser	Thr	His	Ser	Arg	Cys	Thr	Ile	Gly	Gly	Met	Val		
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Thr	Val	Thr	Lys	Asp	Gly	Cys	Asp	Asp	Ala	Glu	Ile	Asn	Gln	Lys	Leu		
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acc	gac	tta	gcg	tcc	aag	aat	cag	gac	ctt	att	agt	aaa	gaa	ctg	ggg	624	
Thr	Asp	Leu	Ala	Ser	Lys	Asn	Gln	Asp	Leu	Ile	Ser	Lys	Glu	Leu	Gly		
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Arg	Phe	Pro	Arg	Gln	Val	Ser	Gly	Tyr	Gly	Leu	His	Tyr	Leu	Ala	His		
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gac	atg	gcc	aaa	gca	atg	gcg	ggc	acc	gag	gga	acc	att	gga	atc	att	720	
Asp	Met	Ala	Lys	Ala	Met	Ala	Gly	Thr	Glu	Gly	Thr	Ile	Gly	Ile	Ile		
225								230				235				240	
act	cgg	ttg	acg	gtg	aag	ttg	ggt	cca	aca	ccc	aaa	gtg	aaa	gcg	ctt	768	
Thr	Arg	Leu	Thr	Val	Lys	Leu	Val	Pro	Thr	Pro	Lys	Val	Lys	Ala	Leu		
245								250				255					
gct	gtc	ctg	gct	ttc	gac	acg	ggt	ttt	gac	gcc	gcc	cga	gca	gcc	gcc	816	
Ala	Val	Leu	Ala	Phe	Asp	Thr	Val	Phe	Asp	Ala	Ala	Arg	Ala	Ala	Ala		
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aaa	ttg	cga	ctg	cct	ggg	gta	gca	acc	att	gaa	ggc	atg	ggc	gga	gat	864	
Lys	Leu	Arg	Leu	Pro	Gly	Val	Ala	Thr	Ile	Glu	Gly	Met	Gly	Gly	Asp		
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ctc	ctc	gct	gcg	ctg	cgc	agt	aaa	cag	gga	caa	tca	gaa	gct	ggg	cag	912	
Leu	Leu	Ala	Ala	Leu	Arg	Ser	Lys	Gln	Gly	Gln	Ser	Glu	Ala	Gly	Gln		
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Asn	Leu	Pro	Gly	Asn	Arg	Ile	Gly	Ile	Glu	Ala	Gly	Gly	Trp	Leu	Tyr		
305								310				315				320	
tgc	gag	aca	gga	agt	gac	acc	ctg	cag	gcc	gcg	gta	caa	gcc	gcc	gag	1008	
Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu		
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gaa gtc gca acc gcc gtt gac acc att gat tac gtg gtc gtg tct gag	1056
Glu Val Ala Thr Ala Val Asp Thr Ile Asp Tyr Val Val Val Ser Glu	
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cct tct gaa atg cgg gaa ttg tgg cgc atc cgt gaa tcc tcg gcg ggc	1104
Pro Ser Glu Met Arg Glu Leu Trp Arg Ile Arg Glu Ser Ser Ala Gly	
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att gtc acg cgc tta gct gat ggt ggg gaa gcg tgg ccg aat tgg gaa	1152
Ile Val Thr Arg Leu Ala Asp Gly Gly Glu Ala Trp Pro Asn Trp Glu	
370 375 380	
gac tcg gcg gtg cct cca gag aat tta gct gat tat ctc cgc gat ctt	1200
Asp Ser Ala Val Pro Pro Glu Asn Leu Ala Asp Tyr Leu Arg Asp Leu	
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tat gcg ctg atg gat aag ttc gat tac cag ggt att cca ttt gga cac	1248
Tyr Ala Leu Met Asp Lys Phe Asp Tyr Gln Gly Ile Pro Phe Gly His	
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Phe Gly Glu Gly Cys Val His Val Arg Ile Ser Phe Asp Phe Ser Thr	
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aag gaa ggc ctg aag aaa ttc gag gcg ttc atg aat gaa gcc tcc acc	1344
Lys Glu Gly Leu Lys Lys Phe Glu Ala Phe Met Asn Glu Ala Ser Thr	
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Arg Ala Arg Ser Ser Phe Leu Asp Arg Met Tyr Ser Ala Glu Met Arg	
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Ala Leu Phe Glu Glu Phe Lys Leu Ile Phe Asp Pro Gln Arg Ile Phe	
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Asn Pro Gly Val Leu Val Trp Ala Asp Pro Val Met Gln Gly Leu Arg	
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Met Asp Pro Gly Gln Arg Ala Leu Asp Ile Thr Pro Val His Lys Phe	
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tct aaa gac aaa ggt tcc atg atc aac gcg gtg aat cgc tgc gtg ggt	1632
Ser Lys Asp Lys Gly Ser Met Ile Asn Ala Val Asn Arg Cys Val Gly	
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gta tcc gca tgc cgc tca gaa tcc gac gcg atg tgc ccg tcc ttc caa	1680
Val Ser Ala Cys Arg Ser Glu Ser Asp Ala Met Cys Pro Ser Phe Gln	
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Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu	
565 570 575	

tct gag atg ttc cgc ggt gaa tcc atc gcc gac ggc tac cgc agc gaa	1776
Ser Glu Met Phe Arg Gly Glu Ser Ile Ala Asp Gly Tyr Arg Ser Glu	
580 585 590	
gaa gtc aat gaa gcc ctt gac ctg tgc ctt tcc tgc aaa gca tgc gca	1824
Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala	
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Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe	
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ctg gac aaa cac tac gcc ggc cga ctt cgc ccc atg gcc cat tac gtc	1920
Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val	
625 630 635 640	
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Met Gly Trp Leu Pro Leu Leu Gly His Val Ala His Lys Ile Pro Leu	
645 650 655	
ctt cct acg ctt atc gac gcc acc atg cag tca gca ctc acc gcc cca	2016
Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro	
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Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe	
675 680 685	
gcc cac cgc tcg ctg cgc aag tac aag ccg aag aaa aac tca ggt gaa	2112
Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu	
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acg gtg gtg ctg tgg ccc gat tcc ttc aac acc aac ctc gac acc gga	2160
Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly	
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cca gct cac gca gcg atc aaa act ctt gaa gcc ctc ggt tac aac gtg	2208
Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val	
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gtc atc cca gat ggc ttc gtc tgc tgt gga ctc acc tgg cat tcc acc	2256
Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr	
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Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val	
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Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro	
770 775 780	
tcg tgc acc gtc atg ctt caa gat gag gca aca gaa ctc tcc gat aac	2400
Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn	
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cct gat ctg gca cgc ctt gca gca ctg acc aaa cca ttc gct gag gtc	2448
Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val	
805 810 815	
atc gca cca aag atc acc gag cta gtc gag tct gga agc ctc cag cta	2496

Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
820 825 830

aca gaa tca act gcg ctt acc cag gtg cac tgc cac gag cgt tcg cta 2544
Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
835 840 845

ggc gac cca caa caa tcg gca ctc gtt ctt gaa gct ttg ggt gta aaa 2592
Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
850 855 860

gat gaa caa att gcc act ggt tgt tgc ggg ctt gcc gga aac tgg ggc 2640
Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
865 870 875 880

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Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
885 890 895

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Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
900 905 910

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915 920 925

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Gln
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Trp Ser Val Val Gly Arg Gly Gly Gly Ser Ser Val Ala Gly Asn Ala
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			260					265					270		
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Cys	Glu	Thr	Gly	Ser	Asp	Thr	Leu	Gln	Ala	Ala	Val	Gln	Ala	Ala	Glu
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Tyr	Ala	Leu	Met	Asp	Lys	Phe	Asp	Tyr	Gln	Gly	Ile	Pro	Phe	Gly	His
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 545 550 555 560
 Ile Thr Gly Asp Glu Val His Ser Thr Arg Gly Arg Ala Arg Leu Leu
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 580 585 590
 Glu Val Asn Glu Ala Leu Asp Leu Cys Leu Ser Cys Lys Ala Cys Ala
 595 600 605
 Ser Glu Cys Pro Val Asn Val Asp Met Ser Thr Tyr Lys Ala Glu Phe
 610 615 620
 Leu Asp Lys His Tyr Ala Gly Arg Leu Arg Pro Met Ala His Tyr Val
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 Leu Pro Thr Leu Ile Asp Ala Thr Met Gln Ser Ala Leu Thr Ala Pro
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 Val Val Arg Lys Val Gly Gly Leu Ala Asp Arg Pro Leu Ile Ser Phe
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 Ala His Arg Ser Leu Arg Lys Tyr Lys Pro Lys Lys Asn Ser Gly Glu
 690 695 700
 Thr Val Val Leu Trp Pro Asp Ser Phe Asn Thr Asn Leu Asp Thr Gly
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 Pro Ala His Ala Ala Ile Lys Thr Leu Glu Ala Leu Gly Tyr Asn Val
 725 730 735
 Val Ile Pro Asp Gly Phe Val Cys Cys Gly Leu Thr Trp His Ser Thr
 740 745 750

Gly Gln Leu Ser Met Thr Lys Lys Val Leu Glu Gln Thr Ala Lys Val
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Met Lys Pro Tyr Leu Asp Gln Gly Leu Thr Val Val Gly Leu Glu Pro
770 775 780

Ser Cys Thr Val Met Leu Gln Asp Glu Ala Thr Glu Leu Ser Asp Asn
785 790 795 800

Pro Asp Leu Ala Arg Leu Ala Ala Leu Thr Lys Pro Phe Ala Glu Val
805 810 815

Ile Ala Pro Lys Ile Thr Glu Leu Val Glu Ser Gly Ser Leu Gln Leu
820 825 830

Thr Glu Ser Thr Ala Leu Thr Gln Val His Cys His Glu Arg Ser Leu
835 840 845

Gly Asp Pro Gln Gln Ser Ala Leu Val Leu Glu Ala Leu Gly Val Lys
850 855 860

Asp Glu Gln Ile Ala Thr Gly Cys Cys Gly Leu Ala Gly Asn Trp Gly
865 870 875 880

Phe Glu Lys Asp His Ala Glu Met Ser Phe Ala Leu Gly Glu Arg Glu
885 890 895

Leu Phe Pro Lys Val Arg Lys Ala Glu Gly His Val Ile Ala Asp Gly
900 905 910

Phe Ser Cys Arg Thr Gln Ile Glu Gln Gly Thr Gly Lys Gln Ala Thr
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930 935 940

Gln
945

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<222> (101)..(1360)

<223> RXA01901

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Met Val Lys Arg Gln
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Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met Lys Phe Lys Lys Pro
10 15 20

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Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser Ala Leu Thr Ile Tyr	
25 30 35	
gac ctg cgt aaa att gct aaa cga cgc acc cca gct gcc gcg ttc gac	259
Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro Ala Ala Phe Asp	
40 45 50	
tac acc gac ggc gca gcc gag gcc gaa ctc tca atc aca cgc gca cgt	307
Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser Ile Thr Arg Ala Arg	
55 60 65	
gaa gca ttc gaa aac atc gaa ttc cac cca gac atc ctc aag cct gca	355
Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp Ile Leu Lys Pro Ala	
70 75 80 85	
gaa cac gta gac acc acc acc caa atc ctg ggc gga acc tcc tcc atg	403
Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly Gly Thr Ser Ser Met	
90 95 100	
cca ttc ggc atc gca cca acc ggc ttc acc cgc ctc atg cag acc gaa	451
Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg Leu Met Gln Thr Glu	
105 110 115	
ggt gaa atc gca ggt gcc gga gct gca ggc gct gca gga att cct ttc	499
Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala Ala Gly Ile Pro Phe	
120 125 130	
acc ctg tcc acc ctg ggc act acc tcc atc gaa gac gtc aag gcc acc	547
Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu Asp Val Lys Ala Thr	
135 140 145	
aac ccc aac ggc cga aac tgg ttc cag ctc tac gtc atg cgc gac cgc	595
Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr Val Met Arg Asp Arg	
150 155 160 165	
gaa atc tcc tac ggc ctc gtc gaa cgc gca gcc aaa gca gga ttc gac	643
Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala Lys Ala Gly Phe Asp	
170 175 180	
acc ctg atg ttc acc gtg gat acc ccc atc gcc ggc tac cgc atc cgc	691
Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala Gly Tyr Arg Ile Arg	
185 190 195	
gat tcc cgc aac gga ttc tcc atc ccg cca cag ctg acc cca tcc acc	739
Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln Leu Thr Pro Ser Thr	
200 205 210	
gtg ctc aat gca atc cca cgc cca tgg tgg tgg atc gac ttc ctg acc	787
Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp Ile Asp Phe Leu Thr	
215 220 225	
acc cca acc ctt gag ttc gca tcc ctt tcc tcg acc ggc gga acc gtg	835
Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser Thr Gly Gly Thr Val	
230 235 240 245	
ggc gac ctc ctc aac tcc gcg atg gat ccc acc att tct tac gaa gac	883
Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr Ile Ser Tyr Glu Asp	
250 255 260	
ctc aag gtc atc cgt gaa atg tgg cca ggc aag ctc gta gtc aag ggt	931

Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys Leu Val Val Lys Gly
 265 270 275
 gtc cag aac gtt gaa gac tcc gtc aaa ctc ctc gac caa ggc gtc gac 979
 Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu Asp Gln Gly Val Asp
 280 285 290
 ggc ctc atc ctc tcc aac cac ggt ggc cgt caa ctc gac cgc gca cca 1027
 Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln Leu Asp Arg Ala Pro
 295 300 305
 gtc cca ttc cac ctc ctg cca cag gta cgc aag gaa gtc gga tct gaa 1075
 Val Pro Phe His Leu Leu Pro Gln Val Arg Lys Glu Val Gly Ser Glu
 310 315 320 325
 cca acc atc atg atc gac acc ggc atc atg aac ggc gcc gac atc gtc 1123
 Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn Gly Ala Asp Ile Val
 330 335 340
 gca gcc gta gcc atg ggc gct gac ttc acc ctc atc ggt cgt gcc tac 1171
 Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu Ile Gly Arg Ala Tyr
 345 350 355
 ctc tac gga ctc atg gcc gga ggc cgc gaa ggc gtc gac cgc acc atc 1219
 Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly Val Asp Arg Thr Ile
 360 365 370
 gcc att ctc cgc agc gag atc acc cgc acc atg gct ctc ctc ggt gtt 1267
 Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met Ala Leu Leu Gly Val
 375 380 385
 tcc tcc ctc gaa gaa ctc gag cca cgc cac gtc acc cag ctg gcc aag 1315
 Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val Thr Gln Leu Ala Lys
 390 395 400 405
 atg gtt cca gtt tct gac gca act cgt tct gca gcg gcg gag att 1360
 Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala Ala Ala Glu Ile
 410 415 420
 taaaagtttc tctccttagc tat 1383

<210> 136

<211> 420

<212> PRT

<213> Corynebacterium glutamicum

<400> 136

Met Val Lys Arg Gln Leu Pro Asn Pro Ala Glu Leu Leu Glu Leu Met
 1 5 10 15

Lys Phe Lys Lys Pro Glu Leu Asn Gly Lys Lys Arg Arg Leu Asp Ser
 20 25 30

Ala Leu Thr Ile Tyr Asp Leu Arg Lys Ile Ala Lys Arg Arg Thr Pro
 35 40 45

Ala Ala Ala Phe Asp Tyr Thr Asp Gly Ala Ala Glu Ala Glu Leu Ser
 50 55 60

Ile Thr Arg Ala Arg Glu Ala Phe Glu Asn Ile Glu Phe His Pro Asp

65	70	75	80
Ile Leu Lys Pro Ala Glu His Val Asp Thr Thr Thr Gln Ile Leu Gly	85	90	95
Gly Thr Ser Ser Met Pro Phe Gly Ile Ala Pro Thr Gly Phe Thr Arg	100	105	110
Leu Met Gln Thr Glu Gly Glu Ile Ala Gly Ala Gly Ala Ala Gly Ala	115	120	125
Ala Gly Ile Pro Phe Thr Leu Ser Thr Leu Gly Thr Thr Ser Ile Glu	130	135	140
Asp Val Lys Ala Thr Asn Pro Asn Gly Arg Asn Trp Phe Gln Leu Tyr	145	150	155
Val Met Arg Asp Arg Glu Ile Ser Tyr Gly Leu Val Glu Arg Ala Ala	165	170	175
Lys Ala Gly Phe Asp Thr Leu Met Phe Thr Val Asp Thr Pro Ile Ala	180	185	190
Gly Tyr Arg Ile Arg Asp Ser Arg Asn Gly Phe Ser Ile Pro Pro Gln	195	200	205
Leu Thr Pro Ser Thr Val Leu Asn Ala Ile Pro Arg Pro Trp Trp Trp	210	215	220
Ile Asp Phe Leu Thr Thr Pro Thr Leu Glu Phe Ala Ser Leu Ser Ser	225	230	235
Thr Gly Gly Thr Val Gly Asp Leu Leu Asn Ser Ala Met Asp Pro Thr	245	250	255
Ile Ser Tyr Glu Asp Leu Lys Val Ile Arg Glu Met Trp Pro Gly Lys	260	265	270
Leu Val Val Lys Gly Val Gln Asn Val Glu Asp Ser Val Lys Leu Leu	275	280	285
Asp Gln Gly Val Asp Gly Leu Ile Leu Ser Asn His Gly Gly Arg Gln	290	295	300
Leu Asp Arg Ala Pro Val Pro Phe His Leu Leu Pro Gln Val Arg Lys	305	310	315
Glu Val Gly Ser Glu Pro Thr Ile Met Ile Asp Thr Gly Ile Met Asn	325	330	335
Gly Ala Asp Ile Val Ala Ala Val Ala Met Gly Ala Asp Phe Thr Leu	340	345	350
Ile Gly Arg Ala Tyr Leu Tyr Gly Leu Met Ala Gly Gly Arg Glu Gly	355	360	365
Val Asp Arg Thr Ile Ala Ile Leu Arg Ser Glu Ile Thr Arg Thr Met	370	375	380
Ala Leu Leu Gly Val Ser Ser Leu Glu Glu Leu Glu Pro Arg His Val	385	390	395
			400

Thr Gln Leu Ala Lys Met Val Pro Val Ser Asp Ala Thr Arg Ser Ala
 405 410 415

Ala Ala Glu Ile
 420

<210> 137

<211> 1836

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1813)

<223> RXN01952

<400> 137

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tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
 Met Thr Gln Pro Gly
 1 5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
 10 15 20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
 25 30 35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg
 40 45 50

ccc ggc acg ctg gtc gag atg tgg cgg gcg ctg cag gta tcc gtc gac 307
 Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu Gln Val Ser Val Asp
 55 60 65

aac aac ctc atc gtc atc ccg cag gca tcg aac acg ggc ctg act ggt 355
 Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn Thr Gly Leu Thr Gly
 70 75 80 85

gga tcc ggc ccc ggc ttc caa gac tac gat cgc ccc att gtg atc atc 403
 Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg Pro Ile Val Ile Ile
 90 95 100

tcg act cac cgc atc gat gag gtg cac ctc atc aac gac gcg cgc gag 451
 Ser Thr His Arg Ile Asp Glu Val His Leu Ile Asn Asp Ala Arg Glu
 105 110 115

gcg atc tcg ctc gcg ggc acc ccg ctg aca cac ctg acc gac gcg ctc 499
 Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His Leu Thr Asp Ala Leu
 120 125 130

gcc aag cac cag cgc gag ccg cac tcg gtg atc ggg tcg aca tca atc 547
 Ala Lys His Gln Arg Glu Pro His Ser Val Ile Gly Ser Thr Ser Ile
 135 140 145

ggc gcc tcg gtc atc ggc ggc atc gcg aac aac tcg ggc ggc agc cag	595
Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn Ser Gly Gly Ser Gln	
150 155 160 165	
att cgc aag ggt ccg gca ttc acg cgc gaa gcg atc ttc gcc cgc gtc	643
Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala Ile Phe Ala Arg Val	
170 175 180	
aac gac gac ggc aag gtc gag ctg gtc aat cac ctg ggc atc tcg ctc	691
Asn Asp Asp Gly Lys Val Glu Leu Val Asn His Leu Gly Ile Ser Leu	
185 190 195	
gga gac gac cct gag gtc gca ctc gac cgt cta cag cgc ggc gag tgg	739
Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu Gln Arg Gly Glu Trp	
200 205 210	
tct ccc gag gat gtc acc cca gct ccc gaa gac tcg aac gag acc gag	787
Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp Ser Asn Glu Thr Glu	
215 220 225	
tac gcc gag cac ttg cgc aag atc gtg cct tcg cct gct cgc tac aat	835
Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser Pro Ala Arg Tyr Asn	
230 235 240 245	
gcg aac ccc gag tac ctg ttc gag gct tcc ggc tcg gcc ggc aag ctg	883
Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly Ser Ala Gly Lys Leu	
250 255 260	
atg gtg ttc gcg gtg cgc acc cgc acc ttc cct cgc gaa gtg cac ccg	931
Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro Arg Glu Val His Pro	
265 270 275	
acc gtg ttt tac atc ggc acg aac aac acg cac gag ctc gaa gag atc	979
Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His Glu Leu Glu Glu Ile	
280 285 290	
cgt cgg ttg ttc ctc gaa gcc gac atg ccg ctg cct atc tct ggt gag	1027
Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu Pro Ile Ser Gly Glu	
295 300 305	
tac atg ggc cgc agt gcc ttc gac ttg gcc gag aag tac ggc aaa gac	1075
Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu Lys Tyr Gly Lys Asp	
310 315 320 325	
acc ttc gtc ttc ctg aag ttc atg agt cca gcg ctg cag acg cgc atg	1123
Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala Leu Gln Thr Arg Met	
330 335 340	
ttc tcg ttc aag acg tgg gcc aac ggc ttg ttc tcg aag att ccc ggc	1171
Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe Ser Lys Ile Pro Gly	
345 350 355	
att ggt ccg acc ttc gcc gac acg gta tcg caa gcc atg ttc agc gtg	1219
Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln Ala Met Phe Ser Val	
360 365 370	
ctg ccc aac cag ctg ccc aag cgc atg atg gag tac cgc aac cgt ttc	1267
Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu Tyr Arg Asn Arg Phe	
375 380 385	
gag cat cac ctg ctg ctc acc gtc agc gag tcg cag aag gcc gcg agc	1315

Glu His His Leu Leu Leu Thr Val Ser Glu Ser Gln Lys Ala Ala Ser
 390 395 400 405
 gag aag atg ctc aag gag ttc ttc gca gag ccc gag cac act ggt gag 1363
 Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro Glu His Thr Gly Glu
 410 415 420
 ttc ttc atc tgc acg tct gat gaa gaa aag agc gcg tcg ctc aac cgg 1411
 Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser Ala Ser Leu Asn Arg
 425 430 435
 ttc ggc gcg gcc agt gcc gcc act cgc tac gcc gcg ttg aag cgc cgg 1459
 Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala Ala Leu Lys Arg Arg
 440 445 450
 cac atc gca ggg ctc atc ccc atc gat gtg gcc ctg cgt cgc gac gat 1507
 His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala Leu Arg Arg Asp Asp
 455 460 465
 tgg aac tgg ctc gag gtg ctg ccg gag gag atc gac gac cag ctt gag 1555
 Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile Asp Asp Gln Leu Glu
 470 475 480 485
 gtc aag gcg tat tac ggg cac ttc ttc tgc cat gtg atg cac cag gac 1603
 Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His Val Met His Gln Asp
 490 495 500
 tat gtc gcc aag cag ggc gtg gat ctc gag gcg ctg cac gac cgc atc 1651
 Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala Leu His Asp Arg Ile
 505 510 515
 cag cac ctg ctg gag gag cgc ggc gcg aag ctg ccc gcc gag cac aac 1699
 Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu Pro Ala Glu His Asn
 520 525 530
 tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac ttc aag 1747
 Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His Phe Lys
 535 540 545
 gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc acg tcg 1795
 Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly Thr Ser
 550 555 560 565
 ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 1836
 Pro His Lys Asp Trp Ala
 570

<210> 138

<211> 571

<212> PRT

<213> Corynebacterium glutamicum

<400> 138

Met Thr Gln Pro Gly Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp
 1 5 10 15

Ala Phe Lys Arg Ile Val Gly Asp Glu His Val Leu Thr Ser Glu Arg
 20 25 30

Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val

35					40					45					
Phe	Ala	Val	Val	Arg	Pro	Gly	Thr	Leu	Val	Glu	Met	Trp	Arg	Ala	Leu
50						55					60				
Gln	Val	Ser	Val	Asp	Asn	Asn	Leu	Ile	Val	Ile	Pro	Gln	Ala	Ser	Asn
65					70					75					80
Thr	Gly	Leu	Thr	Gly	Gly	Ser	Gly	Pro	Gly	Phe	Gln	Asp	Tyr	Asp	Arg
				85					90					95	
Pro	Ile	Val	Ile	Ile	Ser	Thr	His	Arg	Ile	Asp	Glu	Val	His	Leu	Ile
			100					105					110		
Asn	Asp	Ala	Arg	Glu	Ala	Ile	Ser	Leu	Ala	Gly	Thr	Pro	Leu	Thr	His
		115					120					125			
Leu	Thr	Asp	Ala	Leu	Ala	Lys	His	Gln	Arg	Glu	Pro	His	Ser	Val	Ile
130					135					140					
Gly	Ser	Thr	Ser	Ile	Gly	Ala	Ser	Val	Ile	Gly	Gly	Ile	Ala	Asn	Asn
145					150					155					160
Ser	Gly	Gly	Ser	Gln	Ile	Arg	Lys	Gly	Pro	Ala	Phe	Thr	Arg	Glu	Ala
				165					170					175	
Ile	Phe	Ala	Arg	Val	Asn	Asp	Asp	Gly	Lys	Val	Glu	Leu	Val	Asn	His
			180					185					190		
Leu	Gly	Ile	Ser	Leu	Gly	Asp	Asp	Pro	Glu	Val	Ala	Leu	Asp	Arg	Leu
		195					200					205			
Gln	Arg	Gly	Glu	Trp	Ser	Pro	Glu	Asp	Val	Thr	Pro	Ala	Pro	Glu	Asp
	210					215					220				
Ser	Asn	Glu	Thr	Glu	Tyr	Ala	Glu	His	Leu	Arg	Lys	Ile	Val	Pro	Ser
225					230					235					240
Pro	Ala	Arg	Tyr	Asn	Ala	Asn	Pro	Glu	Tyr	Leu	Phe	Glu	Ala	Ser	Gly
				245					250					255	
Ser	Ala	Gly	Lys	Leu	Met	Val	Phe	Ala	Val	Arg	Thr	Arg	Thr	Phe	Pro
			260				265						270		
Arg	Glu	Val	His	Pro	Thr	Val	Phe	Tyr	Ile	Gly	Thr	Asn	Asn	Thr	His
		275					280					285			
Glu	Leu	Glu	Glu	Ile	Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu
	290					295					300				
Pro	Ile	Ser	Gly	Glu	Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu
305					310					315					320
Lys	Tyr	Gly	Lys	Asp	Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala
				325					330					335	
Leu	Gln	Thr	Arg	Met	Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe
			340					345					350		
Ser	Lys	Ile	Pro	Gly	Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln
		355					360					365			

Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
370 375 380

Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
385 390 395 400

Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
405 410 415

Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
420 425 430

Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
435 440 445

Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
450 455 460

Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
465 470 475 480

Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
485 490 495

Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
500 505 510

Leu His Asp Arg Ile Gln His Leu Leu Glu Glu Arg Gly Ala Lys Leu
515 520 525

Pro Ala Glu His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met
530 535 540

Glu Glu His Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly
545 550 555 560

Ile Gly Gly Thr Ser Pro His Lys Asp Trp Ala
565 570

<210> 139

<211> 239

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(216)

<223> FRXA01952

<400> 139

cca gga cta tgt cgc caa gca ggg cgt gga tct caa ggc gct gac gac 48
Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
1 5 10 15

cgc atc cag cac ttg ctg gag gag cac ggc aag aag ctg ccc gcc gag 96
Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
20 25 30

cac aac tac ggt cgc atg tac aag ctg ccg gag tcc atg gaa gag cac 144

His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
 35 40 45

ttc aag gag ctc gat ccg acg aat acg ttc aac gcc ggt atc ggc ggc 192
 Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
 50 55 60

acg tcg ccg cac aag gac tgg gcc taagtcccca aggtagcgcg acg 239
 Thr Ser Pro His Lys Asp Trp Ala
 65 70

<210> 140

<211> 72

<212> PRT

<213> Corynebacterium glutamicum

<400> 140

Pro Gly Leu Cys Arg Gln Ala Gly Arg Gly Ser Gln Gly Ala Asp Asp
 1 5 10 15

Arg Ile Gln His Leu Leu Glu Glu His Gly Lys Lys Leu Pro Ala Glu
 20 25 30

His Asn Tyr Gly Arg Met Tyr Lys Leu Pro Glu Ser Met Glu Glu His
 35 40 45

Phe Lys Glu Leu Asp Pro Thr Asn Thr Phe Asn Ala Gly Ile Gly Gly
 50 55 60

Thr Ser Pro His Lys Asp Trp Ala
 65 70

<210> 141

<211> 1699

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1699)

<223> FRXA01955

<400> 141

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tgacgcgctt gtgatgcaac tgaatatagg aagcttagag atg acg caa cca gga 115
 Met Thr Gln Pro Gly
 1 5

cag acc acc acg act tcg cac gaa gcg atc gat gcg ttc aag aga atc 163
 Gln Thr Thr Thr Thr Ser His Glu Ala Ile Asp Ala Phe Lys Arg Ile
 10 15 20

gtc ggc gac gaa cat gta ctg acc tct gag cgt gcc acg atg cca ttc 211
 Val Gly Asp Glu His Val Leu Thr Ser Glu Arg Ala Thr Met Pro Phe
 25 30 35

agc aaa ggc tat cga ttc ggc gga gga cca gtc ttc gcc gtg gtg cgc 259
 Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val Phe Ala Val Val Arg

40					45					50						
ccc Pro	ggc Gly	acg Thr	ctg Leu	gtc Val	gag Glu	atg Met	tgg Trp	cgg Arg	gcg Ala	ctg Leu	cag Gln	gta Val	tcc Ser	gtc Val	gac Asp	307
55						60				65						
aac Asn	aac Asn	ctc Leu	atc Ile	gtc Val	atc Ile	ccg Pro	cag Gln	gca Ala	tcg Ser	aac Asn	acg Thr	ggc Gly	ctg Leu	act Thr	ggt Gly	355
70						75				80						85
gga Gly	tcc Ser	ggc Gly	ccc Pro	ggc Gly	ttc Phe	caa Gln	gac Asp	tac Tyr	gat Asp	cgc Arg	ccc Pro	att Ile	gtg Val	atc Ile	atc Ile	403
				90				95						100		
tcg Ser	act Thr	cac His	cgc Arg	atc Ile	gat Asp	gag Glu	gtg Val	cac His	ctc Leu	atc Ile	aac Asn	gac Asp	gcg Ala	cgc Arg	gag Glu	451
				105				110				115				
gcg Ala	atc Ile	tcg Ser	ctc Leu	gcg Ala	ggc Gly	acc Thr	ccg Pro	ctg Leu	aca Thr	cac His	ctg Leu	acc Thr	gac Asp	gcg Ala	ctc Leu	499
		120				125						130				
gcc Ala	aag Lys	cac His	cag Gln	cgc Arg	gag Glu	ccg Pro	cac His	tcg Ser	gtg Val	atc Ile	ggg Gly	tcg Ser	aca Thr	tca Ser	atc Ile	547
		135				140				145						
ggc Gly	gcc Ala	tcg Ser	gtc Val	atc Ile	ggc Gly	ggc Gly	atc Ile	gcg Ala	aac Asn	aac Asn	tcg Ser	ggc Gly	ggc Gly	agc Ser	cag Gln	595
150				155		160				165						165
att Ile	cgc Arg	aag Lys	ggt Gly	ccg Pro	gca Ala	ttc Phe	acg Thr	cgc Arg	gaa Glu	gcg Ala	atc Ile	ttc Phe	gcc Ala	cgc Arg	gtc Val	643
				170				175						180		
aac Asn	gac Asp	gac Asp	ggc Gly	aag Lys	gtc Val	gag Glu	ctg Leu	gtc Val	aat Asn	cac His	ctg Leu	ggc Gly	atc Ile	tcg Ser	ctc Leu	691
		185				190		195				195				
gga Gly	gac Asp	gac Asp	cct Pro	gag Glu	gtc Val	gca Ala	ctc Leu	gac Asp	cgt Arg	cta Leu	cag Gln	cgc Arg	ggc Gly	gag Glu	tgg Trp	739
		200				205				210						
tct Ser	ccc Pro	gag Glu	gat Asp	gtc Val	acc Thr	cca Pro	gct Ala	ccc Pro	gaa Glu	gac Asp	tcg Ser	aac Asn	gag Glu	acc Thr	gag Glu	787
		215				220				225						
tac Tyr	gcc Ala	gag Glu	cac His	ttg Leu	cgc Arg	aag Lys	atc Ile	gtg Val	cct Pro	tcg Ser	cct Pro	gct Ala	cgc Arg	tac Tyr	aat Asn	835
230				235						240						245
gcg Ala	aac Asn	ccc Pro	gag Glu	tac Tyr	ctg Leu	ttc Phe	gag Glu	gct Ala	tcc Ser	ggc Gly	tcg Ser	gcc Ala	ggc Gly	aag Lys	ctg Leu	883
				250				255						260		
atg Met	gtg Val	ttc Phe	gcg Ala	gtg Val	cgc Arg	acc Thr	cgc Arg	acc Thr	ttc Phe	cct Pro	cgc Arg	gaa Glu	gtg Val	cac His	ccg Pro	931
		265				270		275				275				
acc Thr	gtg Val	ttt Phe	tac Tyr	atc Ile	ggc Gly	acg Thr	aac Asn	aac Asn	acg Thr	cac His	gag Glu	ctc Leu	gaa Glu	gag Glu	atc Ile	979
		280				285		290				290				

cgt	cgg	ttg	ttc	ctc	gaa	gcc	gac	atg	ccg	ctg	cct	atc	tct	ggg	gag	1027
Arg	Arg	Leu	Phe	Leu	Glu	Ala	Asp	Met	Pro	Leu	Pro	Ile	Ser	Gly	Glu	
	295					300					305					
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Tyr	Met	Gly	Arg	Ser	Ala	Phe	Asp	Leu	Ala	Glu	Lys	Tyr	Gly	Lys	Asp	
310					315					320					325	
acc	ttc	gtc	ttc	ctg	aag	ttc	atg	agt	cca	gcg	ctg	cag	acg	cgc	atg	1123
Thr	Phe	Val	Phe	Leu	Lys	Phe	Met	Ser	Pro	Ala	Leu	Gln	Thr	Arg	Met	
				330					335					340		
ttc	tcg	ttc	aag	acg	tgg	gcc	aac	ggc	ttg	ttc	tcg	aag	att	ccc	ggc	1171
Phe	Ser	Phe	Lys	Thr	Trp	Ala	Asn	Gly	Leu	Phe	Ser	Lys	Ile	Pro	Gly	
			345					350					355			
att	ggg	ccg	acc	ttc	gcc	gac	acg	gta	tcg	caa	gcc	atg	ttc	agc	gtg	1219
Ile	Gly	Pro	Thr	Phe	Ala	Asp	Thr	Val	Ser	Gln	Ala	Met	Phe	Ser	Val	
		360					365					370				
ctg	ccc	aac	cag	ctg	ccc	aag	cgc	atg	atg	gag	tac	cgc	aac	cgt	ttc	1267
Leu	Pro	Asn	Gln	Leu	Pro	Lys	Arg	Met	Met	Glu	Tyr	Arg	Asn	Arg	Phe	
	375					380					385					
gag	cat	cac	ctg	ctg	ctc	acc	gtc	agc	gag	tcg	cag	aag	gcc	gcg	agc	1315
Glu	His	His	Leu	Leu	Leu	Thr	Val	Ser	Glu	Ser	Gln	Lys	Ala	Ala	Ser	
390					395					400					405	
gag	aag	atg	ctc	aag	gag	ttc	ttc	gca	gag	ccc	gag	cac	act	ggg	gag	1363
Glu	Lys	Met	Leu	Lys	Glu	Phe	Phe	Ala	Glu	Pro	Glu	His	Thr	Gly	Glu	
			410					415					420			
ttc	ttc	atc	tgc	acg	tct	gat	gaa	gaa	aag	agc	gcg	tcg	ctc	aac	cgg	1411
Phe	Phe	Ile	Cys	Thr	Ser	Asp	Glu	Glu	Lys	Ser	Ala	Ser	Leu	Asn	Arg	
			425					430					435			
ttc	ggc	gcg	gcc	agt	gcc	gcc	act	cgc	tac	gcc	gcg	ttg	aag	cgc	cgg	1459
Phe	Gly	Ala	Ala	Ser	Ala	Ala	Thr	Arg	Tyr	Ala	Ala	Leu	Lys	Arg	Arg	
		440					445					450				
cac	atc	gca	ggg	ctc	atc	ccc	atc	gat	gtg	gcc	ctg	cgt	cgc	gac	gat	1507
His	Ile	Ala	Gly	Leu	Ile	Pro	Ile	Asp	Val	Ala	Leu	Arg	Arg	Asp	Asp	
	455					460					465					
tgg	aac	tgg	ctc	gag	gtg	ctg	ccg	gag	gag	atc	gac	gac	cag	ctt	gag	1555
Trp	Asn	Trp	Leu	Glu	Val	Leu	Pro	Glu	Glu	Ile	Asp	Asp	Gln	Leu	Glu	
470					475					480					485	
gtc	aag	gcg	tat	tac	ggg	cac	ttc	ttc	tgc	cat	gtg	atg	cac	cag	gac	1603
Val	Lys	Ala	Tyr	Tyr	Gly	His	Phe	Phe	Cys	His	Val	Met	His	Gln	Asp	
			490						495					500		
tat	gtc	gcc	aag	cag	ggc	gtg	gat	ctc	gag	gcg	ctg	cac	gac	cgc	atc	1651
Tyr	Val	Ala	Lys	Gln	Gly	Val	Asp	Leu	Glu	Ala	Leu	His	Asp	Arg	Ile	
			505					510					515			
cag	cac	ctg	ctg	gag	gag	cgc	ggc	gcg	aag	ctg	ccc	gcc	gag	cac	aac	1699
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 <213> Corynebacterium glutamicum

<400> 142

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Ala Thr Met Pro Phe Ser Lys Gly Tyr Arg Phe Gly Gly Gly Pro Val
      35          40          45

Phe Ala Val Val Arg Pro Gly Thr Leu Val Glu Met Trp Arg Ala Leu
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Gln Val Ser Val Asp Asn Asn Leu Ile Val Ile Pro Gln Ala Ser Asn
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Thr Gly Leu Thr Gly Gly Ser Gly Pro Gly Phe Gln Asp Tyr Asp Arg
      85          90          95

Pro Ile Val Ile Ile Ser Thr His Arg Ile Asp Glu Val His Leu Ile
      100          105          110

Asn Asp Ala Arg Glu Ala Ile Ser Leu Ala Gly Thr Pro Leu Thr His
      115          120          125

Leu Thr Asp Ala Leu Ala Lys His Gln Arg Glu Pro His Ser Val Ile
      130          135          140

Gly Ser Thr Ser Ile Gly Ala Ser Val Ile Gly Gly Ile Ala Asn Asn
      145          150          155          160

Ser Gly Gly Ser Gln Ile Arg Lys Gly Pro Ala Phe Thr Arg Glu Ala
      165          170          175

Ile Phe Ala Arg Val Asn Asp Asp Gly Lys Val Glu Leu Val Asn His
      180          185          190

Leu Gly Ile Ser Leu Gly Asp Asp Pro Glu Val Ala Leu Asp Arg Leu
      195          200          205

Gln Arg Gly Glu Trp Ser Pro Glu Asp Val Thr Pro Ala Pro Glu Asp
      210          215          220

Ser Asn Glu Thr Glu Tyr Ala Glu His Leu Arg Lys Ile Val Pro Ser
      225          230          235          240

Pro Ala Arg Tyr Asn Ala Asn Pro Glu Tyr Leu Phe Glu Ala Ser Gly
      245          250          255

Ser Ala Gly Lys Leu Met Val Phe Ala Val Arg Thr Arg Thr Phe Pro
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Arg Glu Val His Pro Thr Val Phe Tyr Ile Gly Thr Asn Asn Thr His
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Glu Leu Glu Glu Ile Arg Arg Leu Phe Leu Glu Ala Asp Met Pro Leu
 290 295 300
 Pro Ile Ser Gly Glu Tyr Met Gly Arg Ser Ala Phe Asp Leu Ala Glu
 305 310 315 320
 Lys Tyr Gly Lys Asp Thr Phe Val Phe Leu Lys Phe Met Ser Pro Ala
 325 330 335
 Leu Gln Thr Arg Met Phe Ser Phe Lys Thr Trp Ala Asn Gly Leu Phe
 340 345 350
 Ser Lys Ile Pro Gly Ile Gly Pro Thr Phe Ala Asp Thr Val Ser Gln
 355 360 365
 Ala Met Phe Ser Val Leu Pro Asn Gln Leu Pro Lys Arg Met Met Glu
 370 375 380
 Tyr Arg Asn Arg Phe Glu His His Leu Leu Leu Thr Val Ser Glu Ser
 385 390 395 400
 Gln Lys Ala Ala Ser Glu Lys Met Leu Lys Glu Phe Phe Ala Glu Pro
 405 410 415
 Glu His Thr Gly Glu Phe Phe Ile Cys Thr Ser Asp Glu Glu Lys Ser
 420 425 430
 Ala Ser Leu Asn Arg Phe Gly Ala Ala Ser Ala Ala Thr Arg Tyr Ala
 435 440 445
 Ala Leu Lys Arg Arg His Ile Ala Gly Leu Ile Pro Ile Asp Val Ala
 450 455 460
 Leu Arg Arg Asp Asp Trp Asn Trp Leu Glu Val Leu Pro Glu Glu Ile
 465 470 475 480
 Asp Asp Gln Leu Glu Val Lys Ala Tyr Tyr Gly His Phe Phe Cys His
 485 490 495
 Val Met His Gln Asp Tyr Val Ala Lys Gln Gly Val Asp Leu Glu Ala
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 Pro Ala Glu His Asn
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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1012)

<223> RXA00293

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				Met	Lys	Ile	Phe	Val								
				1				5								
ggt	ttt	ggc	gat	tat	cca	ctc	acc	acc	aag	gcc	ctt	aag	gag	gca	ggc	163
Gly	Phe	Gly	Asp	Tyr	Pro	Leu	Thr	Thr	Lys	Ala	Leu	Lys	Glu	Ala	Gly	
				10					15					20		
gca	gaa	ata	gtg	gac	tcc	ctc	gaa	aaa	gcc	gag	ggg	ttt	gtc	ttc	act	211
Ala	Glu	Ile	Val	Asp	Ser	Leu	Glu	Lys	Ala	Glu	Gly	Phe	Val	Phe	Thr	
			25					30					35			
caa	aca	cca	ggc	aca	gaa	ttt	ccc	cta	ctt	ccc	gac	gga	gtg	agg	tgg	259
Gln	Thr	Pro	Gly	Thr	Glu	Phe	Pro	Leu	Leu	Pro	Asp	Gly	Val	Arg	Trp	
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gtg	caa	ttt	ccc	aat	gcg	ggg	ctc	aac	gca	tat	ttc	aca	gct	ggg	cag	307
Val	Gln	Phe	Pro	Asn	Ala	Gly	Leu	Asn	Ala	Tyr	Phe	Thr	Ala	Gly	Gln	
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Ile	Asp	Asp	Lys	Arg	Arg	Trp	Ser	Asn	Ala	Ser	Gly	Val	Tyr	Gly	Gln	
	70				75				80						85	
cag	gta	gcc	gaa	gca	gca	atg	gct	ctt	ttg	ctg	gga	ctg	att	cat	atg	403
Gln	Val	Ala	Glu	Ala	Ala	Met	Ala	Leu	Leu	Leu	Gly	Leu	Ile	His	Met	
				90				95						100		
cac	ccc	acc	atg	gtg	cgt	gcc	gat	agt	tgg	gca	cca	agc	act	caa	ata	451
His	Pro	Thr	Met	Val	Arg	Ala	Asp	Ser	Trp	Ala	Pro	Ser	Thr	Gln	Ile	
			105					110					115			
gat	cag	cag	acc	aga	tgg	ctt	gat	ggt	gca	aca	gtt	gcc	att	gtg	gga	499
Asp	Gln	Gln	Thr	Arg	Trp	Leu	Asp	Gly	Ala	Thr	Val	Ala	Ile	Val	Gly	
			120				125					130				
gct	ggt	gga	atc	ggt	aaa	cat	ctg	gca	gcc	atg	ttg	aaa	cct	ttt	ggc	547
Ala	Gly	Gly	Ile	Gly	Lys	His	Leu	Ala	Ala	Met	Leu	Lys	Pro	Phe	Gly	
	135				140						145					
gca	aag	tct	tta	gca	gta	agc	agg	acc	ggt	aca	ccc	acc	caa	gat	ttt	595
Ala	Lys	Ser	Leu	Ala	Val	Ser	Arg	Thr	Gly	Thr	Pro	Thr	Gln	Asp	Phe	
	150				155				160						165	
gat	gca	acg	gaa	cct	ata	tcc	aac	ctg	cac	caa	gta	ctt	gcc	gac	gcc	643
Asp	Ala	Thr	Glu	Pro	Ile	Ser	Asn	Leu	His	Gln	Val	Leu	Ala	Asp	Ala	
			170					175						180		
gac	cat	gtg	gtg	ttg	tgc	gta	ccg	ctt	acc	gca	gac	acc	tat	cat	ctg	691
Asp	His	Val	Val	Leu	Cys	Val	Pro	Leu	Thr	Ala	Asp	Thr	Tyr	His	Leu	
			185				190						195			
atc	gga	aaa	gca	gag	ctt	aaa	gca	atg	cag	tcc	act	gca	att	ttg	atc	739
Ile	Gly	Lys	Ala	Glu	Leu	Lys	Ala	Met	Gln	Ser	Thr	Ala	Ile	Leu	Ile	
		200				205						210				
aac	gtg	gct	cgc	gga	gaa	gta	gta	gat	aca	gaa	gca	tta	gtt	gac	gcc	787
Asn	Val	Ala	Arg	Gly	Glu	Val	Val	Asp	Thr	Glu	Ala	Leu	Val	Asp	Ala	
	215					220					225					

tta gat gcc caa gaa ata tcc ggg gca ggc tta gat gtc acc gat cct 835
 Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu Asp Val Thr Asp Pro
 230 235 240 245

 gaa cca ttg ccg gac gat cat cca ctg tgg ggg cgc agc aat gtg atc 883
 Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly Arg Ser Asn Val Ile
 250 255 260

 att acc ccg cac gta gcc aac acg ttg acc tcg atg gat cgc atg ctt 931
 Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser Met Asp Arg Met Leu
 265 270 275

 gcc cca gtg gtg gca gaa aac tac cga cgg ttt ctc gct gga gaa aag 979
 Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe Leu Ala Gly Glu Lys
 280 285 290

 atg ctg acc gag gtg gac atc cac aaa ggt tac tagagcagtg gctttgaata 1032
 Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
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 tag 1035

<210> 144

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 144

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 20 25 30

 Gly Phe Val Phe Thr Gln Thr Pro Gly Thr Glu Phe Pro Leu Leu Pro
 35 40 45

 Asp Gly Val Arg Trp Val Gln Phe Pro Asn Ala Gly Leu Asn Ala Tyr
 50 55 60

 Phe Thr Ala Gly Gln Ile Asp Asp Lys Arg Arg Trp Ser Asn Ala Ser
 65 70 75 80

 Gly Val Tyr Gly Gln Gln Val Ala Glu Ala Ala Met Ala Leu Leu Leu
 85 90 95

 Gly Leu Ile His Met His Pro Thr Met Val Arg Ala Asp Ser Trp Ala
 100 105 110

 Pro Ser Thr Gln Ile Asp Gln Gln Thr Arg Trp Leu Asp Gly Ala Thr
 115 120 125

 Val Ala Ile Val Gly Ala Gly Gly Ile Gly Lys His Leu Ala Ala Met
 130 135 140

 Leu Lys Pro Phe Gly Ala Lys Ser Leu Ala Val Ser Arg Thr Gly Thr
 145 150 155 160

 Pro Thr Gln Asp Phe Asp Ala Thr Glu Pro Ile Ser Asn Leu His Gln
 165 170 175

Val Leu Ala Asp Ala Asp His Val Val Leu Cys Val Pro Leu Thr Ala
 180 185 190

Asp Thr Tyr His Leu Ile Gly Lys Ala Glu Leu Lys Ala Met Gln Ser
 195 200 205

Thr Ala Ile Leu Ile Asn Val Ala Arg Gly Glu Val Val Asp Thr Glu
 210 215 220

Ala Leu Val Asp Ala Leu Asp Ala Gln Glu Ile Ser Gly Ala Gly Leu
 225 230 235 240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Asp His Pro Leu Trp Gly
 245 250 255

Arg Ser Asn Val Ile Ile Thr Pro His Val Ala Asn Thr Leu Thr Ser
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Met Asp Arg Met Leu Ala Pro Val Val Ala Glu Asn Tyr Arg Arg Phe
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Leu Ala Gly Glu Lys Met Leu Thr Glu Val Asp Ile His Lys Gly Tyr
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (62)..(664)
 <223> RXN01130

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g atg gat ctg gct cgc aag ctt ggt ctt ctt gct ggc aag ctt gtc gac 109
 Met Asp Leu Ala Arg Lys Leu Gly Leu Leu Ala Gly Lys Leu Val Asp
 1 5 10 15

gcc gcc cca gtc tcc att gag gtt gag gct cga ggc gag ctt tct tcc 157
 Ala Ala Pro Val Ser Ile Glu Val Glu Ala Arg Gly Glu Leu Ser Ser
 20 25 30

gag cag gtc aat gca ctt ggt ttg tcc gct gtt cgt ggt ttg ttc tcc 205
 Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
 35 40 45

gga att atc gaa gag tcc gtt act ttc gtc aac gct cct cgc att gct 253
 Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50 55 60

gaa gag cgt ggc ctg gac atc tcc gtg aag acc aac tct gag tct gtt 301
 Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65 70 75 80

act cac cgt tcc gtc ctg cag gtc aag gtc att act ggc agc ggc gcg 349
 Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
 85 90 95

agc gca act gtt gtt ggt gcc ctg act ggt ctt gag cgc gtt gag aag 397
 Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
 100 105 110

atc acc cgc atc aat ggc cgt ggc ctg gat ctg cgc gca gag ggt ctg 445
 Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
 115 120 125

aac ctc ttc ctg cag tac act gac gct cct ggt gca ctg ggt acc gtt 493
 Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
 130 135 140

ggt acc aag ctg ggt gct gct ggc atc aac atc gag gct gct gcg ttg 541
 Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
 145 150 155 160

act cag gct gag aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag 589
 Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
 165 170 175

tcc gct gtc tct gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt 637
 Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
 180 185 190

gct act tcc ttc cag gtt gat ctt gac taattagaga tccatttgct tga 687
 Ala Thr Ser Phe Gln Val Asp Leu Asp
 195 200

<210> 146

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 146

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 20 25 30

Glu Gln Val Asn Ala Leu Gly Leu Ser Ala Val Arg Gly Leu Phe Ser
 35 40 45

Gly Ile Ile Glu Glu Ser Val Thr Phe Val Asn Ala Pro Arg Ile Ala
 50 55 60

Glu Glu Arg Gly Leu Asp Ile Ser Val Lys Thr Asn Ser Glu Ser Val
 65 70 75 80

Thr His Arg Ser Val Leu Gln Val Lys Val Ile Thr Gly Ser Gly Ala
 85 90 95

Ser Ala Thr Val Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys
 100 105 110

Ile Thr Arg Ile Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu
 115 120 125

Asn Leu Phe Leu Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val
 130 135 140

Gly Thr Lys Leu Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu
 145 150 155 160

Thr Gln Ala Glu Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu
 165 170 175

Ser Ala Val Ser Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly
 180 185 190

Ala Thr Ser Phe Gln Val Asp Leu Asp
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<211> 326

<212> DNA

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<222> (1)..(303)

<223> FRXA01130

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 Asn Gly Arg Gly Leu Asp Leu Arg Ala Glu Gly Leu Asn Leu Phe Leu
 20 25 30

cag tac act gac gct cct ggt gca ctg ggt acc gtt ggt acc aag ctg 144
 Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45

ggt gct gct ggc atc aac atc gag gct gct gcg ttg act cag gct gag 192
 Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60

aag ggt gac ggc gct gtc ctg atc ctg cgt gtt gag tcc gct gtc tct 240
 Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
 65 70 75 80

gaa gag ctg gaa gct gaa atc aac gct gag ttg ggt gct act tcc ttc 288
 Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
 85 90 95

cag gtt gat ctt gac taattagaga tccatttgct tga 326
 Gln Val Asp Leu Asp
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<210> 148

<211> 101

<212> PRT

<213> Corynebacterium glutamicum

<400> 148

Val Gly Ala Leu Thr Gly Leu Glu Arg Val Glu Lys Ile Thr Arg Ile
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Gln Tyr Thr Asp Ala Pro Gly Ala Leu Gly Thr Val Gly Thr Lys Leu
 35 40 45

Gly Ala Ala Gly Ile Asn Ile Glu Ala Ala Ala Leu Thr Gln Ala Glu
 50 55 60

Lys Gly Asp Gly Ala Val Leu Ile Leu Arg Val Glu Ser Ala Val Ser
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Glu Glu Leu Glu Ala Glu Ile Asn Ala Glu Leu Gly Ala Thr Ser Phe
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Gln Val Asp Leu Asp
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<210> 149

<211> 604

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(604)

<223> RXN03112

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 Val Glu Ile Phe Gly
 1 5

aaa act gtc ggt atc gtc ggt ttt ggc cac att ggt cag ttg ttt gct 163
 Lys Thr Val Gly Ile Val Gly Phe Gly His Ile Gly Gln Leu Phe Ala
 10 15 20

cag cgt ctt gct gcg ttt gag acc acc att gtt gct tac gat cct tac 211
 Gln Arg Leu Ala Ala Phe Glu Thr Thr Ile Val Ala Tyr Asp Pro Tyr
 25 30 35

gct aac cct gct cgt gcg gct cag ctg aac gtt gag ttg gtt gag ttg 259
 Ala Asn Pro Ala Arg Ala Ala Gln Leu Asn Val Glu Leu Val Glu Leu
 40 45 50

gat gag ctg atg agc cgt tct gac ttt gtc acc att cac ctt cct aag 307
 Asp Glu Leu Met Ser Arg Ser Asp Phe Val Thr Ile His Leu Pro Lys
 55 60 65

acc aag gaa act gct ggc atg ttt gat gcg cac ctc ctt gct aag tcc 355
 Thr Lys Glu Thr Ala Gly Met Phe Asp Ala His Leu Leu Ala Lys Ser

70	75	80	85	
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Lys Lys Gly Gln Ile Ile Ile Asn Ala Ala Arg Gly Gly Leu Val Asp	90	95	100	
gag cag gct ttg gct gat gcg att gag tcc ggt cac att cgt ggc gct				451
Glu Gln Ala Leu Ala Asp Ala Ile Glu Ser Gly His Ile Arg Gly Ala	105	110	115	
ggt ttc gat gtg tac tcc acc gag cct tgc act gat tct cct ttg ttc				499
Gly Phe Asp Val Tyr Ser Thr Glu Pro Cys Thr Asp Ser Pro Leu Phe	120	125	130	
aag ttg cct cag gtt gtt gtg act cct cac ttg ggt gct tct act gaa				547
Lys Leu Pro Gln Val Val Val Thr Pro His Leu Gly Ala Ser Thr Glu	135	140	145	
gag gct caa gat cgt gcg ggt act gac att gct gat tct gtg ctc aag				595
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Ala Leu Ala				

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<211> 168

<212> PRT

<213> Corynebacterium glutamicum

<400> 150

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		20						25						30	

Ala	Tyr	Asp	Pro	Tyr	Ala	Asn	Pro	Ala	Arg	Ala	Ala	Gln	Leu	Asn	Val
		35					40					45			

Glu	Leu	Val	Glu	Leu	Asp	Glu	Leu	Met	Ser	Arg	Ser	Asp	Phe	Val	Thr
	50					55					60				

Ile	His	Leu	Pro	Lys	Thr	Lys	Glu	Thr	Ala	Gly	Met	Phe	Asp	Ala	His
65					70					75				80	

Leu	Leu	Ala	Lys	Ser	Lys	Lys	Gly	Gln	Ile	Ile	Ile	Asn	Ala	Ala	Arg
				85					90					95	

Gly	Gly	Leu	Val	Asp	Glu	Gln	Ala	Leu	Ala	Asp	Ala	Ile	Glu	Ser	Gly
		100						105					110		

His	Ile	Arg	Gly	Ala	Gly	Phe	Asp	Val	Tyr	Ser	Thr	Glu	Pro	Cys	Thr
		115					120					125			

Asp	Ser	Pro	Leu	Phe	Lys	Leu	Pro	Gln	Val	Val	Val	Thr	Pro	His	Leu
	130					135					140				

Gly	Ala	Ser	Thr	Glu	Glu	Ala	Gln	Asp	Arg	Ala	Gly	Thr	Asp	Ile	Ala
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145	150	155	160
Asp Ser Val Leu Lys Ala Leu Ala			
165			
<210> 151 <211> 649 <212> DNA <213> Corynebacterium glutamicum <220> <221> CDS <222> (101)..(649) <223> FRXA01133 <400> 151			
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tgttgtagac ggacattcct agtttttcca ggagtaactt gtg agc cag aat ggc 115			
Val Ser Gln Asn Gly 5			
cgt ccg gta gtc ctc atc gcc gat aag ctt gcg cag tcc act gtt gac 163			
Arg Pro Val Val Ile Ala Asp Lys Leu Ala Gln Ser Thr Val Asp 20			
gcg ctt gga gat gca gta gaa gtc cgt tgg gtt gac gga cct aac cgc 211			
Ala Leu Gly Asp Ala Val Glu Val Arg Trp Val Asp Gly Pro Asn Arg 35			
cca gaa ctg ctt gat gca gtt aag gaa gcg gac gca ctg ctc gtg cgt 259			
Pro Glu Leu Leu Asp Ala Val Lys Glu Ala Asp Ala Leu Leu Val Arg 50			
tct gct acc act gtc gat gct gaa gtc atc gcc gct gcc cct aac ttg 307			
Ser Ala Thr Thr Val Asp Ala Glu Val Ile Ala Ala Ala Pro Asn Leu 65			
aag atc gtc ggt cgt gcc ggc gtg ggc ttg gac aac gtt gac atc cct 355			
Lys Ile Val Gly Arg Ala Gly Val Gly Leu Asp Asn Val Asp Ile Pro 85			
gct gcc act gaa gct ggc gtc atg gtt gct aac gca ccg acc tct aat 403			
Ala Ala Thr Glu Ala Gly Val Met Val Ala Asn Ala Pro Thr Ser Asn 100			
att cac tcc gct tgt gag cac gca att tct ttg ctg ctg tct act gct 451			
Ile His Ser Ala Cys Glu His Ala Ile Ser Leu Leu Leu Ser Thr Ala 115			
cgc cag atc ctg ctg ctg atg cga cgc tgc gtg agg gcg agt gga agc 499			
Arg Gln Ile Leu Leu Leu Met Arg Arg Cys Val Arg Ala Ser Gly Ser 130			
ggt ctt ctt tca acg gtg tgg aaa ttt tcg gaa aaa ctg tcg gta tcg 547			
Gly Leu Leu Ser Thr Val Trp Lys Phe Ser Glu Lys Leu Ser Val Ser 145			
tcg gtt ttg gcc aca ttg gtc agt tgt ttg ctc agc gtc ttg ctg cgt 595			
Ser Val Leu Ala Thr Leu Val Ser Cys Leu Leu Ser Val Leu Leu Arg			

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<210> 152
<211> 183
<212> PRT
<213> Corynebacterium glutamicum
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<210> 153
<211> 1011
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS

<223> RXN00871

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gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca 739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser
200 205 210

cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc 787
 Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile
 215 220 225

gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc 835
 Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly
 230 235 240 245

tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga 883
 Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg
 250 255 260

atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca 931
 Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr
 265 270 275

tgg acc ggg caa gca ttt gat gat cgc ttg cca tat gag aac gca aac 979
 Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro Tyr Glu Asn Ala Asn
 280 285 290

aag gag gga taaaatttca tggctgaaac gaa 1011
 Lys Glu Gly
 295

<210> 154
 <211> 296
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 154
 Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
 1 5 10 15

Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
 20 25 30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
 35 40 45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
 50 55 60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
 65 70 75 80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
 85 90 95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
 100 105 110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
 115 120 125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
 130 135 140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
 145 150 155 160

Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
 165 170 175
 His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
 180 185 190
 Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
 195 200 205
 Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
 210 215 220
 Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
 225 230 235 240
 Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
 245 250 255
 Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
 260 265 270
 Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
 275 280 285
 Tyr Glu Asn Ala Asn Lys Glu Gly
 290 295

<210> 155

<211> 964

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(964)

<223> FRXA00871

<400> 155

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gtttcccaca gaacgattaa ttgaaggaga gcacaggact atg cgt tgg ttc cat 115
 Met Arg Trp Phe His
 1 5

aag aag ggc gaa ctg gcc cga gat ggt tgg caa agc gtt gtc gat gcc 163
 Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln Ser Val Val Asp Ala
 10 15 20

acc acc cca ggt tgg gaa tat acc ggc atc cgc att gcc gaa ctg ggc 211
 Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg Ile Ala Glu Leu Gly
 25 30 35

agt ggt gaa tcg ctt gaa ctg aat gac act ggt gtg gaa cgc atc ttc 259
 Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly Val Glu Arg Ile Phe
 40 45 50

att cca ctt cag ggc agc ttc gat gtt gcc cac cat ggt cag gtg acc 307
 Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His His Gly Gln Val Thr
 55 60 65

cat ctt cac gga aga aag tca gtc ttt gat gga cca acc gat gtg ctc	355
His Leu His Gly Arg Lys Ser Val Phe Asp Gly Pro Thr Asp Val Leu	
70 75 80 85	
tac ctc ccc act gga caa aca gca acg ctc agt ggt cag gga cga gtc	403
Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser Gly Gln Gly Arg Val	
90 95 100	
gcc gtg gcg gaa gct ccc act cag gaa ccc aag gag tgg aag tac atc	451
Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys Glu Trp Lys Tyr Ile	
105 110 115	
gct cca gca gaa act cct gtg gag ttg cgt gga gct ggc cgc tcg agc	499
Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly Ala Gly Arg Ser Ser	
120 125 130	
cga caa gtc cac aac ttt ggc acc ccg gaa gct ctc gat gct gct cga	547
Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala Leu Asp Ala Ala Arg	
135 140 145	
cta atc gtg tgt gaa gta atc acc cca ggt gaa aac tgg agc tct tac	595
Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu Asn Trp Ser Ser Tyr	
150 155 160 165	
cct cca cac aag cat gat gag cac atc cca gga cac gag tcc aag ctg	643
Pro Pro His Lys His Asp Glu His Ile Pro Gly His Glu Ser Lys Leu	
170 175 180	
gag gaa atc tac tac ttc gaa agc gcc cca tcg cga gtt ggt ggc agg	691
Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser Arg Val Gly Gly Arg	
185 190 195	
gcc gaa gca gca gaa gga gct ttc gga atg ttt tcc acc tac tcc tca	739
Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe Ser Thr Tyr Ser Ser	
200 205 210	
cca gcg ggg gag atc gat atc aac gcc atg gtg tac agc ggc gat atc	787
Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val Tyr Ser Gly Asp Ile	
215 220 225	
gcg cta gtt cct ttc gga tac cac ggc cct gcc gtg gca gca cct ggc	835
Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala Val Ala Ala Pro Gly	
230 235 240 245	
tat gac ttg tac tac ctc aac gtc atg gca gga cct gat ccg gag aga	883
Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly Pro Asp Pro Glu Arg	
250 255 260	
atc tgg ctg att aac gat gac cca gcg cac gcc tgg gtt cga gat aca	931
Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala Trp Val Arg Asp Thr	
265 270 275	
tgg acc ggg caa gca ttt gat gat cgc ttg cca	964
Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro	
280 285	

<210> 156

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 156

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Met Arg Trp Phe His Lys Lys Gly Glu Leu Ala Arg Asp Gly Trp Gln
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Ser Val Val Asp Ala Thr Thr Pro Gly Trp Glu Tyr Thr Gly Ile Arg
      20              25              30

Ile Ala Glu Leu Gly Ser Gly Glu Ser Leu Glu Leu Asn Asp Thr Gly
      35              40              45

Val Glu Arg Ile Phe Ile Pro Leu Gln Gly Ser Phe Asp Val Ala His
      50              55              60

His Gly Gln Val Thr His Leu His Gly Arg Lys Ser Val Phe Asp Gly
      65              70              75              80

Pro Thr Asp Val Leu Tyr Leu Pro Thr Gly Gln Thr Ala Thr Leu Ser
      85              90              95

Gly Gln Gly Arg Val Ala Val Ala Glu Ala Pro Thr Gln Glu Pro Lys
      100              105              110

Glu Trp Lys Tyr Ile Ala Pro Ala Glu Thr Pro Val Glu Leu Arg Gly
      115              120              125

Ala Gly Arg Ser Ser Arg Gln Val His Asn Phe Gly Thr Pro Glu Ala
      130              135              140

Leu Asp Ala Ala Arg Leu Ile Val Cys Glu Val Ile Thr Pro Gly Glu
      145              150              155              160

Asn Trp Ser Ser Tyr Pro Pro His Lys His Asp Glu His Ile Pro Gly
      165              170              175

His Glu Ser Lys Leu Glu Glu Ile Tyr Tyr Phe Glu Ser Ala Pro Ser
      180              185              190

Arg Val Gly Gly Arg Ala Glu Ala Ala Glu Gly Ala Phe Gly Met Phe
      195              200              205

Ser Thr Tyr Ser Ser Pro Ala Gly Glu Ile Asp Ile Asn Ala Met Val
      210              215              220

Tyr Ser Gly Asp Ile Ala Leu Val Pro Phe Gly Tyr His Gly Pro Ala
      225              230              235              240

Val Ala Ala Pro Gly Tyr Asp Leu Tyr Tyr Leu Asn Val Met Ala Gly
      245              250              255

Pro Asp Pro Glu Arg Ile Trp Leu Ile Asn Asp Asp Pro Ala His Ala
      260              265              270

Trp Val Arg Asp Thr Trp Thr Gly Gln Ala Phe Asp Asp Arg Leu Pro
      275              280              285

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<220>
<221> CDS
<222> (101)..(373)
<223> RXN02829
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<210> 158
<211> 91
<212> PRT
<213> Corynebacterium glutamicum
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<400> 158
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
1 5 10 15
Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
20 25 30
Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp
35 40 45
Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys
50 55 60
Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn

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65              70              75              80
Arg Leu Thr Asp Asp Gly His Met Thr Trp Asp
      85              90

<210> 159
<211> 376
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(376)
<223> FRXA02829

<400> 159
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ctgaattcgt cagttaaagt gtatcgaaag gagactggac atg caa aaa aat att 115
              Met Gln Lys Asn Ile
              1              5

cta aaa agt ggc atc gaa att tct gaa ctt ggg tta ggt tgc atg agt 163
Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly Leu Gly Cys Met Ser
              10              15              20

tta ggc aca gat tat aaa aaa gcg caa cca att att gaa agt gca att 211
Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile Ile Glu Ser Ala Ile
              25              30              35

gat aat ggt att acg tat ttt gat act gca gat att tac gat caa gga 259
Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp Ile Tyr Asp Gln Gly
              40              45              50

gtt aat gaa gaa att gtt ggt aaa gcc tta aaa aaa tat caa aat cgt 307
Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys Lys Tyr Gln Asn Arg
              55              60              65

gat gac atc gtt atc gga act aaa gtt gga aat cga tta act gac gat 355
Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn Arg Leu Thr Asp Asp
              70              75              80              85

gga cat atg acg tgg gga tcc 376
Gly His Met Thr Trp Gly Ser
              90

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<210> 160
<211> 92
<212> PRT
<213> Corynebacterium glutamicum

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<400> 160
Met Gln Lys Asn Ile Leu Lys Ser Gly Ile Glu Ile Ser Glu Leu Gly
  1              5              10              15

Leu Gly Cys Met Ser Leu Gly Thr Asp Tyr Lys Lys Ala Gln Pro Ile
      20              25              30

Ile Glu Ser Ala Ile Asp Asn Gly Ile Thr Tyr Phe Asp Thr Ala Asp

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35	40	45
Ile Tyr Asp Gln Gly Val Asn Glu Glu Ile Val Gly Lys Ala Leu Lys		
50	55	60
Lys Tyr Gln Asn Arg Asp Asp Ile Val Ile Gly Thr Lys Val Gly Asn		
65	70	75
Arg Leu Thr Asp Asp Gly His Met Thr Trp Gly Ser		
85	90	

<210> 161
 <211> 948
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(925)
 <223> RXN01468

<400> 161
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 ttagcgggaa aatttcgccc aaaacaggga caatggtgtt atg aca gtg aac att 115
 Met Thr Val Asn Ile 5
 tca tat ctg acc gac atg gac ggc gtc ctc atc aaa gag ggc gag ata 163
 Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile Lys Glu Gly Glu Ile 20
 att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211
 Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu Thr Asp Asn Asn Val 35
 gag ttt atg gtt ttg acc aac aac tcc att ttc acc ccg agg gat ctt 259
 Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe Thr Pro Arg Asp Leu 50
 tct gca cgt ctt aag act tcc ggt ttg gat atc ccg ccg gag cgt att 307
 Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile Pro Pro Glu Arg Ile 65
 tgg act tct gca acc gcc act gct cac ttc ctg aaa tcc cag gtc aag 355
 Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu Lys Ser Gln Val Lys 85
 gag ggc aca gcc tat gtt gtt ggc gag tcc ggt ctg acc act gcg ttg 403
 Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly Leu Thr Thr Ala Leu 100
 cat acc gcg ggt tgg att ttg acg gat gca aat cct gag ttt gtt gtc 451
 His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn Pro Glu Phe Val Val 115
 ctg ggc gaa acc cgc aca tat tcc ttc gag gca atc act act gcg ata 499
 Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala Ile Thr Thr Ala Ile 130

aat ctg att ttg ggt ggc gct cgc ttt att tgc acc aac ccg gat gtc 547
 Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys Thr Asn Pro Asp Val
 135 140 145
 act gga cct tca cca agt ggc att ttg cct gct act ggc tct gtc gcc 595
 Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala Thr Gly Ser Val Ala
 150 155 160 165
 gca ctt att acc gca gct act ggc gct gag cct tat tac atc ggc aag 643
 Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro Tyr Tyr Ile Gly Lys
 170 175 180
 cca aac cct gtg atg atg cgc agt gcg ctg aac acc atc ggg gcg cat 691
 Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn Thr Ile Gly Ala His
 185 190 195
 tcc gag cac act gtc atg atc ggc gac cgc atg gac acc gac gtg aaa 739
 Ser Glu His Thr Val Met Ile Gly Asp Arg Met Asp Thr Asp Val Lys
 200 205 210
 tct ggt ttg gaa gcc ggc ctg agc acc gtg ctg gtt cga agc gga att 787
 Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu Val Arg Ser Gly Ile
 215 220 225
 tcc gac gac gcc gag atc cgc cgc tac ccc ttc cgc cca act cac gtg 835
 Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe Arg Pro Thr His Val
 230 235 240 245
 atc aat tcc atc gcc gat ctt gcc gat tgc tgg gac gat cct ttc ggt 883
 Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp Asp Asp Pro Phe Gly
 250 255 260
 gac ggt gca ttt cac gta cca gat gag cag cag ttc act gac 925
 Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln Phe Thr Asp
 265 270 275
 tagtattctg taggtcatgg cat 948

<210> 162

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 162

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
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Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly

85					90					95					
Leu	Thr	Thr	Ala	Leu	His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn
			100					105					110		
Pro	Glu	Phe	Val	Val	Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala
		115					120					125			
Ile	Thr	Thr	Ala	Ile	Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys
		130					135					140			
Thr	Asn	Pro	Asp	Val	Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala
145							150					155			160
Thr	Gly	Ser	Val	Ala	Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro
				165					170					175	
Tyr	Tyr	Ile	Gly	Lys	Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn
			180					185					190		
Thr	Ile	Gly	Ala	His	Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met
		195					200						205		
Asp	Thr	Asp	Val	Lys	Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu
		210					215					220			
Val	Arg	Ser	Gly	Ile	Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe
225							230					235			240
Arg	Pro	Thr	His	Val	Ile	Asn	Ser	Ile	Ala	Asp	Leu	Ala	Asp	Cys	Trp
				245					250					255	
Asp	Asp	Pro	Phe	Gly	Asp	Gly	Ala	Phe	His	Val	Pro	Asp	Glu	Gln	Gln
			260					265					270		
Phe	Thr	Asp													
		275													

<210> 163

<211> 948

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(925)

<223> FRXA01468

<400> 163

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				Met	Thr	Val	Asn	Ile	
				1				5	

tca	tat	ctg	acc	gac	atg	gac	ggc	gtc	ctc	atc	aaa	gag	ggc	gag	ata	163
Ser	Tyr	Leu	Thr	Asp	Met	Asp	Gly	Val	Leu	Ile	Lys	Glu	Gly	Glu	Ile	
				10				15						20		

att ccg ggt gca gat cgt ttt ctt cag tct ctc acc gat aac aat gtg 211

Ile	Pro	Gly	Ala	Asp	Arg	Phe	Leu	Gln	Ser	Leu	Thr	Asp	Asn	Asn	Val		
			25					30					35				
gag	ttt	atg	gtt	ttg	acc	aac	aac	tcc	att	ttc	acc	ccg	agg	gat	ctt	259	
Glu	Phe	Met	Val	Leu	Thr	Asn	Asn	Ser	Ile	Phe	Thr	Pro	Arg	Asp	Leu		
		40					45					50					
tct	gca	cgt	ctt	aag	act	tcc	ggg	ttg	gat	atc	ccg	ccg	gag	cgt	att	307	
Ser	Ala	Arg	Leu	Lys	Thr	Ser	Gly	Leu	Asp	Ile	Pro	Pro	Glu	Arg	Ile		
	55					60					65						
tgg	act	tct	gca	acc	gcc	act	gct	cac	ttc	ctg	aaa	tcc	cag	gtc	aag	355	
Trp	Thr	Ser	Ala	Thr	Ala	Thr	Ala	His	Phe	Leu	Lys	Ser	Gln	Val	Lys		
70					75				80						85		
gag	ggc	aca	gcc	tat	gtt	gtt	ggc	gag	tcc	ggg	ctg	acc	act	gcg	ttg	403	
Glu	Gly	Thr	Ala	Tyr	Val	Val	Gly	Glu	Ser	Gly	Leu	Thr	Thr	Ala	Leu		
			90						95					100			
cat	acc	gcg	ggg	tgg	att	ttg	acg	gat	gca	aat	cct	gag	ttt	gtt	gtc	451	
His	Thr	Ala	Gly	Trp	Ile	Leu	Thr	Asp	Ala	Asn	Pro	Glu	Phe	Val	Val		
			105					110					115				
ctg	ggc	gaa	acc	cgc	aca	tat	tcc	ttc	gag	gca	atc	act	act	gcg	ata	499	
Leu	Gly	Glu	Thr	Arg	Thr	Tyr	Ser	Phe	Glu	Ala	Ile	Thr	Thr	Ala	Ile		
		120					125					130					
aat	ctg	att	ttg	ggg	ggc	gct	cgc	ttt	att	tgc	acc	aac	ccg	gat	gtc	547	
Asn	Leu	Ile	Leu	Gly	Gly	Ala	Arg	Phe	Ile	Cys	Thr	Asn	Pro	Asp	Val		
	135					140					145						
act	gga	cct	tca	cca	agt	ggc	att	ttg	cct	gct	act	ggc	tct	gtc	gcc	595	
Thr	Gly	Pro	Ser	Pro	Ser	Gly	Ile	Leu	Pro	Ala	Thr	Gly	Ser	Val	Ala		
150					155					160					165		
gca	ctt	att	acc	gca	gct	act	ggc	gct	gag	cct	tat	tac	atc	ggc	aag	643	
Ala	Leu	Ile	Thr	Ala	Ala	Thr	Gly	Ala	Glu	Pro	Tyr	Tyr	Ile	Gly	Lys		
				170					175					180			
cca	aac	cct	gtg	atg	atg	cgc	agt	gcg	ctg	aac	acc	atc	ggg	gcg	cat	691	
Pro	Asn	Pro	Val	Met	Met	Arg	Ser	Ala	Leu	Asn	Thr	Ile	Gly	Ala	His		
			185					190					195				
tcc	gag	cac	act	gtc	atg	atc	ggc	gac	cgc	atg	gac	acc	gac	gtg	aaa	739	
Ser	Glu	His	Thr	Val	Met	Ile	Gly	Asp	Arg	Met	Asp	Thr	Asp	Val	Lys		
		200					205					210					
tct	ggg	ttg	gaa	gcc	ggc	ctg	agc	acc	gtg	ctg	gtt	cga	agc	gga	att	787	
Ser	Gly	Leu	Glu	Ala	Gly	Leu	Ser	Thr	Val	Leu	Val	Arg	Ser	Gly	Ile		
	215					220					225						
tcc	gac	gac	gcc	gag	atc	cgc	cgc	tac	ccc	ttc	cgc	cca	act	cac	gtg	835	
Ser	Asp	Asp	Ala	Glu	Ile	Arg	Arg	Tyr	Pro	Phe	Arg	Pro	Thr	His	Val		
230					235					240					245		
atc	aat	tcc	atc	gcc	gat	ctt	gcc	gat	tgc	tgg	gac	gat	cct	ttc	ggg	883	
Ile	Asn	Ser	Ile	Ala	Asp	Leu	Ala	Asp	Cys	Trp	Asp	Asp	Pro	Phe	Gly		
				250					255					260			
gac	ggg	gca	ttt	cac	gta	cca	gat	gag	cag	cag	ttc	act	gac			925	
Asp	Gly	Ala	Phe	His	Val	Pro	Asp	Glu	Gln	Gln	Phe	Thr	Asp				

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270

275

tagtattctg taggtcatgg cat

948

<210> 164

<211> 275

<212> PRT

<213> Corynebacterium glutamicum

<400> 164

Met Thr Val Asn Ile Ser Tyr Leu Thr Asp Met Asp Gly Val Leu Ile
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Lys Glu Gly Glu Ile Ile Pro Gly Ala Asp Arg Phe Leu Gln Ser Leu
 20 25 30

Thr Asp Asn Asn Val Glu Phe Met Val Leu Thr Asn Asn Ser Ile Phe
 35 40 45

Thr Pro Arg Asp Leu Ser Ala Arg Leu Lys Thr Ser Gly Leu Asp Ile
 50 55 60

Pro Pro Glu Arg Ile Trp Thr Ser Ala Thr Ala Thr Ala His Phe Leu
 65 70 75 80

Lys Ser Gln Val Lys Glu Gly Thr Ala Tyr Val Val Gly Glu Ser Gly
 85 90 95

Leu Thr Thr Ala Leu His Thr Ala Gly Trp Ile Leu Thr Asp Ala Asn
 100 105 110

Pro Glu Phe Val Val Leu Gly Glu Thr Arg Thr Tyr Ser Phe Glu Ala
 115 120 125

Ile Thr Thr Ala Ile Asn Leu Ile Leu Gly Gly Ala Arg Phe Ile Cys
 130 135 140

Thr Asn Pro Asp Val Thr Gly Pro Ser Pro Ser Gly Ile Leu Pro Ala
 145 150 155 160

Thr Gly Ser Val Ala Ala Leu Ile Thr Ala Ala Thr Gly Ala Glu Pro
 165 170 175

Tyr Tyr Ile Gly Lys Pro Asn Pro Val Met Met Arg Ser Ala Leu Asn
 180 185 190

Thr Ile Gly Ala His Ser Glu His Thr Val Met Ile Gly Asp Arg Met
 195 200 205

Asp Thr Asp Val Lys Ser Gly Leu Glu Ala Gly Leu Ser Thr Val Leu
 210 215 220

Val Arg Ser Gly Ile Ser Asp Asp Ala Glu Ile Arg Arg Tyr Pro Phe
 225 230 235 240

Arg Pro Thr His Val Ile Asn Ser Ile Ala Asp Leu Ala Asp Cys Trp
 245 250 255

Asp Asp Pro Phe Gly Asp Gly Ala Phe His Val Pro Asp Glu Gln Gln
 260 265 270

Phe Thr Asp
275

<210> 165
<211> 1128
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1105)
<223> RXA00794

<400> 165
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cgtaaccagg tcagatcaag tgccccagga ggcccttcag atg aac cta aag aac 115
Met Asn Leu Lys Asn
1 5
ccc gaa acg cca gac cgt aac ctt gct atg gag ctg gtg cga gtt acg 163
Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu Leu Val Arg Val Thr
10 15 20
gaa gca gct gca ctg gct tct gga cgt tgg gtt gga cgt ggc atg aag 211
Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val Gly Arg Gly Met Lys
25 30 35
aat gaa ggc gac ggt gcc gct gtt gac gcc atg cgc cag ctc atc aac 259
Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met Arg Gln Leu Ile Asn
40 45 50
tca gtg acc atg aag ggc gtc gtt gtt atc ggc gag ggc gaa aaa gac 307
Ser Val Thr Met Lys Gly Val Val Val Ile Gly Glu Gly Glu Lys Asp
55 60 65
gaa gct cca atg ctg tac aac ggc gaa gag gtc gga acc ggc ttt gga 355
Glu Ala Pro Met Leu Tyr Asn Gly Glu Glu Val Gly Thr Gly Phe Gly
70 75 80 85
cct gag gtt gat atc gca gtt gac cca gtt gac ggc acc acc ctg atg 403
Pro Glu Val Asp Ile Ala Val Asp Pro Val Asp Gly Thr Thr Leu Met
90 95 100
gct gag ggt cgc ccc aac gca att tcc att ctc gca gct gca gag cgt 451
Ala Glu Gly Arg Pro Asn Ala Ile Ser Ile Leu Ala Ala Ala Glu Arg
105 110 115
ggc acc atg tac gat cca tcc tcc gtc ttc tac atg aag aag atc gcc 499
Gly Thr Met Tyr Asp Pro Ser Ser Val Phe Tyr Met Lys Lys Ile Ala
120 125 130
gtg gga cct gag gcc gca ggc aag atc gac atc gaa gct cca gtt gcc 547
Val Gly Pro Glu Ala Ala Gly Lys Ile Asp Ile Glu Ala Pro Val Ala
135 140 145
cac aac atc aac gcg gtg gca aag tcc aag gga atc aac cct tcc gac 595
His Asn Ile Asn Ala Val Ala Lys Ser Lys Gly Ile Asn Pro Ser Asp
150 155 160 165

gtc acc gtt gtc gtg ctt gac cgt cct cgc cac atc gaa ctg atc gca 643
 Val Thr Val Val Val Leu Asp Arg Pro Arg His Ile Glu Leu Ile Ala
 170 175 180

gac att cgt cgt gca ggc gca aag gtt cgt ctc atc tcc gac ggc gac 691
 Asp Ile Arg Arg Ala Gly Ala Lys Val Arg Leu Ile Ser Asp Gly Asp
 185 190 195

gtt gca ggt gca gtt gca gca gct cag gat tcc aac tcc gtg gac atc 739
 Val Ala Gly Ala Val Ala Ala Ala Gln Asp Ser Asn Ser Val Asp Ile
 200 205 210

atg atg ggc acc ggc gga acc cca gaa ggc atc atc act gcg tgc gcc 787
 Met Met Gly Thr Gly Gly Thr Pro Glu Gly Ile Ile Thr Ala Cys Ala
 215 220 225

atg aag tgc atg ggt ggc gaa atc cag ggc atc ctg gcc cca atg aac 835
 Met Lys Cys Met Gly Gly Glu Ile Gln Gly Ile Leu Ala Pro Met Asn
 230 235 240 245

gat ttc gag cgc cag aag gca cac gac gct ggt ctg gtt ctt gat cag 883
 Asp Phe Glu Arg Gln Lys Ala His Asp Ala Gly Leu Val Leu Asp Gln
 250 255 260

gtt ctg cac acc aac gat ctg gtg agc tcc gac aac tgc tac ttc gtg 931
 Val Leu His Thr Asn Asp Leu Val Ser Ser Asp Asn Cys Tyr Phe Val
 265 270 275

gca acc ggt gtg acc aac ggt gac atg ctc cgt ggc gtt tcc tac cgc 979
 Ala Thr Gly Val Thr Asn Gly Asp Met Leu Arg Gly Val Ser Tyr Arg
 280 285 290

gca aac ggc gca acc acc cgt tcc ctg gtt atg cgc gca aag tca ggc 1027
 Ala Asn Gly Ala Thr Thr Arg Ser Leu Val Met Arg Ala Lys Ser Gly
 295 300 305

acc atc cgc cac atc gag tct gtc cac cag ctg tcc aag ctg cag gaa 1075
 Thr Ile Arg His Ile Glu Ser Val His Gln Leu Ser Lys Leu Gln Glu
 310 315 320 325

tac tcc gtg gtt gac tac acc acc gcg acc taagagctct tagttcgaaa 1125
 Tyr Ser Val Val Asp Tyr Thr Thr Ala Thr
 330 335

aac 1128

<210> 166

<211> 335

<212> PRT

<213> Corynebacterium glutamicum

<400> 166

Met Asn Leu Lys Asn Pro Glu Thr Pro Asp Arg Asn Leu Ala Met Glu
 1 5 10 15

Leu Val Arg Val Thr Glu Ala Ala Ala Leu Ala Ser Gly Arg Trp Val
 20 25 30

Gly Arg Gly Met Lys Asn Glu Gly Asp Gly Ala Ala Val Asp Ala Met

35					40					45						
Arg	Gln	Leu	Ile	Asn	Ser	Val	Thr	Met	Lys	Gly	Val	Val	Val	Ile	Gly	
50					55					60						
Glu	Gly	Glu	Lys	Asp	Glu	Ala	Pro	Met	Leu	Tyr	Asn	Gly	Glu	Glu	Val	
65					70					75					80	
Gly	Thr	Gly	Phe	Gly	Pro	Glu	Val	Asp	Ile	Ala	Val	Asp	Pro	Val	Asp	
85					90					95						
Gly	Thr	Thr	Leu	Met	Ala	Glu	Gly	Arg	Pro	Asn	Ala	Ile	Ser	Ile	Leu	
100					105					110						
Ala	Ala	Ala	Glu	Arg	Gly	Thr	Met	Tyr	Asp	Pro	Ser	Ser	Val	Phe	Tyr	
115					120					125						
Met	Lys	Lys	Ile	Ala	Val	Gly	Pro	Glu	Ala	Ala	Gly	Lys	Ile	Asp	Ile	
130					135					140						
Glu	Ala	Pro	Val	Ala	His	Asn	Ile	Asn	Ala	Val	Ala	Lys	Ser	Lys	Gly	
145					150					155					160	
Ile	Asn	Pro	Ser	Asp	Val	Thr	Val	Val	Val	Leu	Asp	Arg	Pro	Arg	His	
165					170					175						
Ile	Glu	Leu	Ile	Ala	Asp	Ile	Arg	Arg	Ala	Gly	Ala	Lys	Val	Arg	Leu	
180					185					190						
Ile	Ser	Asp	Gly	Asp	Val	Ala	Gly	Ala	Val	Ala	Ala	Ala	Gln	Asp	Ser	
195					200					205						
Asn	Ser	Val	Asp	Ile	Met	Met	Gly	Thr	Gly	Gly	Thr	Pro	Glu	Gly	Ile	
210					215					220						
Ile	Thr	Ala	Cys	Ala	Met	Lys	Cys	Met	Gly	Gly	Glu	Ile	Gln	Gly	Ile	
225					230					235					240	
Leu	Ala	Pro	Met	Asn	Asp	Phe	Glu	Arg	Gln	Lys	Ala	His	Asp	Ala	Gly	
245					250					255						
Leu	Val	Leu	Asp	Gln	Val	Leu	His	Thr	Asn	Asp	Leu	Val	Ser	Ser	Asp	
260					265					270						
Asn	Cys	Tyr	Phe	Val	Ala	Thr	Gly	Val	Thr	Asn	Gly	Asp	Met	Leu	Arg	
275					280					285						
Gly	Val	Ser	Tyr	Arg	Ala	Asn	Gly	Ala	Thr	Thr	Arg	Ser	Leu	Val	Met	
290					295					300						
Arg	Ala	Lys	Ser	Gly	Thr	Ile	Arg	His	Ile	Glu	Ser	Val	His	Gln	Leu	
305					310					315					320	
Ser	Lys	Leu	Gln	Glu	Tyr	Ser	Val	Val	Asp	Tyr	Thr	Thr	Ala	Thr		
325					330					335						

<210> 167

<211> 1035

<212> DNA

<213> Corynebacterium glutamicum

<223> RXN02920

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gat gtg ttt gtg ctc atc ctg ccg ctg act gat gcc act tat cag atc 691
Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
185 190 195

gtc aat gca gaa act ttg ggc aag atg aag cct tct gcc gtg gtg gtc 739
 Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 200 205 210

aat gtg ggg cgt ggc ccg ctg atc aac acc gat gat ctg gtg gat gca 787
 Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 215 220 225

ttg aac aac ggc acc att gcg ggt gct gcg ctg gac gtt acc gat cct 835
 Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 230 235 240 245

gag cca ctt cct gac agc cac ccg ctg tgg gag atg gac aat gtg gtt 883
 Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 250 255 260

atc act cct cat act gca aac acg aat gag agg att cgt gct ttg acc 931
 Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 265 270 275

ggc gaa ctc acc ttg cgc aac att gag ttg ttt gag gca ggc gag cag 979
 Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 280 285 290

atg gcc acc gag gtc gat gtg gtg gct ggc tac taggcctttt atggtgtgat 1032
 Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 295 300

ccg 1035

<210> 168

<211> 304

<212> PRT

<213> Corynebacterium glutamicum

<400> 168

Met Lys Phe Val Met Tyr Pro His Leu Trp Glu Ser Thr Thr Ala Val
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Ile Glu Gly Gly Gly His Glu Arg Val Glu Asp Ile Lys Asp Ala Asp
 20 25 30

Phe Ile Phe Phe Asn Gly Ser Ala Pro Glu Phe Pro Asp Leu Pro Glu
 35 40 45

Asn Ile Lys Phe Val Gln Ala Ser Met Ala Gly Ile Asp Ala Leu Val
 50 55 60

Lys Arg Gly Val Val Asn Glu Lys Ala Arg Trp Ala Asn Ala Ala Gly
 65 70 75 80

Leu Tyr Ala Asp Thr Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala
 85 90 95

Gln Met His Met His Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val
 100 105 110

Arg Pro Glu Val Glu Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr
 115 120 125

Val Ala Ile Leu Gly Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met
 130 135 140

Leu Lys Pro Phe Asn Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg
 145 150 155 160

Pro Val Glu Gly Ala Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His
 165 170 175

Val Trp Ala Glu Ala Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp
 180 185 190

Ala Thr Tyr Gln Ile Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro
 195 200 205

Ser Ala Val Val Val Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp
 210 215 220

Asp Leu Val Asp Ala Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu
 225 230 235 240

Asp Val Thr Asp Pro Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu
 245 250 255

Met Asp Asn Val Val Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg
 260 265 270

Ile Arg Ala Leu Thr Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe
 275 280 285

Glu Ala Gly Glu Gln Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 290 295 300

<210> 169

<211> 779

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (52)..(756)

<223> FRXA02379

<400> 169

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 Met Arg
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aag cac cgt tgg gca aac gcg gct ggc ctg tac gct gac acc gtt gct 105
 Lys His Arg Trp Ala Asn Ala Ala Gly Leu Tyr Ala Asp Thr Val Ala
 5 10 15

gag tcc acc att ggt tta att ctg gcg cag atg cac atg cat gcg acg 153
 Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His Ala Thr
 20 25 30

act cgt ttg gct aag tcg tgg agc gtg cgg cct gag gtg gaa aac aac 201

Thr	Arg	Leu	Ala	Lys	Ser	Trp	Ser	Val	Arg	Pro	Glu	Val	Glu	Asn	Asn		
35					40					45					50		
aag	tca	tgg	ctg	cat	gac	aat	aaa	act	gtc	gct	att	ttg	ggc	gcc	ggt	249	
Lys	Ser	Trp	Leu	His	Asp	Asn	Lys	Thr	Val	Ala	Ile	Leu	Gly	Ala	Gly		
				55					60					65			
ggc	att	ggc	gtg	cgt	ctg	ctg	gaa	atg	ctc	aag	ccg	ttc	aac	gtg	aag	297	
Gly	Ile	Gly	Val	Arg	Leu	Leu	Glu	Met	Leu	Lys	Pro	Phe	Asn	Val	Lys		
			70					75					80				
acc	att	gcg	gtt	aat	aac	tct	ggt	cgt	ccg	gtg	gaa	ggt	gca	gat	gaa	345	
Thr	Ile	Ala	Val	Asn	Asn	Ser	Gly	Arg	Pro	Val	Glu	Gly	Ala	Asp	Glu		
		85					90					95					
acc	ttc	gcc	atg	gat	aag	gct	gag	cac	gtg	tgg	gct	gag	gct	gat	gtg	393	
Thr	Phe	Ala	Met	Asp	Lys	Ala	Glu	His	Val	Trp	Ala	Glu	Ala	Asp	Val		
	100					105					110						
ttt	gtg	ctc	atc	ctg	ccg	ctg	act	gat	gcc	act	tat	cag	atc	gtc	aat	441	
Phe	Val	Leu	Ile	Leu	Pro	Leu	Thr	Asp	Ala	Thr	Tyr	Gln	Ile	Val	Asn		
115					120				125						130		
gca	gaa	act	ttg	ggc	aag	atg	aag	cct	tct	gcc	gtg	gtg	gtc	aat	gtg	489	
Ala	Glu	Thr	Leu	Gly	Lys	Met	Lys	Pro	Ser	Ala	Val	Val	Val	Asn	Val		
				135				140						145			
ggg	cgt	ggc	ccg	ctg	atc	aac	acc	gat	gat	ctg	gtg	gat	gca	ttg	aac	537	
Gly	Arg	Gly	Pro	Leu	Ile	Asn	Thr	Asp	Asp	Leu	Val	Asp	Ala	Leu	Asn		
			150					155					160				
aac	ggc	acc	att	gcg	ggt	gct	gcg	ctg	gac	gtt	acc	gat	cct	gag	cca	585	
Asn	Gly	Thr	Ile	Ala	Gly	Ala	Ala	Leu	Asp	Val	Thr	Asp	Pro	Glu	Pro		
		165					170					175					
ctt	cct	gac	agc	cac	ccg	ctg	tgg	gag	atg	gac	aat	gtg	gtt	atc	act	633	
Leu	Pro	Asp	Ser	His	Pro	Leu	Trp	Glu	Met	Asp	Asn	Val	Val	Ile	Thr		
	180					185					190						
cct	cat	act	gca	aac	acg	aat	gag	agg	att	cgt	gct	ttg	acc	ggc	gaa	681	
Pro	His	Thr	Ala	Asn	Thr	Asn	Glu	Arg	Ile	Arg	Ala	Leu	Thr	Gly	Glu		
195					200					205				210			
ctc	acc	ttg	cgc	aac	att	gag	ttg	ttt	gag	gca	ggc	gag	cag	atg	gcc	729	
Leu	Thr	Leu	Arg	Asn	Ile	Glu	Leu	Phe	Glu	Ala	Gly	Glu	Gln	Met	Ala		
				215					220					225			
acc	gag	gtc	gat	gtg	gtg	gct	ggc	tac	taggcctttt	atggtgtgat	ccg					779	
Thr	Glu	Val	Asp	Val	Val	Ala	Gly	Tyr									
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<210> 170

<211> 235

<212> PRT

<213> Corynebacterium glutamicum

<400> 170

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Val Ala Glu Ser Thr Ile Gly Leu Ile Leu Ala Gln Met His Met His
 20 25 30
 Ala Thr Thr Arg Leu Ala Lys Ser Trp Ser Val Arg Pro Glu Val Glu
 35 40 45
 Asn Asn Lys Ser Trp Leu His Asp Asn Lys Thr Val Ala Ile Leu Gly
 50 55 60
 Ala Gly Gly Ile Gly Val Arg Leu Leu Glu Met Leu Lys Pro Phe Asn
 65 70 75 80
 Val Lys Thr Ile Ala Val Asn Asn Ser Gly Arg Pro Val Glu Gly Ala
 85 90 95
 Asp Glu Thr Phe Ala Met Asp Lys Ala Glu His Val Trp Ala Glu Ala
 100 105 110
 Asp Val Phe Val Leu Ile Leu Pro Leu Thr Asp Ala Thr Tyr Gln Ile
 115 120 125
 Val Asn Ala Glu Thr Leu Gly Lys Met Lys Pro Ser Ala Val Val Val
 130 135 140
 Asn Val Gly Arg Gly Pro Leu Ile Asn Thr Asp Asp Leu Val Asp Ala
 145 150 155 160
 Leu Asn Asn Gly Thr Ile Ala Gly Ala Ala Leu Asp Val Thr Asp Pro
 165 170 175
 Glu Pro Leu Pro Asp Ser His Pro Leu Trp Glu Met Asp Asn Val Val
 180 185 190
 Ile Thr Pro His Thr Ala Asn Thr Asn Glu Arg Ile Arg Ala Leu Thr
 195 200 205
 Gly Glu Leu Thr Leu Arg Asn Ile Glu Leu Phe Glu Ala Gly Glu Gln
 210 215 220
 Met Ala Thr Glu Val Asp Val Val Ala Gly Tyr
 225 230 235

<210> 171

<211> 792

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(769)

<223> RXN02688

<400> 171

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gggttcgcg agcaagcgaa ggaaggaaac ttaactagcc atg gcc ggc cgg att 115

Met Ala Gly Arg Ile

1

5

att ttg cta cga cac ggg cag act cac aac aac gtc aaa cac ctc ctg 163

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Ile Leu Leu Arg His Gly Gln Thr His Asn Asn Val Lys His Leu Leu
      10                      15                      20

gac acc cgc cca cca gga gct gaa ctc acc gac ctg ggc cgt aaa caa 211
Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp Leu Gly Arg Lys Gln
      25                      30                      35

gcc ctt gaa gtt ggc cac gaa cta gcc acc tac tcc ggt gag cgc ctc 259
Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr Ser Gly Glu Arg Leu
      40                      45                      50

gcc cat gtg tac agc tcc atc gtg ttg cgc gcc caa caa acc gcc gtg 307
Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala Gln Gln Thr Ala Val
      55                      60                      65

ctt gcc acc tct acc ttt gaa aaa gct cgc gac atg cag tcc ggt gcg 355
Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp Met Gln Ser Gly Ala
      70                      75                      80                      85

att cca ctc gac gtt gtg gaa ggc att cag gaa atc aac gtc ggc gac 403
Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu Ile Asn Val Gly Asp
      90                      95                      100

ttt gaa atg cgc ggc gat gaa gaa gcc cac atg aat tac tcc cgc gca 451
Phe Glu Met Arg Gly Asp Glu Glu Ala His Met Asn Tyr Ser Arg Ala
      105                      110                      115

ctc aac ggc tgg ctt cac ggg gat cct gcc gct ggt ctt ccc ggc ggt 499
Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala Gly Leu Pro Gly Gly
      120                      125                      130

gag acc tac aaa gac gtg ctg aac cgc tac cag ccg act ctt gat cga 547
Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln Pro Thr Leu Asp Arg
      135                      140                      145

atc atg gac agc cac gac ctt gac gac gac cgc gac gtt gcc gtt gtc 595
Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg Asp Val Ala Val Val
      150                      155                      160                      165

agc cac ggc gcc gtc atc cgc atc gtg gca aca cac gca act ggt gtg 643
Ser His Gly Ala Val Ile Arg Ile Val Ala Thr His Ala Thr Gly Val
      170                      175                      180

gat ccc aac ttt gcg ttc aac acc tac ctg ggc aac tgc cgc ttc gtg 691
Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly Asn Cys Arg Phe Val
      185                      190                      195

gtg ctg gag cca aac ggt aag aaa ttc agc caa tgg gat gtt gtg cgc 739
Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln Trp Asp Val Val Arg
      200                      205                      210

tgg act gac agc cca ctg cca tgg cag gag taattgagac caaaggctcg 789
Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
      215                      220

gat 792

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<210> 172

<211> 223

<212> PRT

<213> Corynebacterium glutamicum

<400> 172

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Val Lys His Leu Leu Asp Thr Arg Pro Pro Gly Ala Glu Leu Thr Asp
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Leu Gly Arg Lys Gln Ala Leu Glu Val Gly His Glu Leu Ala Thr Tyr
          35           40           45

Ser Gly Glu Arg Leu Ala His Val Tyr Ser Ser Ile Val Leu Arg Ala
          50           55           60

Gln Gln Thr Ala Val Leu Ala Thr Ser Thr Phe Glu Lys Ala Arg Asp
          65           70           75           80

Met Gln Ser Gly Ala Ile Pro Leu Asp Val Val Glu Gly Ile Gln Glu
          85           90           95

Ile Asn Val Gly Asp Phe Glu Met Arg Gly Asp Glu Glu Ala His Met
          100          105          110

Asn Tyr Ser Arg Ala Leu Asn Gly Trp Leu His Gly Asp Pro Ala Ala
          115          120          125

Gly Leu Pro Gly Gly Glu Thr Tyr Lys Asp Val Leu Asn Arg Tyr Gln
          130          135          140

Pro Thr Leu Asp Arg Ile Met Asp Ser His Asp Leu Asp Asp Asp Arg
          145          150          155          160

Asp Val Ala Val Val Ser His Gly Ala Val Ile Arg Ile Val Ala Thr
          165          170          175

His Ala Thr Gly Val Asp Pro Asn Phe Ala Phe Asn Thr Tyr Leu Gly
          180          185          190

Asn Cys Arg Phe Val Val Leu Glu Pro Asn Gly Lys Lys Phe Ser Gln
          195          200          205

Trp Asp Val Val Arg Trp Thr Asp Ser Pro Leu Pro Trp Gln Glu
          210          215          220

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<210> 173

<211> 336

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(313)

<223> RXN03087

<400> 173

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gaatacctgg aaaagagctg atattgatag ggtttaagtc atg aag atc tac gca 115
Met Lys Ile Tyr Ala

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                                1           5
cct ttt gct gga atc gtc cac tat ttt gtc gat gaa ggc gat ccc gtg 163
Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp Glu Gly Asp Pro Val
      10           15           20
gaa acc ggc atg caa ctg gga acg gta gaa acc atc aaa ctc gag gca 211
Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr Ile Lys Leu Glu Ala
      25           30           35
cca atc atg gca ccg gga cct ggc atc gta gct aag gtt tct ttt gat 259
Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala Lys Val Ser Phe Asp
      40           45           50
gat ttc tcc gac gtc acc ggc ggc gat gaa ctc ctc gaa ttg gag gca 307
Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu Leu Glu Leu Glu Ala
      55           60           65
aag aac taatgggtca aaccgcacatc att 336
Lys Asn
      70

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<210> 174
 <211> 71
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 174
Met Lys Ile Tyr Ala Pro Phe Ala Gly Ile Val His Tyr Phe Val Asp
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Glu Gly Asp Pro Val Glu Thr Gly Met Gln Leu Gly Thr Val Glu Thr
      20           25           30
Ile Lys Leu Glu Ala Pro Ile Met Ala Pro Gly Pro Gly Ile Val Ala
      35           40           45
Lys Val Ser Phe Asp Asp Phe Ser Asp Val Thr Gly Gly Asp Glu Leu
      50           55           60
Leu Glu Leu Glu Ala Lys Asn
      65           70

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<210> 175
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 <212> DNA
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<220>
 <221> CDS
 <222> (101)..(310)
 <223> RXN03186

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<400> 175
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cgtataaacg aaataaaaaca ttccaacagg aggtgtggaa atg gcc gat caa gca 115
Met Ala Asp Gln Ala
      1           5

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aaa ctt ggt ggc aag ccc tcg gat gac tct aac ttc gcg atg atc cgc 163
 Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn Phe Ala Met Ile Arg
 10 15 20

gat ggc gtg gca tct tat ttg aac gac tca gat ccg gag gag acc aac 211
 Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp Pro Glu Glu Thr Asn
 25 30 35

gag tgg atg gat tca ctc gac gga tta ctc cag gag tct tct cca gaa 259
 Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln Glu Ser Ser Pro Glu
 40 45 50

cgt gct cgt tac ctc atg ctt cgt ttg ctt gag cgt gca tct gca aag 307
 Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu Arg Ala Ser Ala Lys
 55 60 65

cgc 310
 Arg
 70

<210> 176

<211> 70

<212> PRT

<213> Corynebacterium glutamicum

<400> 176

Met Ala Asp Gln Ala Lys Leu Gly Gly Lys Pro Ser Asp Asp Ser Asn
 1 5 10 15

Phe Ala Met Ile Arg Asp Gly Val Ala Ser Tyr Leu Asn Asp Ser Asp
 20 25 30

Pro Glu Glu Thr Asn Glu Trp Met Asp Ser Leu Asp Gly Leu Leu Gln
 35 40 45

Glu Ser Ser Pro Glu Arg Ala Arg Tyr Leu Met Leu Arg Leu Leu Glu
 50 55 60

Arg Ala Ser Ala Lys Arg
 65 70

<210> 177

<211> 302

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(279)

<223> RXN03187

<400> 177

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 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
 1 5 10 15

tgg gtc cca ggc gac tac acc gtt ctc ggt gca gat ggc ttc ggt ttc 96
 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe

	20	25	30	
tct gat acc cgc cca gct gct cgt cgc ttc ttc aac atc gac gct gag				144
Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu				
	35	40	45	
tcc att gtt gtt gca gtg ctg aac tcc ctg gca cgc gaa ggc aag atc				192
Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile				
	50	55	60	
gac gtc tcc gtt gct gct cag gct gct gag aag ttc aag ttg gat gat				240
Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp				
	65	70	75	80
cct acg agt gtt tcc gta gat cca aac gct cct gag gaa taaatcacct				289
Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu				
	85	90		
caagggacag ata				302

<210> 178
 <211> 93
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 178
 Val Ala Val Ser Asp Phe Ser Thr Asp Leu Pro Asn Gln Ile Arg Glu
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 Trp Val Pro Gly Asp Tyr Thr Val Leu Gly Ala Asp Gly Phe Gly Phe
 20 25 30
 Ser Asp Thr Arg Pro Ala Ala Arg Arg Phe Phe Asn Ile Asp Ala Glu
 35 40 45
 Ser Ile Val Val Ala Val Leu Asn Ser Leu Ala Arg Glu Gly Lys Ile
 50 55 60
 Asp Val Ser Val Ala Ala Gln Ala Ala Glu Lys Phe Lys Leu Asp Asp
 65 70 75 80
 Pro Thr Ser Val Ser Val Asp Pro Asn Ala Pro Glu Glu
 85 90

<210> 179
 <211> 1953
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1930)
 <223> RXN02591

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 ggcgagaact ctgtcgaatg acacaaaatc tggagaagta atg act act gct gca 115
 Met Thr Thr Ala Ala

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atc	agg	ggc	ctt	cag	ggc	gag	gcg	ccg	acc	aag	aat	aag	gaa	ctg	ctg	163															
Ile	Arg	Gly	Leu	Gln	Gly	Glu	Ala	Pro	Thr	Lys	Asn	Lys	Glu	Leu	Leu																
				10					15					20																	
aac	tgg	atc	gca	gac	gcc	gtc	gag	ctc	ttc	cag	cct	gag	gct	gct	gtg	211															
Asn	Trp	Ile	Ala	Asp	Ala	Val	Glu	Leu	Phe	Gln	Pro	Glu	Ala	Val	Val																
				25					30					35																	
ttc	gtt	gat	gga	tcc	cag	gct	gag	tgg	gat	cgc	atg	gcg	gag	gat	ctt	259															
Phe	Val	Asp	Gly	Ser	Gln	Ala	Glu	Trp	Asp	Arg	Met	Ala	Glu	Asp	Leu																
				40					45					50																	
gtt	gaa	gcc	ggt	acc	ctc	atc	aag	ctc	aac	gag	gaa	aag	cgt	ccg	aac	307															
Val	Glu	Ala	Gly	Thr	Leu	Ile	Lys	Leu	Asn	Glu	Glu	Lys	Arg	Pro	Asn																
				55					60					65																	
agc	tac	cta	gct	cgt	tcc	aac	cca	tct	gac	gtt	gcg	cgc	gtt	gag	tcc	355															
Ser	Tyr	Leu	Ala	Arg	Ser	Asn	Pro	Ser	Asp	Val	Ala	Arg	Val	Glu	Ser																
				70					75					80																	
cgc	acc	ttc	atc	tgc	tcc	gag	aag	gaa	gaa	gat	gct	ggc	cca	acc	aac	403															
Arg	Thr	Phe	Ile	Cys	Ser	Glu	Lys	Glu	Glu	Asp	Ala	Gly	Pro	Thr	Asn																
				90					95					100																	
aac	tgg	gct	cca	cca	cag	gca	atg	aag	gac	gaa	atg	tcc	aag	cat	tac	451															
Asn	Trp	Ala	Pro	Pro	Gln	Ala	Met	Lys	Asp	Glu	Met	Ser	Lys	His	Tyr																
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gct	ggt	tcc	atg	aag	ggg	cgc	acc	atg	tac	gtc	gtg	cct	ttc	tgc	atg	499															
Ala	Gly	Ser	Met	Lys	Gly	Arg	Thr	Met	Tyr	Val	Val	Pro	Phe	Cys	Met																
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ggt	cca	atc	agc	gat	ccg	gac	cct	aag	ctt	ggt	gtg	cag	ctc	act	gac	547															
Gly	Pro	Ile	Ser	Asp	Pro	Asp	Pro	Lys	Leu	Gly	Val	Gln	Leu	Thr	Asp																
				135					140					145																	
tcc	gag	tac	gtt	gtc	atg	tcc	atg	cgc	atc	atg	acc	cgc	atg	ggt	att	595															
Ser	Glu	Tyr	Val	Val	Met	Ser	Met	Arg	Ile	Met	Thr	Arg	Met	Gly	Ile																
				150					155					160																	
gaa	gcg	ctg	gac	aag	atc	ggc	gcg	aac	ggc	agc	ttc	gtc	agg	tgc	ctc	643															
Glu	Ala	Leu	Asp	Lys	Ile	Gly	Ala	Asn	Gly	Ser	Phe	Val	Arg	Cys	Leu																
				170					175					180																	
cac	tcc	gtt	ggt	gct	cct	ttg	gag	cca	ggc	cag	gaa	gac	gtt	gca	tgg	691															
His	Ser	Val	Gly	Ala	Pro	Leu	Glu	Pro	Gly	Gln	Glu	Asp	Val	Ala	Trp																
				185					190					195																	
cct	tgc	aac	gac	acc	aag	tac	atc	acc	cag	ttc	cca	gag	acc	aag	gaa	739															
Pro	Cys	Asn	Asp	Thr	Lys	Tyr	Ile	Thr	Gln	Phe	Pro	Glu	Thr	Lys	Glu																
				200					205					210																	
att	tgg	tcc	tac	ggt	tcc	ggc	tac	ggc	gga	aac	gca	atc	ctg	gca	aag	787															
Ile	Trp	Ser	Tyr	Gly																											

tgg atg gct gag cac atg ctc atc ctg aag ctg atc aac cca gag ggc	883
Trp Met Ala Glu His Met Leu Ile Leu Lys Leu Ile Asn Pro Glu Gly	
250 255 260	
aag gcg tac cac atc gca gca gca ttc cca tct gct tgt ggc aag acc	931
Lys Ala Tyr His Ile Ala Ala Ala Phe Pro Ser Ala Cys Gly Lys Thr	
265 270 275	
aac ctc gcc atg atc act cca acc atc cca ggc tgg acc gct cag gtt	979
Asn Leu Ala Met Ile Thr Pro Thr Ile Pro Gly Trp Thr Ala Gln Val	
280 285 290	
gtt ggc gac gac atc gct tgg ctg aag ctg cgc gag gac ggc ctc tac	1027
Val Gly Asp Asp Ile Ala Trp Leu Lys Leu Arg Glu Asp Gly Leu Tyr	
295 300 305	
gca gtt aac cca gaa aat ggt ttc ttc ggt gtt gct cca ggc acc aac	1075
Ala Val Asn Pro Glu Asn Gly Phe Phe Gly Val Ala Pro Gly Thr Asn	
310 315 320 325	
tac gca tcc aac cca atc gcg atg aag acc atg gaa cca ggc aac acc	1123
Tyr Ala Ser Asn Pro Ile Ala Met Lys Thr Met Glu Pro Gly Asn Thr	
330 335 340	
ctg ttc acc aac gtg gca ctc acc gac gac ggc gac atc tgg tgg gaa	1171
Leu Phe Thr Asn Val Ala Leu Thr Asp Asp Gly Asp Ile Trp Trp Glu	
345 350 355	
ggc atg gac ggc gac gcc cca gct cac ctc att gac tgg atg ggc aac	1219
Gly Met Asp Gly Asp Ala Pro Ala His Leu Ile Asp Trp Met Gly Asn	
360 365 370	
gac tgg acc cca gag tcc gac gaa aac gct gct cac cct aac tcc cgt	1267
Asp Trp Thr Pro Glu Ser Asp Glu Asn Ala Ala His Pro Asn Ser Arg	
375 380 385	
tac tgc gta gca atc gac cag tcc cca gca gca gca cct gag ttc aac	1315
Tyr Cys Val Ala Ile Asp Gln Ser Pro Ala Ala Ala Pro Glu Phe Asn	
390 395 400 405	
gac tgg gaa ggc gtc aag atc gac gca atc ctc ttc ggt gga cgt cgc	1363
Asp Trp Glu Gly Val Lys Ile Asp Ala Ile Leu Phe Gly Gly Arg Arg	
410 415 420	
gca gac acc gtc cca ctg gtt acc cag acc tac gac tgg gag cac ggc	1411
Ala Asp Thr Val Pro Leu Val Thr Gln Thr Tyr Asp Trp Glu His Gly	
425 430 435	
acc atg gtt ggt gca ctg ctc gca tcc ggt cag acc gca gct tcc gca	1459
Thr Met Val Gly Ala Leu Leu Ala Ser Gly Gln Thr Ala Ala Ser Ala	
440 445 450	
gaa gca aag gtc ggc aca ctc cgc cac gac cca atg gca atg ctc cca	1507
Glu Ala Lys Val Gly Thr Leu Arg His Asp Pro Met Ala Met Leu Pro	
455 460 465	
ttc att ggc tac aac gct ggt gaa tac ctg cag aac tgg att gac atg	1555
Phe Ile Gly Tyr Asn Ala Gly Glu Tyr Leu Gln Asn Trp Ile Asp Met	
470 475 480 485	

ggt aac aag ggt ggc gac aag atg cca tcc atc ttc ctg gtc aac tgg 1603
 Gly Asn Lys Gly Gly Asp Lys Met Pro Ser Ile Phe Leu Val Asn Trp
 490 495 500

ttc cgc cgt ggc gaa gat gga cgc ttc ctg tgg cct ggc ttc ggc gac 1651
 Phe Arg Arg Gly Glu Asp Gly Arg Phe Leu Trp Pro Gly Phe Gly Asp
 505 510 515

aac tct cgc gtt ctg aag tgg gtc atc gac cgc atc gaa ggc cac gtt 1699
 Asn Ser Arg Val Leu Lys Trp Val Ile Asp Arg Ile Glu Gly His Val
 520 525 530

ggc gca gac gag acc gtt gtt gga cac acc gct aag gcc gaa gac ctc 1747
 Gly Ala Asp Glu Thr Val Val Gly His Thr Ala Lys Ala Glu Asp Leu
 535 540 545

gac ctc gac ggc ctc gac acc cca att gag gat gtc aag gaa gca ctg 1795
 Asp Leu Asp Gly Leu Asp Thr Pro Ile Glu Asp Val Lys Glu Ala Leu
 550 555 560 565

acc gct cct gca gag cag tgg gca aac gac gtt gaa gac aac gcc gag 1843
 Thr Ala Pro Ala Glu Gln Trp Ala Asn Asp Val Glu Asp Asn Ala Glu
 570 575 580

tac ctc act ttc ctc gga cca cgt gtt cct gca gag gtt cac agc cag 1891
 Tyr Leu Thr Phe Leu Gly Pro Arg Val Pro Ala Glu Val His Ser Gln
 585 590 595

ttc gat gct ctg aag gcc cgc att tca gca gct cac gct taaagtccac 1940
 Phe Asp Ala Leu Lys Ala Arg Ile Ser Ala Ala His Ala
 600 605 610

gcttaagaac tgc 1953

<210> 180

<211> 610

<212> PRT

<213> Corynebacterium glutamicum

<400> 180

Met Thr Thr Ala Ala Ile Arg Gly Leu Gln Gly Glu Ala Pro Thr Lys
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Asn Lys Glu Leu Leu Asn Trp Ile Ala Asp Ala Val Glu Leu Phe Gln
 20 25 30

Pro Glu Ala Val Val Phe Val Asp Gly Ser Gln Ala Glu Trp Asp Arg
 35 40 45

Met Ala Glu Asp Leu Val Glu Ala Gly Thr Leu Ile Lys Leu Asn Glu
 50 55 60

Glu Lys Arg Pro Asn Ser Tyr Leu Ala Arg Ser Asn Pro Ser Asp Val
 65 70 75 80

Ala Arg Val Glu Ser Arg Thr Phe Ile Cys Ser Glu Lys Glu Glu Asp
 85 90 95

Ala Gly Pro Thr Asn Asn Trp Ala Pro Pro Gln Ala Met Lys Asp Glu
 100 105 110

Met	Ser	Lys	His	Tyr	Ala	Gly	Ser	Met	Lys	Gly	Arg	Thr	Met	Tyr	Val		
		115					120					125					
Val	Pro	Phe	Cys	Met	Gly	Pro	Ile	Ser	Asp	Pro	Asp	Pro	Lys	Leu	Gly		
	130					135					140						
Val	Gln	Leu	Thr	Asp	Ser	Glu	Tyr	Val	Val	Met	Ser	Met	Arg	Ile	Met		
145					150					155					160		
Thr	Arg	Met	Gly	Ile	Glu	Ala	Leu	Asp	Lys	Ile	Gly	Ala	Asn	Gly	Ser		
				165					170					175			
Phe	Val	Arg	Cys	Leu	His	Ser	Val	Gly	Ala	Pro	Leu	Glu	Pro	Gly	Gln		
			180					185					190				
Glu	Asp	Val	Ala	Trp	Pro	Cys	Asn	Asp	Thr	Lys	Tyr	Ile	Thr	Gln	Phe		
	195						200					205					
Pro	Glu	Thr	Lys	Glu	Ile	Trp	Ser	Tyr	Gly	Ser	Gly	Tyr	Gly	Gly	Asn		
	210					215					220						
Ala	Ile	Leu	Ala	Lys	Lys	Cys	Tyr	Ala	Leu	Arg	Ile	Ala	Ser	Val	Met		
225					230					235					240		
Ala	Arg	Glu	Glu	Gly	Trp	Met	Ala	Glu	His	Met	Leu	Ile	Leu	Lys	Leu		
				245					250					255			
Ile	Asn	Pro	Glu	Gly	Lys	Ala	Tyr	His	Ile	Ala	Ala	Ala	Phe	Pro	Ser		
			260					265					270				
Ala	Cys	Gly	Lys	Thr	Asn	Leu	Ala	Met	Ile	Thr	Pro	Thr	Ile	Pro	Gly		
		275					280					285					
Trp	Thr	Ala	Gln	Val	Val	Gly	Asp	Asp	Ile	Ala	Trp	Leu	Lys	Leu	Arg		
	290					295					300						
Glu	Asp	Gly	Leu	Tyr	Ala	Val	Asn	Pro	Glu	Asn	Gly	Phe	Phe	Gly	Val		
305					310					315					320		
Ala	Pro	Gly	Thr	Asn	Tyr	Ala	Ser	Asn	Pro	Ile	Ala	Met	Lys	Thr	Met		
				325					330					335			
Glu	Pro	Gly	Asn	Thr	Leu	Phe	Thr	Asn	Val	Ala	Leu	Thr	Asp	Asp	Gly		
			340					345					350				
Asp	Ile	Trp	Trp	Glu	Gly	Met	Asp	Gly	Asp	Ala	Pro	Ala	His	Leu	Ile		
		355					360					365					
Asp	Trp	Met	Gly	Asn	Asp	Trp	Thr	Pro	Glu	Ser	Asp	Glu	Asn	Ala	Ala		
	370					375					380						
His	Pro	Asn	Ser	Arg	Tyr	Cys	Val	Ala	Ile	Asp	Gln	Ser	Pro	Ala	Ala		
385					390					395					400		
Ala	Pro	Glu	Phe	Asn	Asp	Trp	Glu	Gly	Val	Lys	Ile	Asp	Ala	Ile	Leu		
				405					410					415			
Phe	Gly	Gly	Arg	Arg	Ala	Asp	Thr	Val	Pro	Leu	Val	Thr	Gln	Thr	Tyr		
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<210> 181
<211> 1305
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1282)  
<223> RXS01260
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ctttaccat  gagagaaga ccttcggcat caatggcgaa gtg acc ttc aac tat 115
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              Val Thr Phe Asn Tyr
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gag gat gct cac aag cgt tcc cgt ggc gtt tcc gac aag atc gtt gga 163
Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser Asp Lys Ile Val Gly
              10              15              20

ggc gtt cat tac ttg atg aag aag aac aag atc atc gaa att cat ggt 211
Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile Ile Glu Ile His Gly
              25              30              35

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ctt gga aac ttc aag gat gct aag act ctt gag gtc acc gac ggt aag	259
Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu Val Thr Asp Gly Lys	
40 45 50	
gat gct ggc aag acc atc acc ttt gat gac tgc atc atc gca acc ggt	307
Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys Ile Ile Ala Thr Gly	
55 60 65	
tcg gta gtc aac acc ctc cgt ggc gtt gac ttc tca gag aac gtt gtg	355
Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe Ser Glu Asn Val Val	
70 75 80 85	
tct ttt gaa gag cag att ctt aac cct gtt gcg cca aag aag atg gtc	403
Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala Pro Lys Lys Met Val	
90 95 100	
att gtt ggt gca ggc gca att gga atg gaa ttc gcc tac gtt ctt ggt	451
Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe Ala Tyr Val Leu Gly	
105 110 115	
aac tac ggt gta gat gta acc gtc atc gag ttc atg gat cgt gtg ctt	499
Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe Met Asp Arg Val Leu	
120 125 130	
cca aat gaa gat gct gaa gtc tcc aag gtt att gca aag gcc tac aag	547
Pro Asn Glu Asp Ala Glu Val Ser Lys Val Ile Ala Lys Ala Tyr Lys	
135 140 145	
aag atg ggc gtt aag ctt ctt cct ggc cat gca acc act gct gtt cgg	595
Lys Met Gly Val Lys Leu Leu Pro Gly His Ala Thr Thr Ala Val Arg	
150 155 160 165	
gac aac ggt gac ttt gtc gag gtt gat tac cag aag aag ggc tct gac	643
Asp Asn Gly Asp Phe Val Glu Val Asp Tyr Gln Lys Lys Gly Ser Asp	
170 175 180	
aag aca gag act ctt act gtt gat cga gtc atg gtt tcc gtt ggt ttc	691
Lys Thr Glu Thr Leu Thr Val Asp Arg Val Met Val Ser Val Gly Phe	
185 190 195	
cgt cca cgc gtt gag gga ttt ggt ctt gaa aac act ggc gtt aag ctc	739
Arg Pro Arg Val Glu Gly Phe Gly Leu Glu Asn Thr Gly Val Lys Leu	
200 205 210	
acc gag cgt ggc gca atc gag atc gat gat tac atg cgt acc aac gtc	787
Thr Glu Arg Gly Ala Ile Glu Ile Asp Asp Tyr Met Arg Thr Asn Val	
215 220 225	
gat ggc att tac gcc atc ggt gac gtg acc gcc aag ctt cag ctt gct	835
Asp Gly Ile Tyr Ala Ile Gly Asp Val Thr Ala Lys Leu Gln Leu Ala	
230 235 240 245	
cac gtc gca gaa gca cag ggc att gtt gcc gca gag act att gct ggt	883
His Val Ala Glu Ala Gln Gly Ile Val Ala Ala Glu Thr Ile Ala Gly	
250 255 260	
gca gaa act cag act ctt ggt gat tac atg atg atg cca cgt gca acc	931
Ala Glu Thr Gln Thr Leu Gly Asp Tyr Met Met Met Pro Arg Ala Thr	
265 270 275	

ttc tgc aac cca cag gtt tct tcc ttt ggt tac acc gaa gag cag gcc 979
 Phe Cys Asn Pro Gln Val Ser Ser Phe Gly Tyr Thr Glu Glu Gln Ala
 280 285 290

aag gag aag tgg cca gat cgt gag atc aag gtt gct tcc ttc cca ttc 1027
 Lys Glu Lys Trp Pro Asp Arg Glu Ile Lys Val Ala Ser Phe Pro Phe
 295 300 305

tct gca aac ggt aaa gca gtt ggc ctg gca gaa act gat ggt ttc gca 1075
 Ser Ala Asn Gly Lys Ala Val Gly Leu Ala Glu Thr Asp Gly Phe Ala
 310 315 320 325

aag atc gtt gct gat gca gaa ttc ggt gag ctg ctc ggt gca cac ctg 1123
 Lys Ile Val Ala Asp Ala Glu Phe Gly Glu Leu Leu Gly Ala His Leu
 330 335 340

gtt gga gca aat gca tca gag ctc atc aat gaa ttg gtg ctt gct cag 1171
 Val Gly Ala Asn Ala Ser Glu Leu Ile Asn Glu Leu Val Leu Ala Gln
 345 350 355

aac tgg gat ctc acc act gaa gag atc tct cgt agc gtc cat att cac 1219
 Asn Trp Asp Leu Thr Thr Glu Glu Ile Ser Arg Ser Val His Ile His
 360 365 370

cca acg cta tct gag gca gtt aag gaa gct gca cac ggt atc tct gga 1267
 Pro Thr Leu Ser Glu Ala Val Lys Glu Ala Ala His Gly Ile Ser Gly
 375 380 385

cac atg atc aac ttc tagaatccac ctcgttggcc ctg 1305
 His Met Ile Asn Phe
 390

<210> 182

<211> 394

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 182

Val Thr Phe Asn Tyr Glu Asp Ala His Lys Arg Ser Arg Gly Val Ser
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Asp Lys Ile Val Gly Gly Val His Tyr Leu Met Lys Lys Asn Lys Ile
 20 25 30

Ile Glu Ile His Gly Leu Gly Asn Phe Lys Asp Ala Lys Thr Leu Glu
 35 40 45

Val Thr Asp Gly Lys Asp Ala Gly Lys Thr Ile Thr Phe Asp Asp Cys
 50 55 60

Ile Ile Ala Thr Gly Ser Val Val Asn Thr Leu Arg Gly Val Asp Phe
 65 70 75 80

Ser Glu Asn Val Val Ser Phe Glu Glu Gln Ile Leu Asn Pro Val Ala
 85 90 95

Pro Lys Lys Met Val Ile Val Gly Ala Gly Ala Ile Gly Met Glu Phe
 100 105 110

Ala Tyr Val Leu Gly Asn Tyr Gly Val Asp Val Thr Val Ile Glu Phe

115					120					125						
Met	Asp	Arg	Val	Leu	Pro	Asn	Glu	Asp	Ala	Glu	Val	Ser	Lys	Val	Ile	
130					135					140						
Ala	Lys	Ala	Tyr	Lys	Lys	Met	Gly	Val	Lys	Leu	Leu	Pro	Gly	His	Ala	
145					150					155					160	
Thr	Thr	Ala	Val	Arg	Asp	Asn	Gly	Asp	Phe	Val	Glu	Val	Asp	Tyr	Gln	
165					170					175						
Lys	Lys	Gly	Ser	Asp	Lys	Thr	Glu	Thr	Leu	Thr	Val	Asp	Arg	Val	Met	
180					185					190						
Val	Ser	Val	Gly	Phe	Arg	Pro	Arg	Val	Glu	Gly	Phe	Gly	Leu	Glu	Asn	
195					200					205						
Thr	Gly	Val	Lys	Leu	Thr	Glu	Arg	Gly	Ala	Ile	Glu	Ile	Asp	Asp	Tyr	
210					215					220						
Met	Arg	Thr	Asn	Val	Asp	Gly	Ile	Tyr	Ala	Ile	Gly	Asp	Val	Thr	Ala	
225					230					235					240	
Lys	Leu	Gln	Leu	Ala	His	Val	Ala	Glu	Ala	Gln	Gly	Ile	Val	Ala	Ala	
245					250					255						
Glu	Thr	Ile	Ala	Gly	Ala	Glu	Thr	Gln	Thr	Leu	Gly	Asp	Tyr	Met	Met	
260					265					270						
Met	Pro	Arg	Ala	Thr	Phe	Cys	Asn	Pro	Gln	Val	Ser	Ser	Phe	Gly	Tyr	
275					280					285						
Thr	Glu	Glu	Gln	Ala	Lys	Glu	Lys	Trp	Pro	Asp	Arg	Glu	Ile	Lys	Val	
290					295					300						
Ala	Ser	Phe	Pro	Phe	Ser	Ala	Asn	Gly	Lys	Ala	Val	Gly	Leu	Ala	Glu	
305					310					315					320	
Thr	Asp	Gly	Phe	Ala	Lys	Ile	Val	Ala	Asp	Ala	Glu	Phe	Gly	Glu	Leu	
325					330					335						
Leu	Gly	Ala	His	Leu	Val	Gly	Ala	Asn	Ala	Ser	Glu	Leu	Ile	Asn	Glu	
340					345					350						
Leu	Val	Leu	Ala	Gln	Asn	Trp	Asp	Leu	Thr	Thr	Glu	Glu	Ile	Ser	Arg	
355					360					365						
Ser	Val	His	Ile	His	Pro	Thr	Leu	Ser	Glu	Ala	Val	Lys	Glu	Ala	Ala	
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His	Gly	Ile	Ser	Gly	His	Met	Ile	Asn	Phe							
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<211> 294

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<223> RXS01261

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gat caa aaa cgc tgaagttgcc cataccttta ccc 294
Asp Gln Lys Arg
55

<213> Corynebacterium glutamicum

Pro Ser Lys Val Ser Asp Gln Lys Arg
50 55

<213> Corynebacterium glutamicum

<223> RXA02640

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aaacactgct tagtggccca atacgtgcaa aaataaggcc atg aga atc tca aag 115
Met Arg Ile Ser Lys

1												5				
gcc	aat	gcg	tat	gtt	gca	gcg	att	gac	caa	ggc	acc	act	tcc	act	cgg	163
Ala	Asn	Ala	Tyr	Val	Ala	Ala	Ile	Asp	Gln	Gly	Thr	Thr	Ser	Thr	Arg	
				10					15					20		
tgc	atc	ttc	att	gat	gcc	caa	gga	aaa	gtg	gtg	tct	tct	gct	tcc	aag	211
Cys	Ile	Phe	Ile	Asp	Ala	Gln	Gly	Lys	Val	Val	Ser	Ser	Ala	Ser	Lys	
				25					30					35		
gag	cac	cgc	caa	atc	ttc	cca	caa	cag	ggc	tgg	gta	gag	cac	gat	cct	259
Glu	His	Arg	Gln	Ile	Phe	Pro	Gln	Gln	Gly	Trp	Val	Glu	His	Asp	Pro	
				40					45					50		
gaa	gaa	att	tgg	gac	aac	att	cga	tct	gtc	gtc	agc	cag	gcg	atg	gtc	307
Glu	Glu	Ile	Trp	Asp	Asn	Ile	Arg	Ser	Val	Val	Ser	Gln	Ala	Met	Val	
				55					60					65		
tcc	att	gac	atc	acc	cca	cac	gag	gtt	gca	tcg	ctg	gga	gtc	acc	aac	355
Ser	Ile	Asp	Ile	Thr	Pro	His	Glu	Val	Ala	Ser	Leu	Gly	Val	Thr	Asn	
				70					75					80		
cag	cgc	gaa	acc	acc	gtg	gtg	tgg	gac	aag	cac	acc	ggc	gaa	cct	gtc	403
Gln	Arg	Glu	Thr	Thr	Val	Val	Trp	Asp	Lys	His	Thr	Gly	Glu	Pro	Val	
				90					95					100		
tac	aac	gca	atc	gtg	tgg	caa	gac	acc	cgc	acc	tct	gac	att	tgc	cta	451
Tyr	Asn	Ala	Ile	Val	Trp	Gln	Asp	Thr	Arg	Thr	Ser	Asp	Ile	Cys	Leu	
				105					110					115		
gag	atc	gcg	ggc	gaa	gaa	ggc	cag	gaa	aag	tgg	ctt	gac	cgc	acc	ggc	499
Glu	Ile	Ala	Gly	Glu	Glu	Gly	Gln	Glu	Lys	Trp	Leu	Asp	Arg	Thr	Gly	
				120					125					130		
ctg	ctg	atc	aac	tcc	tac	cca	tcg	ggg	ccc	aaa	atc	aag	tgg	att	ctc	547
Leu	Leu	Ile	Asn	Ser	Tyr	Pro	Ser	Gly	Pro	Lys	Ile	Lys	Trp	Ile	Leu	
				135					140					145		
gac	aac	gtt	gag	gga	gct	cgc	gaa	cgc	gcc	gaa	aag	ggc	gac	ctt	ttg	595
Asp	Asn	Val	Glu	Gly	Ala	Arg	Glu	Arg	Ala	Glu	Lys	Gly	Asp	Leu	Leu	
				150					155					160		
ttt	ggc	acc	atg	gat	acc	tgg	gtg	ctg	tgg	aac	ctg	acc	ggc	ggg	gtc	643
Phe	Gly	Thr	Met	Asp	Thr	Trp	Val	Leu	Trp	Asn	Leu	Thr	Gly	Gly	Val	
				170					175					180		
cgc	ggc	gac	gac	ggg	gat	gat	gcc	atc	cac	gtc	acc	gat	gtc	acc	aac	691
Arg	Gly	Asp	Asp	Gly	Asp	Asp	Ala	Ile	His	Val	Thr	Asp	Val	Thr	Asn	
				185					190					195		
gca	tcc	cgc	aca	cta	ttg	atg	gat	ctc	cgc	acg	caa	cag	tgg	gat	cca	739
Ala	Ser	Arg	Thr	Leu	Leu	Met	Asp	Leu	Arg	Thr	Gln	Gln	Trp	Asp	Pro	
				200					205					210		
gaa	cta	tgc	gaa	gcc	cta	gac	att	ccg	atg	tcc	atg	ctc	cct	gag	att	787
Glu	Leu	Cys	Glu	Ala	Leu	Asp	Ile	Pro	Met	Ser	Met	Leu	Pro	Glu	Ile	
				215					220					225		
cgt	ccc	tcc	gtc	gga	gaa	ttc	cgc	tcc	gtg	cgc	cac	cgc	gga	acc	cta	835
Arg	Pro	Ser	Val	Gly	Glu	Phe	Arg	Ser	Val	Arg	His	Arg	Gly	Thr	Leu	
				230					235					240		

gcc gac gtc ccg att act ggc gtg ctc ggc gac cag caa gcg gcc ctt	883
Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp Gln Gln Ala Ala Leu	
250 255 260	
ttt ggt cag ggc gga ttc cac gaa ggt gct gct aaa aat acc tac ggc	931
Phe Gly Gln Gly Gly Phe His Glu Gly Ala Ala Lys Asn Thr Tyr Gly	
265 270 275	
acc ggc ctc ttc ctg ctg atg aac acc ggc acc tcg ttg aag att tcc	979
Thr Gly Leu Phe Leu Leu Met Asn Thr Gly Thr Ser Leu Lys Ile Ser	
280 285 290	
gag cac ggc ctg ctg tcc acc atc gcc tat caa cgg gaa gga tcc gct	1027
Glu His Gly Leu Leu Ser Thr Ile Ala Tyr Gln Arg Glu Gly Ser Ala	
295 300 305	
ccg gtc tac gcg ctg gaa ggt tcc gta tcc atg ggc ggt tcc ttg gtg	1075
Pro Val Tyr Ala Leu Glu Gly Ser Val Ser Met Gly Gly Ser Leu Val	
310 315 320 325	
cag tgg ctg cgc gac aac cta cag cta atc ccc aac gca cca gcg att	1123
Gln Trp Leu Arg Asp Asn Leu Gln Leu Ile Pro Asn Ala Pro Ala Ile	
330 335 340	
gaa aac ctc gcc cga gaa gtc gaa gac aac ggt ggc gtt cat gtt gtc	1171
Glu Asn Leu Ala Arg Glu Val Glu Asp Asn Gly Gly Val His Val Val	
345 350 355	
cca gca ttc acc gga ctg ttc gca cca cgt tgg cgc ccc gat gct cgt	1219
Pro Ala Phe Thr Gly Leu Phe Ala Pro Arg Trp Arg Pro Asp Ala Arg	
360 365 370	
ggc gtc att aca ggc ctc acc cgt ttt gcc aac cgc aaa cac atc gcc	1267
Gly Val Ile Thr Gly Leu Thr Arg Phe Ala Asn Arg Lys His Ile Ala	
375 380 385	
cgc gca gtc ctt gaa gcc aac gcc ttc caa acc cgc gaa gtt gtg gac	1315
Arg Ala Val Leu Glu Ala Asn Ala Phe Gln Thr Arg Glu Val Val Asp	
390 395 400 405	
gcc atg gcc aaa gac gca ggc aaa gcc ctc gaa tcc ctc cgc gtc gac	1363
Ala Met Ala Lys Asp Ala Gly Lys Ala Leu Glu Ser Leu Arg Val Asp	
410 415 420	
ggt gcg atg gtg gaa aat gac ctc ctc atg caa atg caa gcc gac ttc	1411
Gly Ala Met Val Glu Asn Asp Leu Leu Met Gln Met Gln Ala Asp Phe	
425 430 435	
ctc ggc atc gac gtc caa cgt ctc gag gac gta gaa acc acc gcc gtc	1459
Leu Gly Ile Asp Val Gln Arg Leu Glu Asp Val Glu Thr Thr Ala Val	
440 445 450	
ggc gtc gca ttc gct gca ggt ctc ggc tct gga ttc ttc aaa aca act	1507
Gly Val Ala Phe Ala Ala Gly Leu Gly Ser Gly Phe Phe Lys Thr Thr	
455 460 465	
gac gag atc gaa aaa ctt att gca gtg aag aaa gtc tgg aac cct gac	1555
Asp Glu Ile Glu Lys Leu Ile Ala Val Lys Lys Val Trp Asn Pro Asp	
470 475 480 485	

atg agc gaa gaa gag cgc gaa cgt cgc tat gcc gaa tgg aat agg gca 1603
 Met Ser Glu Glu Glu Arg Glu Arg Arg Tyr Ala Glu Trp Asn Arg Ala
 490 495 500

gtg gag cat tct tat gac cag gcc tagctgattt gggtcggcct tta 1650
 Val Glu His Ser Tyr Asp Gln Ala
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<210> 186

<211> 509

<212> PRT

<213> Corynebacterium glutamicum

<400> 186

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 20 25 30

Ser Ser Ala Ser Lys Glu His Arg Gln Ile Phe Pro Gln Gln Gly Trp
 35 40 45

Val Glu His Asp Pro Glu Glu Ile Trp Asp Asn Ile Arg Ser Val Val
 50 55 60

Ser Gln Ala Met Val Ser Ile Asp Ile Thr Pro His Glu Val Ala Ser
 65 70 75 80

Leu Gly Val Thr Asn Gln Arg Glu Thr Thr Val Val Trp Asp Lys His
 85 90 95

Thr Gly Glu Pro Val Tyr Asn Ala Ile Val Trp Gln Asp Thr Arg Thr
 100 105 110

Ser Asp Ile Cys Leu Glu Ile Ala Gly Glu Glu Gly Gln Glu Lys Trp
 115 120 125

Leu Asp Arg Thr Gly Leu Leu Ile Asn Ser Tyr Pro Ser Gly Pro Lys
 130 135 140

Ile Lys Trp Ile Leu Asp Asn Val Glu Gly Ala Arg Glu Arg Ala Glu
 145 150 155 160

Lys Gly Asp Leu Leu Phe Gly Thr Met Asp Thr Trp Val Leu Trp Asn
 165 170 175

Leu Thr Gly Gly Val Arg Gly Asp Asp Gly Asp Asp Ala Ile His Val
 180 185 190

Thr Asp Val Thr Asn Ala Ser Arg Thr Leu Leu Met Asp Leu Arg Thr
 195 200 205

Gln Gln Trp Asp Pro Glu Leu Cys Glu Ala Leu Asp Ile Pro Met Ser
 210 215 220

Met Leu Pro Glu Ile Arg Pro Ser Val Gly Glu Phe Arg Ser Val Arg
 225 230 235 240

His Arg Gly Thr Leu Ala Asp Val Pro Ile Thr Gly Val Leu Gly Asp

245										250					255				
Gln	Gln	Ala	Ala	Leu	Phe	Gly	Gln	Gly	Gly	Phe	His	Glu	Gly	Ala	Ala				
			260					265					270						
Lys	Asn	Thr	Tyr	Gly	Thr	Gly	Leu	Phe	Leu	Leu	Met	Asn	Thr	Gly	Thr				
		275					280					285							
Ser	Leu	Lys	Ile	Ser	Glu	His	Gly	Leu	Leu	Ser	Thr	Ile	Ala	Tyr	Gln				
	290					295					300								
Arg	Glu	Gly	Ser	Ala	Pro	Val	Tyr	Ala	Leu	Glu	Gly	Ser	Val	Ser	Met				
305					310					315					320				
Gly	Gly	Ser	Leu	Val	Gln	Trp	Leu	Arg	Asp	Asn	Leu	Gln	Leu	Ile	Pro				
				325					330					335					
Asn	Ala	Pro	Ala	Ile	Glu	Asn	Leu	Ala	Arg	Glu	Val	Glu	Asp	Asn	Gly				
			340					345					350						
Gly	Val	His	Val	Val	Pro	Ala	Phe	Thr	Gly	Leu	Phe	Ala	Pro	Arg	Trp				
		355					360					365							
Arg	Pro	Asp	Ala	Arg	Gly	Val	Ile	Thr	Gly	Leu	Thr	Arg	Phe	Ala	Asn				
	370					375					380								
Arg	Lys	His	Ile	Ala	Arg	Ala	Val	Leu	Glu	Ala	Asn	Ala	Phe	Gln	Thr				
385					390					395					400				
Arg	Glu	Val	Val	Asp	Ala	Met	Ala	Lys	Asp	Ala	Gly	Lys	Ala	Leu	Glu				
				405					410					415					
Ser	Leu	Arg	Val	Asp	Gly	Ala	Met	Val	Glu	Asn	Asp	Leu	Leu	Met	Gln				
			420					425					430						
Met	Gln	Ala	Asp	Phe	Leu	Gly	Ile	Asp	Val	Gln	Arg	Leu	Glu	Asp	Val				
		435					440					445							
Glu	Thr	Thr	Ala	Val	Gly	Val	Ala	Phe	Ala	Ala	Gly	Leu	Gly	Ser	Gly				
	450					455					460								
Phe	Phe	Lys	Thr	Thr	Asp	Glu	Ile	Glu	Lys	Leu	Ile	Ala	Val	Lys	Lys				
465					470					475					480				
Val	Trp	Asn	Pro	Asp	Met	Ser	Glu	Glu	Glu	Arg	Glu	Arg	Arg	Tyr	Ala				
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Glu	Trp	Asn	Arg	Ala	Val	Glu	His	Ser	Tyr	Asp	Gln	Ala							
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<210> 187

<211> 1119

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1096)

<223> RXN01025

<400> 187

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ctgagacggt taaatatcgt ttctgaaagg tgggtttcgc gtg gtt tct gta agc 115
Val Val Ser Val Ser
1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca 211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala
25 30 35

agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att 259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile
40 45 50

acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta 307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu
55 60 65

gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt 355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg
70 75 80 85

ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg 403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu
90 95 100

gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg cgg atg agt 451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser
105 110 115

gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg 499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val
120 125 130

ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca 547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala
135 140 145

gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag 595
Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln
150 155 160 165

gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg 643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val
170 175 180

gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc 691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala
185 190 195

tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg 739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser
200 205 210

ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg 787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu

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ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg			835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu			
230	235	240	245
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag			883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu			
	250	255	260
cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat			931
Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn			
	265	270	275
ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt			979
Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu			
	280	285	290
gcc acc aag ctt ggt gtg gag atg ccg atc acc cag gct gtc tac ggt			1027
Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln Ala Val Tyr Gly			
	295	300	305
gtg tgc cac cga gat atg aaa gta act gac atg att gtg gct ctc atg			1075
Val Cys His Arg Asp Met Lys Val Thr Asp Met Ile Val Ala Leu Met			
310	315	320	325
ggc agg tct aag aag gct gag tagtcttagg ttgtaagctt caa			1119
Gly Arg Ser Lys Lys Ala Glu			
	330		

<210> 188

<211> 332

<212> PRT

<213> Corynebacterium glutamicum

<400> 188

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	20 25 30
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	35 40 45
Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser	
	50 55 60
Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro	
	65 70 75 80
Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro	
	85 90 95
Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr	
	100 105 110
His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro	
	115 120 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140
 Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160
 Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175
 Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190
 Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205
 Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220
 Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala
 225 230 235 240
 Gly Met Gly Asp Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn
 245 250 255
 Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala
 260 265 270
 Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln
 275 280 285
 Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr
 290 295 300
 Gln Ala Val Tyr Gly Val Cys His Arg Asp Met Lys Val Thr Asp Met
 305 310 315 320
 Ile Val Ala Leu Met Gly Arg Ser Lys Lys Ala Glu
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<210> 189

<211> 1015

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1015)

<223> FRXA01025

<400> 189

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 Val Val Ser Val Ser
 1 5

gtg atg ggt gca ggt tcc tgg gga acc acg ttg gcc aag gtc ttc tct 163
 Val Met Gly Ala Gly Ser Trp Gly Thr Thr Leu Ala Lys Val Phe Ser
 10 15 20

gat gct ggc aac gct gtg acg ttg tgg gcg agg cgg gaa gag ttg gca	211
Asp Ala Gly Asn Ala Val Thr Leu Trp Ala Arg Arg Glu Glu Leu Ala	
25 30 35	
agc acc atc cgt gac agc cat gaa aac cgt gat tac ctt ccg ggg att	259
Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp Tyr Leu Pro Gly Ile	
40 45 50	
acg ttg ccg gag tcg ctg cag gtc aca tca tcg gca acg gag gct tta	307
Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser Ala Thr Glu Ala Leu	
55 60 65	
gag ggc gca gcc att gtg gtg ttg gcg att cct tcg cag gcg ttg cgt	355
Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro Ser Gln Ala Leu Arg	
70 75 80 85	
ggc aat ttg gcg gag tgg aaa gag acg atc ccg cag gat gcg acc ttg	403
Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro Gln Asp Ala Thr Leu	
90 95 100	
gtg tcc ttg gct aaa ggt att gaa aag ggc acg cac ctg ccg atg agt	451
Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr His Leu Arg Met Ser	
105 110 115	
gaa gtg atc gcg gag gtg acg gaa gcg gat cct tca cgc atc gcg gtg	499
Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro Ser Arg Ile Ala Val	
120 125 130	
ttg tcg ggg cca aac ctt gct cgt gag atc gcg gag ggg cag cct gca	547
Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala Glu Gly Gln Pro Ala	
135 140 145	
gct acg gtg att gct tgc cct gat gaa aac cga gcg aaa ctt gtg cag	595
Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg Ala Lys Leu Val Gln	
150 155 160 165	
gct gca gtg gct gcg ccg tat ttc cgc ccg tac acc aac act gat gtg	643
Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr Thr Asn Thr Asp Val	
170 175 180	
gtg ggc act gaa atc ggt ggt gcg tgt aag aac gtc atc gcg ctg gcc	691
Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn Val Ile Ala Leu Ala	
185 190 195	
tgt ggt att tcc cat ggt tac ggc ctg ggt gag aac acc aat gca tcg	739
Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu Asn Thr Asn Ala Ser	
200 205 210	
ttg att act cgt ggc ctt gca gag atc gca cgc ctc ggt gcc aca ttg	787
Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg Leu Gly Ala Thr Leu	
215 220 225	
ggt gcg gat gcg aag act ttt tct ggc ctt gcg gga atg ggc gac ttg	835
Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala Gly Met Gly Asp Leu	
230 235 240 245	
gtg gct acg tgt tca tca ccg ctg tcg cgt aac cgc agc ttc ggt gag	883
Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn Arg Ser Phe Gly Glu	
250 255 260	
cgt ttg ggt cag ggt gaa tcc cta gag aag gct cgc gag gca acc aat	931

Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala Arg Glu Ala Thr Asn
 265 270 275

ggt cag gtt gcg gag ggt gtt att tcc tcg cag tcg att ttt gat ctt 979
 Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln Ser Ile Phe Asp Leu
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 Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr Gln
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<213> Corynebacterium glutamicum

<400> 190

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 20 25 30

Arg Glu Glu Leu Ala Ser Thr Ile Arg Asp Ser His Glu Asn Arg Asp
 35 40 45

Tyr Leu Pro Gly Ile Thr Leu Pro Glu Ser Leu Gln Val Thr Ser Ser
 50 55 60

Ala Thr Glu Ala Leu Glu Gly Ala Ala Ile Val Val Leu Ala Ile Pro
 65 70 75 80

Ser Gln Ala Leu Arg Gly Asn Leu Ala Glu Trp Lys Glu Thr Ile Pro
 85 90 95

Gln Asp Ala Thr Leu Val Ser Leu Ala Lys Gly Ile Glu Lys Gly Thr
 100 105 110

His Leu Arg Met Ser Glu Val Ile Ala Glu Val Thr Glu Ala Asp Pro
 115 120 125

Ser Arg Ile Ala Val Leu Ser Gly Pro Asn Leu Ala Arg Glu Ile Ala
 130 135 140

Glu Gly Gln Pro Ala Ala Thr Val Ile Ala Cys Pro Asp Glu Asn Arg
 145 150 155 160

Ala Lys Leu Val Gln Ala Ala Val Ala Ala Pro Tyr Phe Arg Pro Tyr
 165 170 175

Thr Asn Thr Asp Val Val Gly Thr Glu Ile Gly Gly Ala Cys Lys Asn
 180 185 190

Val Ile Ala Leu Ala Cys Gly Ile Ser His Gly Tyr Gly Leu Gly Glu
 195 200 205

Asn Thr Asn Ala Ser Leu Ile Thr Arg Gly Leu Ala Glu Ile Ala Arg
 210 215 220

Leu Gly Ala Thr Leu Gly Ala Asp Ala Lys Thr Phe Ser Gly Leu Ala

225		230		235		240
Gly Met Gly Asp	Leu Val Ala Thr Cys Ser Ser Pro Leu Ser Arg Asn					
	245		250		255	
Arg Ser Phe Gly Glu Arg Leu Gly Gln Gly Glu Ser Leu Glu Lys Ala						
	260		265		270	
Arg Glu Ala Thr Asn Gly Gln Val Ala Glu Gly Val Ile Ser Ser Gln						
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Ser Ile Phe Asp Leu Ala Thr Lys Leu Gly Val Glu Met Pro Ile Thr						
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Gln
305

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 <222> (101)..(1786)
 <223> RXA01851

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 Met Thr Ser Ala His
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ttt gaa tcc cgc cgg att ggc cct ccg ctt cgc gat aat tat gac gtc 163
 Phe Glu Ser Arg Arg Ile Gly Pro Pro Leu Arg Asp Asn Tyr Asp Val
 10 15 20

att gtg att ggc ggt ggt atc tca ggt gta cag att gcg cga cat gct 211
 Ile Val Ile Gly Gly Gly Ile Ser Gly Val Gln Ile Ala Arg His Ala
 25 30 35

caa ggc cgc ggt tta cgc act gtg atg ttt gag gcc aga gat tat tct 259
 Gln Gly Arg Gly Leu Arg Thr Val Met Phe Glu Ala Arg Asp Tyr Ser
 40 45 50

tct gga aca tca tcg aca acc tcc aag atg att cat ggt ggt ttg cgc 307
 Ser Gly Thr Ser Ser Thr Thr Ser Lys Met Ile His Gly Gly Leu Arg
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tat ttg gag cag tac gat ttc ggc gtg gtc cag gaa gcc gtg aag gaa 355
 Tyr Leu Glu Gln Tyr Asp Phe Gly Val Val Gln Glu Ala Val Lys Glu
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cgc cgg tac cta ggt atc gcc gct ccg cat ttg gtg gct cca cgc agt 403
 Arg Arg Tyr Leu Gly Ile Ala Ala Pro His Leu Val Ala Pro Arg Ser
 90 95 100

ttc atg ctc acg gcg ttt gat tgg tca gag ccg aaa gcc cct atg ttg 451
 Phe Met Leu Thr Ala Phe Asp Trp Ser Glu Pro Lys Ala Pro Met Leu

105							110					115					
ggt	gct	ggt	gtg	gcg	ttg	tat	gaa	acg	atg	gcg	tgg	cag	cgt	aac	cag		499
Gly	Ala	Gly	Val	Ala	Leu	Tyr	Glu	Thr	Met	Ala	Trp	Gln	Arg	Asn	Gln		
		120						125					130				
ggg	caa	tcg	aag	gaa	aac	cac	tcg	ccg	cgt	ttc	cgg	tgg	att	cct	aaa		547
Gly	Gln	Ser	Lys	Glu	Asn	His	Ser	Pro	Arg	Phe	Arg	Trp	Ile	Pro	Lys		
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aat	gca	ctg	ctc	aag	gaa	gtc	ccg	tgg	ctt	gac	ccg	gag	ggc	ttg	aag		595
Asn	Ala	Leu	Leu	Lys	Glu	Val	Pro	Trp	Leu	Asp	Pro	Glu	Gly	Leu	Lys		
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Gly	Ala	Trp	Arg	His	Asp	Asp	Thr	Leu	Asn	Leu	His	Ala	Glu	Arg	Leu		
				170					175						180		
ctc	ctc	gcg	gtg	att	aaa	gct	ttt	gcg	gca	gat	ggc	gga	acg	gcg	atc		691
Leu	Leu	Ala	Val	Ile	Lys	Ala	Phe	Ala	Ala	Asp	Gly	Gly	Thr	Ala	Ile		
			185					190					195				
aac	cac	gcc	aaa	gtc	act	cgc	att	ctc	cgg	aac	gtg	gaa	gaa	ggc	cgc		739
Asn	His	Ala	Lys	Val	Thr	Arg	Ile	Leu	Arg	Asn	Val	Glu	Glu	Gly	Arg		
		200					205					210					
gtc	aag	ggt	gta	gaa	gtg	act	gat	cag	gtc	acc	aac	acc	acg	cat	gag		787
Val	Lys	Gly	Val	Glu	Val	Thr	Asp	Gln	Val	Thr	Asn	Thr	Thr	His	Glu		
	215					220					225						
gtg	aat	gcc	cct	gtg	gtg	atc	aac	gct	gcg	ggt	ccg	tgg	gtt	gcg	cag		835
Val	Asn	Ala	Pro	Val	Val	Ile	Asn	Ala	Ala	Gly	Pro	Trp	Val	Ala	Gln		
230					235					240					245		
gcg	ttg	ggt	gat	ttg	gcg	gag	gta	acc	aag	ttg	aag	gtg	cgc	caa	tcc		883
Ala	Leu	Gly	Asp	Leu	Ala	Glu	Val	Thr	Lys	Leu	Lys	Val	Arg	Gln	Ser		
				250					255					260			
aag	gga	gtg	cat	ttg	ctc	act	ggt	gat	ttg	ggc	agc	cag	agt	ggc	gtg		931
Lys	Gly	Val	His	Leu	Leu	Thr	Gly	Asp	Leu	Gly	Ser	Gln	Ser	Gly	Val		
			265					270				275					
ttt	gtg	cgt	ggc	aaa	aac	ggc	aag	cat	gtg	atc	gtg	aat	ccg	tgg	atg		979
Phe	Val	Arg	Gly	Lys	Asn	Gly	Lys	His	Val	Ile	Val	Asn	Pro	Trp	Met		
		280					285					290					
ggg	cgc	acc	ctt	att	ggt	cca	acc	gac	acc	atg	att	gac	ggt	gac	gct		1027
Gly	Arg	Thr	Leu	Ile	Gly	Pro	Thr	Asp	Thr	Met	Ile	Asp	Gly	Asp	Ala		
		295				300					305						
gat	gat	gcg	gct	gca	gat	gaa	agc	gat	atc	gat	ttg	ctg	ctt	gag	acc		1075
Asp	Asp	Ala	Ala	Ala	Asp	Glu	Ser	Asp	Ile	Asp	Leu	Leu	Leu	Glu	Thr		
310					315					320					325		
atc	gat	tcg	gta	cgc	gct	aca	ccg	ctt	gat	cgc	aaa	gag	atc	atc	tcc		1123
Ile	Asp	Ser	Val	Arg	Ala	Thr	Pro	Leu	Asp	Arg	Lys	Glu	Ile	Ile	Ser		
				330					335					340			
acg	ctg	gtg	ggt	gtg	cgc	ccg	ctt	gtt	gat	gac	ggc	acc	gac	acc	tac		1171
Thr	Leu	Val	Gly	Val	Arg	Pro	Leu	Val	Asp	Asp	Gly	Thr	Asp	Thr	Tyr		
			345					350					355				

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acg tcc tct cgc cgt ttc gat att tcc gat cac gcc aac gtc ggc att 1219
Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His Ala Asn Val Gly Ile
360 365 370

gat ggt ttg gtg tct gtc tct ggc ggc aag tgg acc act tcc cgc gtg 1267
Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp Thr Thr Ser Arg Val
375 380 385

atg ggg tac aag gtg att gag cat gtg gtg gag cac caa gct gcg gtg 1315
Met Gly Tyr Lys Val Ile Glu His Val Val Glu His Gln Ala Ala Val
390 395 400 405

tta cct ccg ctg cgc cac ttt gac tcc agg cag atg ccg ttg agt act 1363
Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln Met Pro Leu Ser Thr
410 415 420

tct ttt ggc gcg tat gag tcc gtg gct gat tcc ttt gag tca gcg ctt 1411
Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser Phe Glu Ser Ala Leu
425 430 435

cgc agc cac ccc gag ctg gat gtg gat gat gaa atc cgc gtg cat ctg 1459
Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu Ile Arg Val His Leu
440 445 450

gcc aga ctg tat gga act gag cat gaa aaa gtg ctg gat ctc gtc gca 1507
Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val Leu Asp Leu Val Ala
455 460 465

aag caa ccc gac ctg ggg cgc cga ctt gac cca gac aac ctt gat atc 1555
Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro Asp Asn Leu Asp Ile
470 475 480 485

gcg gcg cag gcc gtt ttt gct gtc gcc gag gag gcg gcc gtc gac ctg 1603
Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu Ala Ala Val Asp Leu
490 495 500

gcg gac gtg ctg gat cgt cgc atc gtg ctc ggc acg ctg ggt tat gtg 1651
Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly Thr Leu Gly Tyr Val
505 510 515

caa ccg gct gcc gtg cgt gcg acg gcc gaa gca atg gcg cag gtc acc 1699
Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala Met Ala Gln Val Thr
520 525 530

ggg tgg tca gct gag ctt atc gac gcc cag tgc cag tcc tac ctc gcc 1747
Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys Gln Ser Tyr Leu Ala
535 540 545

aag caa gac aaa atc caa gcc gtg tta aag ccg tac cgc taacactccg 1796
Lys Gln Asp Lys Ile Gln Ala Val Leu Lys Pro Tyr Arg
550 555 560

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<211> 562

<212> PRT

<213> Corynebacterium glutamicum

<400> 192

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Ile	Ala	Arg	His	Ala	Gln	Gly	Arg	Gly	Leu	Arg	Thr	Val	Met	Phe	Glu	35	40	45	
Ala	Arg	Asp	Tyr	Ser	Ser	Gly	Thr	Ser	Ser	Thr	Thr	Ser	Lys	Met	Ile	50	55	60	
His	Gly	Gly	Leu	Arg	Tyr	Leu	Glu	Gln	Tyr	Asp	Phe	Gly	Val	Val	Gln	65	70	75	80
Glu	Ala	Val	Lys	Glu	Arg	Arg	Tyr	Leu	Gly	Ile	Ala	Ala	Pro	His	Leu	85	90	95	
Val	Ala	Pro	Arg	Ser	Phe	Met	Leu	Thr	Ala	Phe	Asp	Trp	Ser	Glu	Pro	100	105	110	
Lys	Ala	Pro	Met	Leu	Gly	Ala	Gly	Val	Ala	Leu	Tyr	Glu	Thr	Met	Ala	115	120	125	
Trp	Gln	Arg	Asn	Gln	Gly	Gln	Ser	Lys	Glu	Asn	His	Ser	Pro	Arg	Phe	130	135	140	
Arg	Trp	Ile	Pro	Lys	Asn	Ala	Leu	Leu	Lys	Glu	Val	Pro	Trp	Leu	Asp	145	150	155	160
Pro	Glu	Gly	Leu	Lys	Gly	Ala	Trp	Arg	His	Asp	Asp	Thr	Leu	Asn	Leu	165	170	175	
His	Ala	Glu	Arg	Leu	Leu	Leu	Ala	Val	Ile	Lys	Ala	Phe	Ala	Ala	Asp	180	185	190	
Gly	Gly	Thr	Ala	Ile	Asn	His	Ala	Lys	Val	Thr	Arg	Ile	Leu	Arg	Asn	195	200	205	
Val	Glu	Glu	Gly	Arg	Val	Lys	Gly	Val	Glu	Val	Thr	Asp	Gln	Val	Thr	210	215	220	
Asn	Thr	Thr	His	Glu	Val	Asn	Ala	Pro	Val	Val	Ile	Asn	Ala	Ala	Gly	225	230	235	240
Pro	Trp	Val	Ala	Gln	Ala	Leu	Gly	Asp	Leu	Ala	Glu	Val	Thr	Lys	Leu	245	250	255	
Lys	Val	Arg	Gln	Ser	Lys	Gly	Val	His	Leu	Leu	Thr	Gly	Asp	Leu	Gly	260	265	270	
Ser	Gln	Ser	Gly	Val	Phe	Val	Arg	Gly	Lys	Asn	Gly	Lys	His	Val	Ile	275	280	285	
Val	Asn	Pro	Trp	Met	Gly	Arg	Thr	Leu	Ile	Gly	Pro	Thr	Asp	Thr	Met	290	295	300	
Ile	Asp	Gly	Asp	Ala	Asp	Asp	Ala	Ala	Ala	Asp	Glu	Ser	Asp	Ile	Asp	305	310	315	320

Leu Leu Leu Glu Thr Ile Asp Ser Val Arg Ala Thr Pro Leu Asp Arg
 325 330 335
 Lys Glu Ile Ile Ser Thr Leu Val Gly Val Arg Pro Leu Val Asp Asp
 340 345 350
 Gly Thr Asp Thr Tyr Thr Ser Ser Arg Arg Phe Asp Ile Ser Asp His
 355 360 365
 Ala Asn Val Gly Ile Asp Gly Leu Val Ser Val Ser Gly Gly Lys Trp
 370 375 380
 Thr Thr Ser Arg Val Met Gly Tyr Lys Val Ile Glu His Val Val Glu
 385 390 395 400
 His Gln Ala Ala Val Leu Pro Pro Leu Arg His Phe Asp Ser Arg Gln
 405 410 415
 Met Pro Leu Ser Thr Ser Phe Gly Ala Tyr Glu Ser Val Ala Asp Ser
 420 425 430
 Phe Glu Ser Ala Leu Arg Ser His Pro Glu Leu Asp Val Asp Asp Glu
 435 440 445
 Ile Arg Val His Leu Ala Arg Leu Tyr Gly Thr Glu His Glu Lys Val
 450 455 460
 Leu Asp Leu Val Ala Lys Gln Pro Asp Leu Gly Arg Arg Leu Asp Pro
 465 470 475 480
 Asp Asn Leu Asp Ile Ala Ala Gln Ala Val Phe Ala Val Ala Glu Glu
 485 490 495
 Ala Ala Val Asp Leu Ala Asp Val Leu Asp Arg Arg Ile Val Leu Gly
 500 505 510
 Thr Leu Gly Tyr Val Gln Pro Ala Ala Val Arg Ala Thr Ala Glu Ala
 515 520 525
 Met Ala Gln Val Thr Gly Trp Ser Ala Glu Leu Ile Asp Ala Gln Cys
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<211> 900

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<223> RXA01242

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	Met Tyr Ala Glu Glu	
	1 5	
cgc cgt cga cag att gcc tca tta acg gca gtt gag gga cgt gta aat	163	
Arg Arg Arg Gln Ile Ala Ser Leu Thr Ala Val Glu Gly Arg Val Asn		
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gtc aca gaa tta gcg ggc cga ttc gat gtc act gca gag acg att cga	211	
Val Thr Glu Leu Ala Gly Arg Phe Asp Val Thr Ala Glu Thr Ile Arg		
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cga gac ctt gcg gtg cta gac cgc gag gga att gtt cac cgc gtt cac	259	
Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile Val His Arg Val His		
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ggt ggc gca gta gcc acc caa tct ttc caa acc aca gag ttg agc ttg	307	
Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr Thr Glu Leu Ser Leu		
	55 60 65	
gat act cgt ttc agg tct gca tcg tca gca aag tac tcc att gcc aag	355	
Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys Tyr Ser Ile Ala Lys		
	70 75 80 85	
gca gcg atg cag ttc ctg ccc gct gag cat ggc gga ctg ttc ctc gat	403	
Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly Gly Leu Phe Leu Asp		
	90 95 100	
gcg gga act act gtt act gct ttg gcc gat ctc att tct gag cat cct	451	
Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu Ile Ser Glu His Pro		
	105 110 115	
agc tcc aag cag tgg tcg atc gtg acc aac tgc ctc ccc atc gca ctt	499	
Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys Leu Pro Ile Ala Leu		
	120 125 130	
aat ctg gcc aac gcc ggg ctt gat gat gtc cag ctg ctt gga gga agc	547	
Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln Leu Leu Gly Gly Ser		
	135 140 145	
gtt cgc gcg atc acc cag gct gtt gtg ggt gac act gcg ctt cgt act	595	
Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp Thr Ala Leu Arg Thr		
	150 155 160 165	
ctc gcg ctg atg cgt gcg gat gta gtg ttc atc ggc acc aac gcg ttg	643	
Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile Gly Thr Asn Ala Leu		
	170 175 180	
acg ttg gat cac gga ttg tct acg gcc gat tcc caa gag gct gcc atg	691	
Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser Gln Glu Ala Ala Met		
	185 190 195	
aaa tct gcg atg atc acc aac gcc cac aag gtg gtg gtg ttg tgt gac	739	
Lys Ser Ala Met Ile Thr Asn Ala His Lys Val Val Val Leu Cys Asp		
	200 205 210	
tcc acc aag atg ggc acc gac tac ctc gtg agc ttt ggc gca atc agc	787	
Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser Phe Gly Ala Ile Ser		
	215 220 225	

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 Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala Pro Ala Ser Phe Val
 230 235 240 245

gag cag ttg cga gaa cgc gat gta gaa gtt gtg att gca gaa 877
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<211> 259

<212> PRT

<213> Corynebacterium glutamicum

<400> 194

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 20 25 30

Ala Glu Thr Ile Arg Arg Asp Leu Ala Val Leu Asp Arg Glu Gly Ile
 35 40 45

Val His Arg Val His Gly Gly Ala Val Ala Thr Gln Ser Phe Gln Thr
 50 55 60

Thr Glu Leu Ser Leu Asp Thr Arg Phe Arg Ser Ala Ser Ser Ala Lys
 65 70 75 80

Tyr Ser Ile Ala Lys Ala Ala Met Gln Phe Leu Pro Ala Glu His Gly
 85 90 95

Gly Leu Phe Leu Asp Ala Gly Thr Thr Val Thr Ala Leu Ala Asp Leu
 100 105 110

Ile Ser Glu His Pro Ser Ser Lys Gln Trp Ser Ile Val Thr Asn Cys
 115 120 125

Leu Pro Ile Ala Leu Asn Leu Ala Asn Ala Gly Leu Asp Asp Val Gln
 130 135 140

Leu Leu Gly Gly Ser Val Arg Ala Ile Thr Gln Ala Val Val Gly Asp
 145 150 155 160

Thr Ala Leu Arg Thr Leu Ala Leu Met Arg Ala Asp Val Val Phe Ile
 165 170 175

Gly Thr Asn Ala Leu Thr Leu Asp His Gly Leu Ser Thr Ala Asp Ser
 180 185 190

Gln Glu Ala Ala Met Lys Ser Ala Met Ile Thr Asn Ala His Lys Val
 195 200 205

Val Val Leu Cys Asp Ser Thr Lys Met Gly Thr Asp Tyr Leu Val Ser
 210 215 220

Phe Gly Ala Ile Ser Asp Ile Asp Val Val Val Thr Asp Ala Gly Ala
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Pro Ala Ser Phe Val Glu Gln Leu Arg Glu Arg Asp Val Glu Val Val
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Ile Ala Glu

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<211> 969

<212> DNA

<213> Corynebacterium glutamicum

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<223> RXA02288

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 Met Ser Gln Val Ile
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ccc gcc agc tca caa gaa aag cgt cgt gag cgc atc gtt tct tat gtc 163
 Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg Ile Val Ser Tyr Val
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acc cgt cat gga ttc gct cgt gtt gaa gca tta gct gag ctt ttt gag 211
 Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu Ala Glu Leu Phe Glu
 25 30 35

gtc agc gca atg acc att cac cgt gat ttg gag gcg ctg gct gca gac 259
 Val Ser Ala Met Thr Ile His Arg Asp Leu Glu Ala Leu Ala Ala Asp
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aat ttg gtg gag cgc att agg ggt ggc gcg cgt tcg gtg tcg ccg tcg 307
 Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg Ser Val Ser Pro Ser
 55 60 65

atg agt gag ttg gca gtg gag cag cgt cgg cat ttg cat cgc act gtt 355
 Met Ser Glu Leu Ala Val Glu Gln Arg Arg His Leu His Arg Thr Val
 70 75 80 85

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 Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu Ile Pro Glu Gly Ala
 90 95 100

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 Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu Ser Leu Val Glu Lys
 105 110 115

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 Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr His Ser Leu Lys Thr
 120 125 130

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 Met Ala Asp His Arg Val Arg Ala Gly Met Ser Asp Ile Arg Leu Ile
 135 140 145

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 Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp Ser Phe Leu Gly Lys
 150 155 160 165

 gca act tca gcg cag ttg aat gag ctg tcg gcg gat att tct ttt gtt 643
 Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala Asp Ile Ser Phe Val
 170 175 180

 tct acg act gcg gtg cgc gct acg ggg gag gtt ccg gcg ctg ttt cat 691
 Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val Pro Ala Leu Phe His
 185 190 195

 cct gat atg gag gct gct gat acg aag cgg gcg ttg att ggg att ggt 739
 Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala Leu Ile Gly Ile Gly
 200 205 210

 agc gtg cgt gtg ttg gtg gtg gat tct agt aaa ttt ggt tcg gct ggt 787
 Ser Val Arg Val Leu Val Val Asp Ser Ser Lys Phe Gly Ser Ala Gly
 215 220 225

 gtg ttc aag gtt gct tcg att gag gag ttt gac cac atc atc att gat 835
 Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp His Ile Ile Ile Asp
 230 235 240 245

 cag cag tgc acc cgt gag cag cgg gat ctt ttg cgt aat tcg cgc gcg 883
 Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu Arg Asn Ser Arg Ala
 250 255 260

 cag atc cat gtg att gac cac aat ggt gat gaa att ttg gat acc cca 931
 Gln Ile His Val Ile Asp His Asn Gly Asp Glu Ile Leu Asp Thr Pro
 265 270 275

 acg gaa gag gat ttt taagatggct ttggttcttg gaa 969
 Thr Glu Asp Phe
 280

<210> 196

<211> 282

<212> PRT

<213> Corynebacterium glutamicum

<400> 196

Met Ser Gln Val Ile Pro Ala Ser Ser Gln Glu Lys Arg Arg Glu Arg
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 Ile Val Ser Tyr Val Thr Arg His Gly Phe Ala Arg Val Glu Ala Leu
 20 25 30

 Ala Glu Leu Phe Glu Val Ser Ala Met Thr Ile His Arg Asp Leu Glu
 35 40 45

 Ala Leu Ala Ala Asp Asn Leu Val Glu Arg Ile Arg Gly Gly Ala Arg
 50 55 60

 Ser Val Ser Pro Ser Met Ser Glu Leu Ala Val Glu Gln Arg Arg His
 65 70 75 80

 Leu His Arg Thr Val Lys Glu Ala Leu Cys Thr Ala Ala Ala Arg Leu
 85 90 95

Ile Pro Glu Gly Ala Val Val Ala Ile Asp Asp Ser Thr Thr Leu Glu
 100 105 110
 Ser Leu Val Glu Lys Leu Pro Gln Arg Ser Pro Ser Ala Leu Ile Thr
 115 120 125
 His Ser Leu Lys Thr Met Ala Asp His Arg Val Arg Ala Gly Met Ser
 130 135 140
 Asp Ile Arg Leu Ile Ala Cys Ala Gly Leu Tyr Phe Ala Glu Thr Asp
 145 150 155 160
 Ser Phe Leu Gly Lys Ala Thr Ser Ala Gln Leu Asn Glu Leu Ser Ala
 165 170 175
 Asp Ile Ser Phe Val Ser Thr Thr Ala Val Arg Ala Thr Gly Glu Val
 180 185 190
 Pro Ala Leu Phe His Pro Asp Met Glu Ala Ala Asp Thr Lys Arg Ala
 195 200 205
 Leu Ile Gly Ile Gly Ser Val Arg Val Leu Val Val Asp Ser Ser Lys
 210 215 220
 Phe Gly Ser Ala Gly Val Phe Lys Val Ala Ser Ile Glu Glu Phe Asp
 225 230 235 240
 His Ile Ile Ile Asp Gln Gln Cys Thr Arg Glu Gln Arg Asp Leu Leu
 245 250 255
 Arg Asn Ser Arg Ala Gln Ile His Val Ile Asp His Asn Gly Asp Glu
 260 265 270
 Ile Leu Asp Thr Pro Thr Glu Glu Asp Phe
 275 280

<210> 197
 <211> 887
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(864)
 <223> RXN01891

<400> 197
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 Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
 1 5 10 15
 tac aac aag gat ctg tgg gct aag gct ggc ctg gaa gat cgt ggc cca 96
 Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
 20 25 30
 gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa gcg 144
 Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
 35 40 45
 atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac ctt 192

Met	Asp	Ser	Gly	Phe	Ala	His	Gly	Trp	Gly	Asp	Ala	Thr	Asn	Tyr	Leu	
50						55					60					
tct	tgg	act	ttc	gaa	ggc	cca	atg	tgg	tcc	ctc	ggc	ggc	aac	tac	tct	240
Ser	Trp	Thr	Phe	Glu	Gly	Pro	Met	Trp	Ser	Leu	Gly	Gly	Asn	Tyr	Ser	80
65					70					75						
gaa	ggg	tgg	gag	tcc	cgt	ctg	act	acc	cca	gag	acc	atc	cgt	gca	gtt	288
Glu	Gly	Trp	Glu	Ser	Arg	Leu	Thr	Thr	Pro	Glu	Thr	Ile	Arg	Ala	Val	
				85					90					95		
gag	tgg	ctc	aag	tcc	acc	gtt	gat	gaa	ggg	ttc	gca	acc	gtc	tcc	acc	336
Glu	Trp	Leu	Lys	Ser	Thr	Val	Asp	Glu	Gly	Phe	Ala	Thr	Val	Ser	Thr	
			100				105						110			
gac	gtc	acc	aac	gag	ttc	gca	acc	ggc	ctg	atc	ggg	tca	tgc	atc	cag	384
Asp	Val	Thr	Asn	Glu	Phe	Ala	Thr	Gly	Leu	Ile	Gly	Ser	Cys	Ile	Gln	
		115					120					125				
tcc	acc	ggg	gat	ctg	tct	tcg	gtt	gcc	ggc	gct	gca	agc	ttc	gac	tgg	432
Ser	Thr	Gly	Asp	Leu	Ser	Ser	Val	Ala	Gly	Ala	Ala	Ser	Phe	Asp	Trp	
			130			135					140					
ggc	gta	gca	gca	ctt	cct	aac	cca	acc	ggc	gag	ggc	gct	tgc	cca	acc	480
Gly	Val	Ala	Ala	Leu	Pro	Asn	Pro	Thr	Gly	Glu	Gly	Ala	Cys	Pro	Thr	
145					150					155					160	
ggg	ggc	gca	ggc	ctg	gga	atc	cca	tct	ggc	atc	tct	gag	cag	cgt	cag	528
Gly	Gly	Ala	Gly	Leu	Gly	Ile	Pro	Ser	Gly	Ile	Ser	Glu	Gln	Arg	Gln	
				165					170					175		
gac	aac	gcc	ctg	aag	ttc	atc	gac	ttc	ctc	acc	aac	gcc	gcg	aac	act	576
Asp	Asn	Ala	Leu	Lys	Phe	Ile	Asp	Phe	Leu	Thr	Asn	Ala	Ala	Asn	Thr	
			180					185				190				
ggc	tac	tgg	tcc	cgc	gag	acc	ggg	tat	gtt	cca	gtt	cgt	aag	gat	gct	624
Gly	Tyr	Trp	Ser	Arg	Glu	Thr	Gly	Tyr	Val	Pro	Val	Arg	Lys	Asp	Ala	
		195					200					205				
gca	tct	gat	cca	gat	cac	gca	gca	ttc	ctc	gag	gag	aac	cct	gca	tac	672
Ala	Ser	Asp	Pro	Asp	His	Ala	Ala	Phe	Leu	Glu	Glu	Asn	Pro	Ala	Tyr	
	210					215				220						
aac	gtt	gca	gtg	gag	cag	ctt	cct	gat	acc	cgt	tcc	cag	gac	aac	ttc	720
Asn	Val	Ala	Val	Glu	Gln	Leu	Pro	Asp	Thr	Arg	Ser	Gln	Asp	Asn	Phe	
225					230					235					240	
cgc	gtg	ctg	ctg	cca	aac	ggg	gac	cgc	acc	atc	ggg	gac	gca	ctg	gag	768
Arg	Val	Leu	Leu	Pro	Asn	Gly	Asp	Arg	Thr	Ile	Gly	Asp	Ala	Leu	Glu	
				245					250					255		
aag	atc	tgc	ctg	act	ggg	gca	gac	atc	gat	gtc	acc	ctg	gct	gag	gtt	816
Lys	Ile	Cys	Leu	Thr	Gly	Ala	Asp	Ile	Asp	Val	Thr	Leu	Ala	Glu	Val	
			260					265				270				
gag	acc	aag	ctg	aac	acc	atc	tac	acc	cgc	gac	atc	gaa	cca	ctt	att	864
Glu	Thr	Lys	Leu	Asn	Thr	Ile	Tyr	Thr	Arg	Asp	Ile	Glu	Pro	Leu	Ile	
		275					280					285				
taatccgaqc acttcaqcta cac																887

<210> 198

<211> 288

<212> PRT

<213> Corynebacterium glutamicum

<400> 198

Gly Gly His Tyr Gly Leu Pro Phe Ala Arg Ser Thr Val Leu Phe Tyr
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Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly Pro
 20 25 30

Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu Ala
 35 40 45

Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr Leu
 50 55 60

Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr Ser
 65 70 75 80

Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala Val
 85 90 95

Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser Thr
 100 105 110

Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile Gln
 115 120 125

Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp Trp
 130 135 140

Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro Thr
 145 150 155 160

Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg Gln
 165 170 175

Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn Thr
 180 185 190

Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp Ala
 195 200 205

Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala Tyr
 210 215 220

Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn Phe
 225 230 235 240

Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu Glu
 245 250 255

Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu Val
 260 265 270

Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu Ile
 275 280 285

<210> 199
 <211> 842
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(819)
 <223> FRXA01891

<400> 199
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 Tyr Tyr Asn Lys Asp Leu Trp Ala Lys Ala Gly Leu Glu Asp Arg Gly
 1 5 10 15
 cca gag tca tgg gaa gag ttc tcc gag tgg ggt cca aag ctg cag gaa 96
 Pro Glu Ser Trp Glu Glu Phe Ser Glu Trp Gly Pro Lys Leu Gln Glu
 20 25 30
 gcg atg gac agt ggt ttc gca cac ggt tgg gga gat gca acc aac tac 144
 Ala Met Asp Ser Gly Phe Ala His Gly Trp Gly Asp Ala Thr Asn Tyr
 35 40 45
 ctt tct tgg act ttc gaa ggc cca atg tgg tcc ctc ggc ggc aac tac 192
 Leu Ser Trp Thr Phe Glu Gly Pro Met Trp Ser Leu Gly Gly Asn Tyr
 50 55 60
 tct gaa ggt tgg gag tcc cgt ctg act acc cca gag acc atc cgt gca 240
 Ser Glu Gly Trp Glu Ser Arg Leu Thr Thr Pro Glu Thr Ile Arg Ala
 65 70 75 80
 gtt gag tgg ctc aag tcc acc gtt gat gaa ggt ttc gca acc gtc tcc 288
 Val Glu Trp Leu Lys Ser Thr Val Asp Glu Gly Phe Ala Thr Val Ser
 85 90 95
 acc gac gtc acc aac gag ttc gca acc ggc ctg atc ggt tca tgc atc 336
 Thr Asp Val Thr Asn Glu Phe Ala Thr Gly Leu Ile Gly Ser Cys Ile
 100 105 110
 cag tcc acc ggt gat ctg tct tcc gtt gcc ggc gct gca agc ttc gac 384
 Gln Ser Thr Gly Asp Leu Ser Ser Val Ala Gly Ala Ala Ser Phe Asp
 115 120 125
 tgg ggc gta gca gca ctt cct aac cca acc ggc gag ggc gct tgc cca 432
 Trp Gly Val Ala Ala Leu Pro Asn Pro Thr Gly Glu Gly Ala Cys Pro
 130 135 140
 acc ggt ggc gca ggc ctg gga atc cca tct ggc atc tct gag cag cgt 480
 Thr Gly Gly Ala Gly Leu Gly Ile Pro Ser Gly Ile Ser Glu Gln Arg
 145 150 155 160
 cag gac aac gcc ctg aag ttc atc gac ttc ctc acc aac gcc gcg aac 528
 Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn
 165 170 175
 act ggc tac tgg tcc cgc gag acc ggt tat gtt cca gtt cgt aag gat 576
 Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp

180										185					190					
gct	gca	tct	gat	cca	gat	cac	gca	gca	ttc	ctc	gag	gag	aac	cct	gca	624				
Ala	Ala	Ser	Asp	Pro	Asp	His	Ala	Ala	Phe	Leu	Glu	Glu	Asn	Pro	Ala					
		195					200						205							
tac	aac	gtt	gca	gtg	gag	cag	ctt	cct	gat	acc	cgt	tcc	cag	gac	aac	672				
Tyr	Asn	Val	Ala	Val	Glu	Gln	Leu	Pro	Asp	Thr	Arg	Ser	Gln	Asp	Asn					
	210					215					220									
ttc	cgc	gtg	ctg	ctg	cca	aac	ggc	gac	cgc	acc	atc	ggc	gac	gca	ctg	720				
Phe	Arg	Val	Leu	Leu	Pro	Asn	Gly	Asp	Arg	Thr	Ile	Gly	Asp	Ala	Leu					
225					230				235						240					
gag	aag	atc	tgc	ctg	act	ggc	gca	gac	atc	gat	gtc	acc	ctg	gct	gag	768				
Glu	Lys	Ile	Cys	Leu	Thr	Gly	Ala	Asp	Ile	Asp	Val	Thr	Leu	Ala	Glu					
				245					250					255						
gtt	gag	acc	aag	ctg	aac	acc	atc	tac	acc	cgc	gac	atc	gaa	cca	ctt	816				
Val	Glu	Thr	Lys	Leu	Asn	Thr	Ile	Tyr	Thr	Arg	Asp	Ile	Glu	Pro	Leu					
			260					265					270							
att	taatccgagc	acttcagcta	cac													842				
Ile																				

<210> 200

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 200

Tyr	Tyr	Asn	Lys	Asp	Leu	Trp	Ala	Lys	Ala	Gly	Leu	Glu	Asp	Arg	Gly
1				5					10					15	

Pro	Glu	Ser	Trp	Glu	Glu	Phe	Ser	Glu	Trp	Gly	Pro	Lys	Leu	Gln	Glu
			20					25					30		

Ala	Met	Asp	Ser	Gly	Phe	Ala	His	Gly	Trp	Gly	Asp	Ala	Thr	Asn	Tyr
		35					40					45			

Leu	Ser	Trp	Thr	Phe	Glu	Gly	Pro	Met	Trp	Ser	Leu	Gly	Gly	Asn	Tyr
	50					55					60				

Ser	Glu	Gly	Trp	Glu	Ser	Arg	Leu	Thr	Thr	Pro	Glu	Thr	Ile	Arg	Ala
65					70					75					80

Val	Glu	Trp	Leu	Lys	Ser	Thr	Val	Asp	Glu	Gly	Phe	Ala	Thr	Val	Ser
				85					90					95	

Thr	Asp	Val	Thr	Asn	Glu	Phe	Ala	Thr	Gly	Leu	Ile	Gly	Ser	Cys	Ile
		100						105					110		

Gln	Ser	Thr	Gly	Asp	Leu	Ser	Ser	Val	Ala	Gly	Ala	Ala	Ser	Phe	Asp
		115					120					125			

Trp	Gly	Val	Ala	Ala	Leu	Pro	Asn	Pro	Thr	Gly	Glu	Gly	Ala	Cys	Pro
	130					135					140				

Thr	Gly	Gly	Ala	Gly	Leu	Gly	Ile	Pro	Ser	Gly	Ile	Ser	Glu	Gln	Arg
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145		150		155		160
Gln Asp Asn Ala Leu Lys Phe Ile Asp Phe Leu Thr Asn Ala Ala Asn						
		165		170		175
Thr Gly Tyr Trp Ser Arg Glu Thr Gly Tyr Val Pro Val Arg Lys Asp						
		180		185		190
Ala Ala Ser Asp Pro Asp His Ala Ala Phe Leu Glu Glu Asn Pro Ala						
		195		200		205
Tyr Asn Val Ala Val Glu Gln Leu Pro Asp Thr Arg Ser Gln Asp Asn						
		210		215		220
Phe Arg Val Leu Leu Pro Asn Gly Asp Arg Thr Ile Gly Asp Ala Leu						
		225		230		240
Glu Lys Ile Cys Leu Thr Gly Ala Asp Ile Asp Val Thr Leu Ala Glu						
		245		250		255
Val Glu Thr Lys Leu Asn Thr Ile Tyr Thr Arg Asp Ile Glu Pro Leu						
		260		265		270

Ile

<210> 201

<211> 776

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (7)..(753)

<223> RXA02414

<400> 201

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Met	Ser	Tyr	Asn	Ser	Pro	Tyr	Asn	Asn	Thr	Asn	Phe	Ser	Thr	Thr
1				5					10				15	

ggc gcg ttc caa cct gct ggt ggg ccg gtg aag ccg tgg aat aag ccc 99

Gly	Ala	Phe	Gln	Pro	Ala	Gly	Gly	Pro	Val	Lys	Pro	Trp	Asn	Lys	Pro
			20					25					30		

gat gcc agc ctg aat cag cag ctg aaa aac aaa tcc cgt gtg cgc aca 147

Asp	Ala	Ser	Leu	Asn	Gln	Gln	Leu	Lys	Asn	Lys	Ser	Arg	Val	Arg	Thr
			35				40					45			

ggt ctt acc atc gcc atc ggt tat gta gtg gtg att tgg gcg gtg cat 195

Gly	Leu	Thr	Ile	Ala	Ile	Gly	Tyr	Val	Val	Val	Ile	Trp	Ala	Val	His
		50				55					60				

ttg gca tcc atc gtc att gcg ctg ctc act ggc ttc aac ctg acc aac 243

Leu	Ala	Ser	Ile	Val	Ile	Ala	Leu	Leu	Thr	Gly	Phe	Asn	Leu	Thr	Asn
	65					70				75					

ttt ggt att cat ccg ctg gat acc agt gca ctg tgg ggt att ttc acc 291

Phe	Gly	Ile	His	Pro	Leu	Asp	Thr	Ser	Ala	Leu	Trp	Gly	Ile	Phe	Thr
	80				85					90				95	

tca ccg ctg ttg cat gga agc ttc agc cac ctc att gga aat acc gtt 339
 Ser Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val
 100 105 110

cca ggc ttt ata ttc agt ttc ctc atc ggt atg agt ggc aag cgc gtg 387
 Pro Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val
 115 120 125

ttc tgg gaa gtc acg att atc gca ggt ctc atc ggc ggt ctt ggt aca 435
 Phe Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr
 130 135 140

tgg att ttc ggt gga atc ggc acc aac cac atc ggt gcg tcc ggc ctg 483
 Trp Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu
 145 150 155

att tat ggc tgg ctt ggc tac ctg atc gtg cgt gga att ttc aac aag 531
 Ile Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys
 160 165 170 175

gat att aaa cag ttc ctg ctt ggc ata gtt ttg gcg ttc att tac tcc 579
 Asp Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser
 180 185 190

ggt ttg ttc tgg ggt ctg cta cct act caa atc ggt gtg tcc tgg cag 627
 Gly Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln
 195 200 205

ggc cac ctt ttc ggt gca ctt ggt gga atc ggt gcg ggt gct ttt atc 675
 Gly His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile
 210 215 220

gcc tcg gat gac ccg gca gcg ttg aaa gcg aag aag caa cag aag aaa 723
 Ala Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys
 225 230 235

tta gaa aag caa caa cgc caa aga ggc tta tagttttcac ctagecgacta 773
 Leu Glu Lys Gln Gln Arg Gln Arg Gly Leu
 240 245

cac 776

<210> 202

<211> 249

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 202

Met Ser Tyr Asn Ser Pro Tyr Asn Asn Thr Asn Phe Ser Thr Thr Gly
 1 5 10 15

Ala Phe Gln Pro Ala Gly Gly Pro Val Lys Pro Trp Asn Lys Pro Asp
 20 25 30

Ala Ser Leu Asn Gln Gln Leu Lys Asn Lys Ser Arg Val Arg Thr Gly
 35 40 45

Leu Thr Ile Ala Ile Gly Tyr Val Val Val Ile Trp Ala Val His Leu
 50 55 60

Ala Ser Ile Val Ile Ala Leu Leu Thr Gly Phe Asn Leu Thr Asn Phe
65 70 75 80

Gly Ile His Pro Leu Asp Thr Ser Ala Leu Trp Gly Ile Phe Thr Ser
85 90 95

Pro Leu Leu His Gly Ser Phe Ser His Leu Ile Gly Asn Thr Val Pro
100 105 110

Gly Phe Ile Phe Ser Phe Leu Ile Gly Met Ser Gly Lys Arg Val Phe
115 120 125

Trp Glu Val Thr Ile Ile Ala Gly Leu Ile Gly Gly Leu Gly Thr Trp
130 135 140

Ile Phe Gly Gly Ile Gly Thr Asn His Ile Gly Ala Ser Gly Leu Ile
145 150 155 160

Tyr Gly Trp Leu Gly Tyr Leu Ile Val Arg Gly Ile Phe Asn Lys Asp
165 170 175

Ile Lys Gln Phe Leu Leu Gly Ile Val Leu Ala Phe Ile Tyr Ser Gly
180 185 190

Leu Phe Trp Gly Leu Leu Pro Thr Gln Ile Gly Val Ser Trp Gln Gly
195 200 205

His Leu Phe Gly Ala Leu Gly Gly Ile Gly Ala Gly Ala Phe Ile Ala
210 215 220

Ser Asp Asp Pro Ala Ala Leu Lys Ala Lys Lys Gln Gln Lys Lys Leu
225 230 235 240

Glu Lys Gln Gln Arg Gln Arg Gly Leu
245

<210> 203

<211> 840

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(817)

<223> RXN01580

<400> 203

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tcaactttgc tccctatcct taaaaagccc acagaaaagg atg tat aag aat atg 115
Met Tyr Lys Asn Met
1 5

cac att gtt gcc cat cgc ggt gcg gaa gat ctg cac ctc gaa aac acc 163
His Ile Val Ala His Arg Gly Ala Glu Asp Leu His Leu Glu Asn Thr
10 15 20

atg acc gct ttc cag gct gcc gcg ccc gct gac gct ttt gag ctg gat 211
Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp Ala Phe Glu Leu Asp

25										30					35					
atc	cac	gcc	acc	gct	gac	aat	cag	gtc	gtc	gtt	atc	cac	gac	cgc	acc	259				
Ile	His	Ala	Thr	Ala	Asp	Asn	Gln	Val	Val	Val	Ile	His	Asp	Arg	Thr					
40				45				50												
gca	gcg	cgt	gtt	gcc	gcg	cca	gat	tcc	ctg	cac	cgc	gac	acc	ccg	gtt	307				
Ala	Ala	Arg	Val	Ala	Ala	Pro	Asp	Ser	Leu	His	Arg	Asp	Thr	Pro	Val					
55				60				65												
gcg	cgc	tta	agc	gcc	gcg	caa	atc	aag	gag	ata	acg	ctt	atc	gac	gga	355				
Ala	Arg	Leu	Ser	Ala	Ala	Gln	Ile	Lys	Glu	Ile	Thr	Leu	Ile	Asp	Gly					
70				75				80				85								
tcc	ccc	gta	cca	acc	ctg	gag	gaa	gtt	cta	ctc	cag	acg	agc	ctg	ccg	403				
Ser	Pro	Val	Pro	Thr	Leu	Glu	Glu	Val	Leu	Leu	Gln	Thr	Ser	Leu	Pro					
90				95				100												
atc	caa	gtg	gaa	atc	aaa	tct	gcc	ggt	gca	gtt	cca	gca	gcc	gca	gca	451				
Ile	Gln	Val	Glu	Ile	Lys	Ser	Ala	Gly	Ala	Val	Pro	Ala	Ala	Ala	Ala					
105				110				115												
tta	ttg	cag	aaa	tac	cca	gag	cac	ctg	gag	cgc	ctg	ctg	ttc	atc	agt	499				
Leu	Leu	Gln	Lys	Tyr	Pro	Glu	His	Leu	Glu	Arg	Leu	Leu	Phe	Ile	Ser					
120				125				130												
ttc	atc	gat	gca	gca	ctg	gtg	gaa	atc	gtg	gat	cga	ctg	cca	gaa	gct	547				
Phe	Ile	Asp	Ala	Ala	Leu	Val	Glu	Ile	Val	Asp	Arg	Leu	Pro	Glu	Ala					
135				140				145												
cgc	gtg	gga	atc	ttg	cgc	gat	gcg	tcc	atg	gat	gat	ctg	cgc	att	ctt	595				
Arg	Val	Gly	Ile	Leu	Arg	Asp	Ala	Ser	Met	Asp	Asp	Leu	Arg	Ile	Leu					
150				155				160				165								
gat	tac	atc	ccg	cta	aaa	aat	gtg	ggc	gcg	atc	ttg	ccc	tcg	tgg	aaa	643				
Asp	Tyr	Ile	Pro	Leu	Lys	Asn	Val	Gly	Ala	Ile	Leu	Pro	Ser	Trp	Lys					
170				175				180												
gca	cta	aac	gtg	gcg	tca	att	gct	gat	cta	cat	acc	aag	gga	atc	aag	691				
Ala	Leu	Asn	Val	Ala	Ser	Ile	Ala	Asp	Leu	His	Thr	Lys	Gly	Ile	Lys					
185				190				195												
gtt	ggc	tgc	tgg	aca	att	cgg	gat	gaa	aat	gcg	ttt	ggg	atc	gca	caa	739				
Val	Gly	Cys	Trp	Thr	Ile	Arg	Asp	Glu	Asn	Ala	Phe	Gly	Ile	Ala	Gln					
200				205				210												
caa	gct	ggc	gtt	gat	tac	gcc	act	gtt	agc	gat	ccc	tct	cgt	ttc	ctc	787				
Gln	Ala	Gly	Val	Asp	Tyr	Ala	Thr	Val	Ser	Asp	Pro	Ser	Arg	Phe	Leu					
215				220				225												
gcg	ccc	tcc	cct	gct	ggg	gag	ttg	cac	tgg	taaataatct	agtgaccaga				837					
Ala	Pro	Ser	Pro	Ala	Gly	Glu	Leu	His	Trp											
230				235																
ctg															840					

<210> 204

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 204

Met Tyr Lys Asn Met His Ile Val Ala His Arg Gly Ala Glu Asp Leu
 1 5 10 15

His Leu Glu Asn Thr Met Thr Ala Phe Gln Ala Ala Ala Pro Ala Asp
 20 25 30

Ala Phe Glu Leu Asp Ile His Ala Thr Ala Asp Asn Gln Val Val Val
 35 40 45

Ile His Asp Arg Thr Ala Ala Arg Val Ala Ala Pro Asp Ser Leu His
 50 55 60

Arg Asp Thr Pro Val Ala Arg Leu Ser Ala Ala Gln Ile Lys Glu Ile
 65 70 75 80

Thr Leu Ile Asp Gly Ser Pro Val Pro Thr Leu Glu Glu Val Leu Leu
 85 90 95

Gln Thr Ser Leu Pro Ile Gln Val Glu Ile Lys Ser Ala Gly Ala Val
 100 105 110

Pro Ala Ala Ala Ala Leu Leu Gln Lys Tyr Pro Glu His Leu Glu Arg
 115 120 125

Leu Leu Phe Ile Ser Phe Ile Asp Ala Ala Leu Val Glu Ile Val Asp
 130 135 140

Arg Leu Pro Glu Ala Arg Val Gly Ile Leu Arg Asp Ala Ser Met Asp
 145 150 155 160

Asp Leu Arg Ile Leu Asp Tyr Ile Pro Leu Lys Asn Val Gly Ala Ile
 165 170 175

Leu Pro Ser Trp Lys Ala Leu Asn Val Ala Ser Ile Ala Asp Leu His
 180 185 190

Thr Lys Gly Ile Lys Val Gly Cys Trp Thr Ile Arg Asp Glu Asn Ala
 195 200 205

Phe Gly Ile Ala Gln Gln Ala Gly Val Asp Tyr Ala Thr Val Ser Asp
 210 215 220

Pro Ser Arg Phe Leu Ala Pro Ser Pro Ala Gly Glu Leu His Trp
 225 230 235

<210> 205

<211> 1314

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1291)

<223> RXA01436

<400> 205

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cagtagccat cacagcaatt caggcaggag gacgcagcta	atg gca ttg gca ctt	115
	Met Ala Leu Ala Leu	
	1 5	
ggt ttg aac tcc ggt tca tct tcc atc aaa ttc cag ctg gtc aac ccc	163	
Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe Gln Leu Val Asn Pro		
10 15 20		
gaa aac tct gcc atc gac gag cca tat gtt tct ggt ctt gtg gag cag	211	
Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser Gly Leu Val Glu Gln		
25 30 35		
att ggt gag cca aac ggc cgc atc gta ctc aaa ata gag ggt gaa aaa	259	
Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys Ile Glu Gly Glu Lys		
40 45 50		
tat acc cta gag aca ccc atc gca gat cac tcc gaa ggc cta aac ctg	307	
Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser Glu Gly Leu Asn Leu		
55 60 65		
gcg ttc gat ctc atg gac cag cac aac tgt ggt cct tcc caa ctg gaa	355	
Ala Phe Asp Leu Met Asp Gln His Asn Cys Gly Pro Ser Gln Leu Glu		
70 75 80 85		
atc acc gca gtt gga cac cgc gtg gtc cac ggc gga atc ttg ttc tcc	403	
Ile Thr Ala Val Gly His Arg Val Val His Gly Gly Ile Leu Phe Ser		
90 95 100		
gca ccg gaa ctt atc act gat gaa atc gtg gaa atg atc cgc gat ctc	451	
Ala Pro Glu Leu Ile Thr Asp Glu Ile Val Glu Met Ile Arg Asp Leu		
105 110 115		
att cca ctc gca cca ctg cac aac cct gca aac gtt gac ggc att gat	499	
Ile Pro Leu Ala Pro Leu His Asn Pro Ala Asn Val Asp Gly Ile Asp		
120 125 130		
ggt gct cga aaa att ctc ccc gat gtc cca cac gta gct gtc ttt gac	547	
Val Ala Arg Lys Ile Leu Pro Asp Val Pro His Val Ala Val Phe Asp		
135 140 145		
acc ggt ttc ttc cac tca ctt cca cca gca gct gcg ctg tat gcc atc	595	
Thr Gly Phe Phe His Ser Leu Pro Pro Ala Ala Leu Tyr Ala Ile		
150 155 160 165		
aac aag gat gtc gca gct gaa cac gga atc agg cgc tat ggt ttc cac	643	
Asn Lys Asp Val Ala Ala Glu His Gly Ile Arg Arg Tyr Gly Phe His		
170 175 180		
ggc acc tcc cat gaa ttt gtg tcc aag cgc gtg gtg gaa att ctg gaa	691	
Gly Thr Ser His Glu Phe Val Ser Lys Arg Val Val Glu Ile Leu Glu		
185 190 195		
aag ccc acc gaa gac atc aac acc atc acc ttc cac ctg ggc aac ggc	739	
Lys Pro Thr Glu Asp Ile Asn Thr Ile Thr Phe His Leu Gly Asn Gly		
200 205 210		
gca tcc atg gct gct gtt caa ggt ggc cgt gcg gta gat act tcc atg	787	
Ala Ser Met Ala Ala Val Gln Gly Gly Arg Ala Val Asp Thr Ser Met		
215 220 225		
ggt atg aca cct ctc gcg ggc ctt gtc atg ggt acc cga agc ggt gac	835	

Gly Met Thr Pro Leu Ala Gly Leu Val Met Gly Thr Arg Ser Gly Asp
 230 235 240 245
 att gat cca ggt atc gtc ttc cac ctt tcc cgc acc gct ggc atg agc 883
 Ile Asp Pro Gly Ile Val Phe His Leu Ser Arg Thr Ala Gly Met Ser
 250 255 260
 atc gat gag atc gat aat ctg ctg aac aaa aag tcg ggt gta aag gga 931
 Ile Asp Glu Ile Asp Asn Leu Leu Asn Lys Lys Ser Gly Val Lys Gly
 265 270 275
 ctt tcc ggt gtt aat gat ttc cgt gaa ctg cgg gaa atg atc gac aac 979
 Leu Ser Gly Val Asn Asp Phe Arg Glu Leu Arg Glu Met Ile Asp Asn
 280 285 290
 aat gat caa gat gcc tgg tcc gcg tac aac att tac ata cac caa ctc 1027
 Asn Asp Gln Asp Ala Trp Ser Ala Tyr Asn Ile Tyr Ile His Gln Leu
 295 300 305
 cgc cgc tac ctc ggt tcc tac atg gtg gca ctg gga cgg gta gac acc 1075
 Arg Arg Tyr Leu Gly Ser Tyr Met Val Ala Leu Gly Arg Val Asp Thr
 310 315 320 325
 atc gtg ttc acc gcc ggt gtc ggt gaa aat gcc cag ttt gtc cgt gag 1123
 Ile Val Phe Thr Ala Gly Val Gly Glu Asn Ala Gln Phe Val Arg Glu
 330 335 340
 gat gcc ttg gca ggt ttg gaa atg tac gga att gag atc gat cca gag 1171
 Asp Ala Leu Ala Gly Leu Glu Met Tyr Gly Ile Glu Ile Asp Pro Glu
 345 350 355
 cgt aac gca ttg cca aac gat ggt cct cga ttg att tcc acc gat gcc 1219
 Arg Asn Ala Leu Pro Asn Asp Gly Pro Arg Leu Ile Ser Thr Asp Ala
 360 365 370
 tcc aag gtg aag gtg ttt gtt att cca act aat gaa gag tta gct atc 1267
 Ser Lys Val Lys Val Phe Val Ile Pro Thr Asn Glu Glu Leu Ala Ile
 375 380 385
 gct agg tac gcg gtg aag ttc gct tagctctcct ggtaggatac cac 1314
 Ala Arg Tyr Ala Val Lys Phe Ala
 390 395

<210> 206

<211> 397

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 206

Met Ala Leu Ala Leu Val Leu Asn Ser Gly Ser Ser Ser Ile Lys Phe
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 Gln Leu Val Asn Pro Glu Asn Ser Ala Ile Asp Glu Pro Tyr Val Ser
 20 25 30
 Gly Leu Val Glu Gln Ile Gly Glu Pro Asn Gly Arg Ile Val Leu Lys
 35 40 45
 Ile Glu Gly Glu Lys Tyr Thr Leu Glu Thr Pro Ile Ala Asp His Ser
 50 55 60

Glu	Gly	Leu	Asn	Leu	Ala	Phe	Asp	Leu	Met	Asp	Gln	His	Asn	Cys	Gly	65	70	75	80
Pro	Ser	Gln	Leu	Glu	Ile	Thr	Ala	Val	Gly	His	Arg	Val	Val	His	Gly	85	90	95	
Gly	Ile	Leu	Phe	Ser	Ala	Pro	Glu	Leu	Ile	Thr	Asp	Glu	Ile	Val	Glu	100	105	110	
Met	Ile	Arg	Asp	Leu	Ile	Pro	Leu	Ala	Pro	Leu	His	Asn	Pro	Ala	Asn	115	120	125	
Val	Asp	Gly	Ile	Asp	Val	Ala	Arg	Lys	Ile	Leu	Pro	Asp	Val	Pro	His	130	135	140	
Val	Ala	Val	Phe	Asp	Thr	Gly	Phe	Phe	His	Ser	Leu	Pro	Pro	Ala	Ala	145	150	155	160
Ala	Leu	Tyr	Ala	Ile	Asn	Lys	Asp	Val	Ala	Ala	Glu	His	Gly	Ile	Arg	165	170	175	
Arg	Tyr	Gly	Phe	His	Gly	Thr	Ser	His	Glu	Phe	Val	Ser	Lys	Arg	Val	180	185	190	
Val	Glu	Ile	Leu	Glu	Lys	Pro	Thr	Glu	Asp	Ile	Asn	Thr	Ile	Thr	Phe	195	200	205	
His	Leu	Gly	Asn	Gly	Ala	Ser	Met	Ala	Ala	Val	Gln	Gly	Gly	Arg	Ala	210	215	220	
Val	Asp	Thr	Ser	Met	Gly	Met	Thr	Pro	Leu	Ala	Gly	Leu	Val	Met	Gly	225	230	235	240
Thr	Arg	Ser	Gly	Asp	Ile	Asp	Pro	Gly	Ile	Val	Phe	His	Leu	Ser	Arg	245	250	255	
Thr	Ala	Gly	Met	Ser	Ile	Asp	Glu	Ile	Asp	Asn	Leu	Leu	Asn	Lys	Lys	260	265	270	
Ser	Gly	Val	Lys	Gly	Leu	Ser	Gly	Val	Asn	Asp	Phe	Arg	Glu	Leu	Arg	275	280	285	
Glu	Met	Ile	Asp	Asn	Asn	Asp	Gln	Asp	Ala	Trp	Ser	Ala	Tyr	Asn	Ile	290	295	300	
Tyr	Ile	His	Gln	Leu	Arg	Arg	Tyr	Leu	Gly	Ser	Tyr	Met	Val	Ala	Leu	305	310	315	320
Gly	Arg	Val	Asp	Thr	Ile	Val	Phe	Thr	Ala	Gly	Val	Gly	Glu	Asn	Ala	325	330	335	
Gln	Phe	Val	Arg	Glu	Asp	Ala	Leu	Ala	Gly	Leu	Glu	Met	Tyr	Gly	Ile	340	345	350	
Glu	Ile	Asp	Pro	Glu	Arg	Asn	Ala	Leu	Pro	Asn	Asp	Gly	Pro	Arg	Leu	355	360	365	
Ile	Ser	Thr	Asp	Ala	Ser	Lys	Val	Lys	Val	Phe	Val	Ile	Pro	Thr	Asn	370	375	380	

Glu Glu Leu Ala Ile Ala Arg Tyr Ala Val Lys Phe Ala
 385 390 395

<210> 207

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(904)

<223> RXA00686

<400> 207

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ttcatcggag tgccagggga acttagagga gcattaaata atg gcg gga gga aat 115
 Met Ala Gly Gly Asn
 1 5

cgc gaa cct gga cgt aca gtc acc tcc aag gtg atc gcc gta ctg gga 163
 Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val Ile Ala Val Leu Gly
 10 15 20

gct ttt gaa cac acc atg cgt cca ctt ggt gtc act gaa atc gct gag 211
 Ala Phe Glu His Thr Met Arg Pro Leu Gly Val Thr Glu Ile Ala Glu
 25 30 35

ctg gca gac ctc cca cca agt acc acc cac cgt ctc gtt tct gaa tta 259
 Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg Leu Val Ser Glu Leu
 40 45 50

acc gaa ggc gga cta ctc agc aag aaa tct gat ggg cgc tac caa ttg 307
 Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp Gly Arg Tyr Gln Leu
 55 60 65

ggc tta cgt atc tgg gaa ctc gcc caa aat aca gga cgg cag tta cgc 355
 Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr Gly Arg Gln Leu Arg
 70 75 80 85

gac act gca cgc ccg ttc atc caa gag ctc tac tca ctt act tcc gag 403
 Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr Ser Leu Thr Ser Glu
 90 95 100

act gcg cag cta gtg gtc cgc gat aaa gat gaa gca ctt ttg att gac 451
 Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu Ala Leu Leu Ile Asp
 105 110 115

cga gcc tac ggc acg aag aaa att cca cgc tcg gct cga gtc ggt ggt 499
 Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser Ala Arg Val Gly Gly
 120 125 130

cga cta cct ctg aac tcc act gcg gtt ggc aag att ctc ctt gcg ttt 547
 Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys Ile Leu Leu Ala Phe
 135 140 145

gat gag cca tgg gta aaa cag tcc tat ctc aag ctg cca ctc aac gcc 595
 Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys Leu Pro Leu Asn Ala
 150 155 160 165

tcc acc cca aag aca att gtg aat ccc gac gtc ttg gct gcg cag ctg 643
 Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val Leu Ala Ala Gln Leu
 170 175 180

aaa caa att cac tcg caa ggc ttt gcc atc aca cat gac gag caa cga 691
 Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr His Asp Glu Gln Arg
 185 190 195

atc ggc ggc gca tcg atc gcc gta ccg gtc tgg cat aca gga aaa ctg 739
 Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp His Thr Gly Lys Leu
 200 205 210

gga gca gca ctg ggg ttg gtg gtt ccc acc gca cag gct gca aat ctt 787
 Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala Gln Ala Ala Asn Leu
 215 220 225

gag cgc tat ctc ccg atc ctt cag gcg aca agt cag aga att aca aaa 835
 Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser Gln Arg Ile Thr Lys
 230 235 240 245

gca acc gcg ctc att cct ttg gac aca ctt ttg gct tca cac aaa aat 883
 Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu Ala Ser His Lys Asn
 250 255 260

gca gaa cga aaa ggc gat acc taaacccgcc ctccatctgc ata 927
 Ala Glu Arg Lys Gly Asp Thr
 265

<210> 208

<211> 268

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 208

Met Ala Gly Gly Asn Arg Glu Pro Gly Arg Thr Val Thr Ser Lys Val
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Ile Ala Val Leu Gly Ala Phe Glu His Thr Met Arg Pro Leu Gly Val
 20 25 30

Thr Glu Ile Ala Glu Leu Ala Asp Leu Pro Pro Ser Thr Thr His Arg
 35 40 45

Leu Val Ser Glu Leu Thr Glu Gly Gly Leu Leu Ser Lys Lys Ser Asp
 50 55 60

Gly Arg Tyr Gln Leu Gly Leu Arg Ile Trp Glu Leu Ala Gln Asn Thr
 65 70 75 80

Gly Arg Gln Leu Arg Asp Thr Ala Arg Pro Phe Ile Gln Glu Leu Tyr
 85 90 95

Ser Leu Thr Ser Glu Thr Ala Gln Leu Val Val Arg Asp Lys Asp Glu
 100 105 110

Ala Leu Leu Ile Asp Arg Ala Tyr Gly Thr Lys Lys Ile Pro Arg Ser
 115 120 125

Ala Arg Val Gly Gly Arg Leu Pro Leu Asn Ser Thr Ala Val Gly Lys
 130 135 140

Ile Leu Leu Ala Phe Asp Glu Pro Trp Val Lys Gln Ser Tyr Leu Lys
145 150 155 160

Leu Pro Leu Asn Ala Ser Thr Pro Lys Thr Ile Val Asn Pro Asp Val
165 170 175

Leu Ala Ala Gln Leu Lys Gln Ile His Ser Gln Gly Phe Ala Ile Thr
180 185 190

His Asp Glu Gln Arg Ile Gly Gly Ala Ser Ile Ala Val Pro Val Trp
195 200 205

His Thr Gly Lys Leu Gly Ala Ala Leu Gly Leu Val Val Pro Thr Ala
210 215 220

Gln Ala Ala Asn Leu Glu Arg Tyr Leu Pro Ile Leu Gln Ala Thr Ser
225 230 235 240

Gln Arg Ile Thr Lys Ala Thr Ala Leu Ile Pro Leu Asp Thr Leu Leu
245 250 255

Ala Ser His Lys Asn Ala Glu Arg Lys Gly Asp Thr
260 265

<210> 209

<211> 1158

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1135)

<223> RXA00246

<400> 209

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gcaatttgcc aagtaatcca agcgagaagg agtgagtttt atg acc act gct gca 115
Met Thr Thr Ala Ala
1 5

ccc caa gaa ttt acc gct gct gtt gtt gaa aaa ttc ggt cat gac gtg 163
Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys Phe Gly His Asp Val
10 15 20

acc gtg aag gat att gac ctt cca aag cca ggg cca cac cag gca ttg 211
Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly Pro His Gln Ala Leu
25 30 35

gtg aag gta ctc acc tcc ggc atc tgc cac acc gac ctc cac gcc ttg 259
Val Lys Val Leu Thr Ser Gly Ile Cys His Thr Asp Leu His Ala Leu
40 45 50

gag ggc gat tgg cca gta aag ccg gaa cca cca ttc gta cca gga cac 307
Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro Phe Val Pro Gly His
55 60 65

gaa ggt gta ggt gaa gtt gtt gag ctc gga cca ggt gaa cac gat gtg 355
Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro Gly Glu His Asp Val

70				75				80				85				
aag	gtc	ggc	gat	att	gtc	ggc	aat	gcg	tgg	ctc	tgg	tca	gcg	tgt	ggc	403
Lys	Val	Gly	Asp	Ile	Val	Gly	Asn	Ala	Trp	Leu	Trp	Ser	Ala	Cys	Gly	
				90					95					100		
acc	tgc	gaa	tac	tgc	atc	acc	ggc	agg	gaa	act	cag	tgc	aac	gaa	gct	451
Thr	Cys	Glu	Tyr	Cys	Ile	Thr	Gly	Arg	Glu	Thr	Gln	Cys	Asn	Glu	Ala	
			105					110					115			
gag	tat	ggg	ggc	tac	acc	caa	aat	gga	tcc	ttc	ggc	cag	tac	atg	ctg	499
Glu	Tyr	Gly	Gly	Tyr	Thr	Gln	Asn	Gly	Ser	Phe	Gly	Gln	Tyr	Met	Leu	
		120					125					130				
gtg	gat	acc	cgt	tac	gcc	gct	cgc	atc	cca	gac	ggc	gtg	gac	tac	ctc	547
Val	Asp	Thr	Arg	Tyr	Ala	Ala	Arg	Ile	Pro	Asp	Gly	Val	Asp	Tyr	Leu	
	135					140					145					
gaa	gca	gca	cca	att	ctg	tgt	gca	ggc	gtg	act	gtc	tac	aag	gca	ctc	595
Glu	Ala	Ala	Pro	Ile	Leu	Cys	Ala	Gly	Val	Thr	Val	Tyr	Lys	Ala	Leu	
150					155					160					165	
aaa	gtc	tct	gaa	acc	cgc	ccg	ggc	caa	ttc	atg	gtg	atc	tcc	ggg	gtc	643
Lys	Val	Ser	Glu	Thr	Arg	Pro	Gly	Gln	Phe	Met	Val	Ile	Ser	Gly	Val	
				170					175					180		
ggc	gga	ctt	ggc	cac	atc	gca	gtc	caa	tac	gca	gcg	gcg	atg	ggc	atg	691
Gly	Gly	Leu	Gly	His	Ile	Ala	Val	Gln	Tyr	Ala	Ala	Ala	Met	Gly	Met	
		185						190					195			
cgt	gtc	att	gcg	gta	gat	att	gcc	gat	gac	aag	ctg	gaa	ctt	gcc	cgt	739
Arg	Val	Ile	Ala	Val	Asp	Ile	Ala	Asp	Asp	Lys	Leu	Glu	Leu	Ala	Arg	
		200					205					210				
aag	cac	ggg	gcg	gaa	ttt	acc	gtg	aat	gcg	cgt	aat	gaa	gat	tca	ggc	787
Lys	His	Gly	Ala	Glu	Phe	Thr	Val	Asn	Ala	Arg	Asn	Glu	Asp	Ser	Gly	
	215					220					225					
gaa	gct	gta	cag	aag	tac	acc	aac	ggg	ggc	gca	cac	ggc	gtg	ctt	gtg	835
Glu	Ala	Val	Gln	Lys	Tyr	Thr	Asn	Gly	Gly	Ala	His	Gly	Val	Leu	Val	
230					235					240					245	
act	gca	gtt	cac	gag	gca	gca	ttc	ggc	cag	gca	ctg	gat	atg	gct	cga	883
Thr	Ala	Val	His	Glu	Ala	Ala	Phe	Gly	Gln	Ala	Leu	Asp	Met	Ala	Arg	
				250					255					260		
cgt	gca	gga	aca	att	gtg	ttc	aac	ggg	ctg	cca	ccg	gga	gag	ttc	cca	931
Arg	Ala	Gly	Thr	Ile	Val	Phe	Asn	Gly	Leu	Pro	Pro	Gly	Glu	Phe	Pro	
			265					270					275			
gca	tcc	gtg	ttc	aac	atc	gta	ttc	aag	ggc	ctg	acc	atc	cgt	gga	tcc	979
Ala	Ser	Val	Phe	Asn	Ile	Val	Phe	Lys	Gly	Leu	Thr	Ile	Arg	Gly	Ser	
		280					285					290				
ctc	gtg	gga	acc	cgc	caa	gac	ttg	gcc	gaa	gcg	ctc	gat	ttc	ttt	gca	1027
Leu	Val	Gly	Thr	Arg	Gln	Asp	Leu	Ala	Glu	Ala	Leu	Asp	Phe	Phe	Ala	
	295					300					305					
cgc	gga	cta	atc	aag	cca	acc	gtg	agt	gag	tgc	tcc	ctc	gat	gag	gtc	1075
Arg	Gly	Leu	Ile	Lys	Pro	Thr	Val	Ser	Glu	Cys	Ser	Leu	Asp	Glu	Val	
310					315					320					325	

aat ggt gtg ctt gac cgc atg cga aac ggc aag atc gat ggt cgt gtg 1123
 Asn Gly Val Leu Asp Arg Met Arg Asn Gly Lys Ile Asp Gly Arg Val
 330 335 340

gcg att cgt ttc taacggattg tggtgaaact gct 1158
 Ala Ile Arg Phe
 345

<210> 210

<211> 345

<212> PRT

<213> Corynebacterium glutamicum

<400> 210

Met Thr Thr Ala Ala Pro Gln Glu Phe Thr Ala Ala Val Val Glu Lys
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Phe Gly His Asp Val Thr Val Lys Asp Ile Asp Leu Pro Lys Pro Gly
 20 25 30

Pro His Gln Ala Leu Val Lys Val Leu Thr Ser Gly Ile Cys His Thr
 35 40 45

Asp Leu His Ala Leu Glu Gly Asp Trp Pro Val Lys Pro Glu Pro Pro
 50 55 60

Phe Val Pro Gly His Glu Gly Val Gly Glu Val Val Glu Leu Gly Pro
 65 70 75 80

Gly Glu His Asp Val Lys Val Gly Asp Ile Val Gly Asn Ala Trp Leu
 85 90 95

Trp Ser Ala Cys Gly Thr Cys Glu Tyr Cys Ile Thr Gly Arg Glu Thr
 100 105 110

Gln Cys Asn Glu Ala Glu Tyr Gly Gly Tyr Thr Gln Asn Gly Ser Phe
 115 120 125

Gly Gln Tyr Met Leu Val Asp Thr Arg Tyr Ala Ala Arg Ile Pro Asp
 130 135 140

Gly Val Asp Tyr Leu Glu Ala Ala Pro Ile Leu Cys Ala Gly Val Thr
 145 150 155 160

Val Tyr Lys Ala Leu Lys Val Ser Glu Thr Arg Pro Gly Gln Phe Met
 165 170 175

Val Ile Ser Gly Val Gly Gly Leu Gly His Ile Ala Val Gln Tyr Ala
 180 185 190

Ala Ala Met Gly Met Arg Val Ile Ala Val Asp Ile Ala Asp Asp Lys
 195 200 205

Leu Glu Leu Ala Arg Lys His Gly Ala Glu Phe Thr Val Asn Ala Arg
 210 215 220

Asn Glu Asp Ser Gly Glu Ala Val Gln Lys Tyr Thr Asn Gly Gly Ala
 225 230 235 240

<400> 211																
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cgctcgtagg cgcttttgat ttttcggtag gctaactggg																115
<div>Val Ser Ile Ser Val</div> <div>1 5</div>																
aaa gca cta caa aag tcc ggc cca gaa gca cct ttc gag gtc aag atc																163
<div>Lys Ala Leu Gln Lys Ser Gly Pro Glu Ala Pro Phe Glu Val Lys Ile</div> <div>10 15 20</div>																
att gaa cgc cgt gac cca cgc gca gat gat gtg gtt att gat atc aaa																211
<div>Ile Glu Arg Arg Asp Pro Arg Ala Asp Val Val Ile Asp Ile Lys</div> <div>25 30 35</div>																
gct gcg ggc atc tgc cac agc gat atc cac acc atc cgc aac gaa tgg																259
<div>Ala Ala Gly Ile Cys His Ser Asp Ile His Thr Ile Arg Asn Glu Trp</div> <div>40 45 50</div>																
ggc gag gcg cac ttc ccg ctc acc gtc ggc cac gaa atc gca ggc gtt																307
<div>Gly Glu Ala His Phe Pro Leu Thr Val Gly His Glu Ile Ala Gly Val</div> <div>55 60 65</div>																
gtc tct gcg gtt gga tcc gat gta acc aaa tgg aaa gtc ggc gac cgc																355
<div>Val Ser Ala Val Gly Ser Asp Val Thr Lys Trp Lys Val Gly Asp Arg</div> <div>70 75 80 85</div>																
gtg ggc gtc ggc tgc ctc gtt aac tcc tgc ggc gaa tgc gaa cag tgc																403
<div>Val Gly Val Gly Cys Leu Val Asn Ser Cys Gly Glu Cys Glu Gln Cys</div>																

90										95					100					
gtc	gca	gga	ttt	gaa	aac	aac	tgc	ctt	cgc	gga	aac	gtc	gga	acc	tac	451				
Val	Ala	Gly	Phe	Glu	Asn	Asn	Cys	Leu	Arg	Gly	Asn	Val	Gly	Thr	Tyr					
			105						110					115						
aac	tct	aac	gac	gtc	gac	ggc	acc	atc	acc	caa	ggc	ggc	tac	gct	gaa	499				
Asn	Ser	Asn	Asp	Val	Asp	Gly	Thr	Ile	Thr	Gln	Gly	Gly	Tyr	Ala	Glu					
		120					125						130							
aag	gta	gtg	gtc	aac	gaa	cgt	ttc	ctg	tgc	agc	atc	cca	gag	gaa	ctt	547				
Lys	Val	Val	Val	Asn	Glu	Arg	Phe	Leu	Cys	Ser	Ile	Pro	Glu	Glu	Leu					
		135				140					145									
aac	ttc	gat	gtc	gca	gca	cca	ctg	ctg	tgc	gca	ggc	atc	acc	acc	tac	595				
Asn	Phe	Asp	Val	Ala	Ala	Pro	Leu	Leu	Cys	Ala	Gly	Ile	Thr	Thr	Tyr					
					155					160					165					
tcc	cca	atc	gct	cgc	tgg	aac	gtt	aaa	gaa	ggc	gac	aaa	gta	gca	gtc	643				
Ser	Pro	Ile	Ala	Arg	Trp	Asn	Val	Lys	Glu	Gly	Asp	Lys	Val	Ala	Val					
				170					175					180						
atg	ggc	ctc	ggc	ggg	act	cgg	aca	cat	ggg	tgt	cca	gat	cgc	tgc	agc	691				
Met	Gly	Leu	Gly	Gly	Thr	Arg	Thr	His	Gly	Cys	Pro	Asp	Arg	Cys	Ser					
			185					190					195							
caa	ggg	tgc	tgaggttacc	gttctgtccc	gtt											723				
Gln	Gly	Cys																		
		200																		

<210> 212

<211> 200

<212> PRT

<213> Corynebacterium glutamicum

<400> 212

Val	Ser	Ile	Ser	Val	Lys	Ala	Leu	Gln	Lys	Ser	Gly	Pro	Glu	Ala	Pro
1				5					10					15	

Phe	Glu	Val	Lys	Ile	Ile	Glu	Arg	Arg	Asp	Pro	Arg	Ala	Asp	Asp	Val
			20					25					30		

Val	Ile	Asp	Ile	Lys	Ala	Ala	Gly	Ile	Cys	His	Ser	Asp	Ile	His	Thr
		35					40					45			

Ile	Arg	Asn	Glu	Trp	Gly	Glu	Ala	His	Phe	Pro	Leu	Thr	Val	Gly	His
	50					55					60				

Glu	Ile	Ala	Gly	Val	Val	Ser	Ala	Val	Gly	Ser	Asp	Val	Thr	Lys	Trp
	65				70					75					80

Lys	Val	Gly	Asp	Arg	Val	Gly	Val	Gly	Cys	Leu	Val	Asn	Ser	Cys	Gly
				85					90					95	

Glu	Cys	Glu	Gln	Cys	Val	Ala	Gly	Phe	Glu	Asn	Asn	Cys	Leu	Arg	Gly
			100					105					110		

Asn	Val	Gly	Thr	Tyr	Asn	Ser	Asn	Asp	Val	Asp	Gly	Thr	Ile	Thr	Gln
		115					120					125			

Gly Gly Tyr Ala Glu Lys Val Val Val Asn Glu Arg Phe Leu Cys Ser
 130 135 140

Ile Pro Glu Glu Leu Asn Phe Asp Val Ala Ala Pro Leu Leu Cys Ala
 145 150 155 160

Gly Ile Thr Thr Tyr Ser Pro Ile Ala Arg Trp Asn Val Lys Glu Gly
 165 170 175

Asp Lys Val Ala Val Met Gly Leu Gly Gly Thr Arg Thr His Gly Cys
 180 185 190

Pro Asp Arg Cys Ser Gln Gly Cys
 195 200

<210> 213
 <211> 615
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(592)
 <223> RXA01572

<400> 213
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gacaaagtag cagtcacggg cctcggcggg actcggacac atg ggt gtc cag atc 115
 Met Gly Val Gln Ile
 1 5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc 163
 Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
 10 15 20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act 211
 Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
 25 30 35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc 259
 Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
 40 45 50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt 307
 Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
 55 60 65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag 355
 Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
 70 75 80 85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc 403
 Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
 90 95 100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc 451
 Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
 105 110 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac 499
 Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
 120 125 130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc 547
 Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
 135 140 145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt 592
 Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
 150 155 160

taggtttact gaagttcaga ctt 615

<210> 214

<211> 164

<212> PRT

<213> Corynebacterium glutamicum

<400> 214

Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
 1 5 10 15

Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
 20 25 30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
 35 40 45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
 50 55 60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
 65 70 75 80

Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
 85 90 95

Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
 100 105 110

Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
 115 120 125

Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
 130 135 140

Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
 145 150 155 160

Val Glu Ala Val

<210> 215

<211> 1140

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1117)

<223> RXA01758

<400> 215

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gatagcgcgc tcagaagttc tttagtga aa gcagaaccaa atg ccc aaa tac att 115
                               Met Pro Lys Tyr Ile
                               1           5

gcc atg cag gta tcc gaa tcc ggt gca ccg tta gcc gcg aat ctc gtg 163
Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu Ala Ala Asn Leu Val
                10                15                20

caa cct gct ccg ttg aaa tcg agg gaa gtc cgc gtg gaa atc gct gct 211
Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg Val Glu Ile Ala Ala
                25                30                35

agt ggt gtg tgc cat gca gat att ggc acg gca gca gca tcg ggg aag 259
Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala Ala Ala Ser Gly Lys
                40                45                50

cac act gtt ttt cct gtt acc cct ggt cat gag att gca gga acc atc 307
His Thr Val Phe Pro Val Thr Pro Gly His Glu Ile Ala Gly Thr Ile
                55                60                65

gcg gaa att ggt gaa aac gta tct cgg tgg acg gtt ggt gat cgc gtt 355
Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr Val Gly Asp Arg Val
                70                75                80                85

gca atc ggt tgg ttt ggt ggc aat tgc ggt gac tgc gct ttt tgt cgt 403
Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp Cys Ala Phe Cys Arg
                90                95                100

gca ggt gat cct gtg cat tgc aga gag cgg aag att cct ggc gtt tct 451
Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys Ile Pro Gly Val Ser
                105                110                115

tat gcg ggt ggt tgg gca cag aat att gtt gtt cca gcg gag gct ctt 499
Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val Pro Ala Glu Ala Leu
                120                125                130

gct gcg att cca gat ggc atg gac ttt tac gag ccc gcc ccg atg ggc 547
Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu Pro Ala Pro Met Gly
                135                140                145

tgc gca ggt gtg aca aca ttc aat gcg ttg cga aac ctg aag ctg gat 595
Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg Asn Leu Lys Leu Asp
                150                155                160                165

ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta 643
Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu
                170                175                180

gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc 691
Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala
                185                190                195

cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac 739
Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His

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200	205	210	
tac atc gat agc aat gat	ctg cac cct ggc cag gcg	tta ttt gaa ctt	787
Tyr Ile Asp Ser Asn Asp	Leu His Pro Gly Gln Ala	Leu Phe Glu Leu	
215	220	225	
ggc ggg gct gac ttg atc	ttg tct act gcg tcc acc	acg gag cct ctt	835
Gly Gly Ala Asp Leu Ile	Leu Ser Thr Ala Ser Thr	Thr Glu Pro Leu	
230	235	240 245	
tcg gag ttg tct acc ggt	ctt tct att ggc ggg	cag cta acc att atc	883
Ser Glu Leu Ser Thr Gly	Leu Ser Ile Gly Gly	Gln Leu Thr Ile Ile	
250	255	260	
gga gtt gat ggg gga gat	atc acc gtt tcg gca gcc	caa ttg atg atg	931
Gly Val Asp Gly Gly Asp	Ile Thr Val Ser Ala Ala	Gln Leu Met Met	
265	270	275	
aac cgt cag atc atc aca	ggt cac ctc act gga agt	gcg aat gac acg	979
Asn Arg Gln Ile Ile Thr	Gly His Leu Thr Gly Ser	Ala Asn Asp Thr	
280	285	290	
gaa cag act atg aaa ttt	gct cat ctc cat ggc	gtg aaa ccg ctt att	1027
Glu Gln Thr Met Lys Phe	Ala His Leu His Gly Val	Lys Pro Leu Ile	
295	300	305	
gaa cgg atg cct ctc gat	caa gcc aac gag gct	att gca cgt att tca	1075
Glu Arg Met Pro Leu Asp	Gln Ala Asn Glu Ala Ile	Ala Arg Ile Ser	
310	315	320 325	
gct ggt aaa cca cgt ttc	cgt att gtc ttg gag ccg	aat tca	1117
Ala Gly Lys Pro Arg Phe	Arg Ile Val Leu Glu Pro	Asn Ser	
330	335		
taatgccaac agcaagccca att			1140

<210> 216

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 216

Met Pro Lys Tyr Ile Ala Met Gln Val Ser Glu Ser Gly Ala Pro Leu
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Ala Ala Asn Leu Val Gln Pro Ala Pro Leu Lys Ser Arg Glu Val Arg
20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
35 40 45

Ala Ala Ser Gly Lys His Thr Val Phe Pro Val Thr Pro Gly His Glu
50 55 60

Ile Ala Gly Thr Ile Ala Glu Ile Gly Glu Asn Val Ser Arg Trp Thr
65 70 75 80

Val Gly Asp Arg Val Ala Ile Gly Trp Phe Gly Gly Asn Cys Gly Asp
85 90 95

Cys Ala Phe Cys Arg Ala Gly Asp Pro Val His Cys Arg Glu Arg Lys
 100 105 110
 Ile Pro Gly Val Ser Tyr Ala Gly Gly Trp Ala Gln Asn Ile Val Val
 115 120 125
 Pro Ala Glu Ala Leu Ala Ala Ile Pro Asp Gly Met Asp Phe Tyr Glu
 130 135 140
 Pro Ala Pro Met Gly Cys Ala Gly Val Thr Thr Phe Asn Ala Leu Arg
 145 150 155 160
 Asn Leu Lys Leu Asp Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly
 165 170 175
 Gly Leu Val Arg Leu Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg
 180 185 190
 Thr Ile Thr Ile Ala Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln
 195 200 205
 Leu Gly Ala Asn His Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln
 210 215 220
 Ala Leu Phe Glu Leu Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser
 225 230 235 240
 Thr Thr Glu Pro Leu Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly
 245 250 255
 Gln Leu Thr Ile Ile Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala
 260 265 270
 Ala Gln Leu Met Met Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly
 275 280 285
 Ser Ala Asn Asp Thr Glu Gln Thr Met Lys Phe Ala His Leu His Gly
 290 295 300
 Val Lys Pro Leu Ile Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala
 305 310 315 320
 Ile Ala Arg Ile Ser Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu
 325 330 335

Pro Asn Ser

<210> 217

<211> 1641

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1618)

<223> RXA02539

<400> 217

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acaggtagtg	ctcaggtgga	ggtggcccaa	aggagaccca	atg	act	gtc	tac	gca	115
				Met	Thr	Val	Tyr	Ala	
				1				5	
aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag	163								
Asn Pro Gly Thr	Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu								
10	15	20							
aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt	211								
Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu									
25	30	35							
gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt	259								
Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg									
40	45	50							
ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc	307								
Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala									
55	60	65							
gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg	355								
Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu									
70	75	80	85						
cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt	403								
His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val									
90	95	100							
gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca	451								
Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala									
105	110	115							
gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc	499								
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile									
120	125	130							
cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct	547								
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala									
135	140	145							
tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg	595								
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp									
150	155	160	165						
aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct	643								
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala									
170	175	180							
gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc	691								
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser									
185	190	195							
att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc	739								
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val									
200	205	210							
ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc	787								
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser									
215	220	225							

ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val 230 235 240 245	835
ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr 250 255 260	883
ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu 265 270 275	931
tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met 280 285 290	979
ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu 295 300 305	1027
gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg 310 315 320 325	1075
gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met 330 335 340	1123
ggc gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu 345 350 355	1171
aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val 360 365 370	1219
aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val 375 380 385	1267
ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly 390 395 400 405	1315
cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg 410 415 420	1363
att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg 425 430 435	1411
gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg 440 445 450	1459
gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly 455 460 465	1507
gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg	1555

Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
 470 475 480 485

aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac 1603
 Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
 490 495 500

cca acc gga ctg ttc tgatctaagc gttaagtcct aga 1641
 Pro Thr Gly Leu Phe
 505

<210> 218

<211> 506

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 218

Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
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Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
 20 25 30

Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
 35 40 45

Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
 50 55 60

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65 70 75 80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
 85 90 95

Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
 100 105 110

Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
 115 120 125

Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
 130 135 140

His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
 145 150 155 160

Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
 165 170 175

Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
 180 185 190

Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
 195 200 205

Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
 210 215 220

Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr

225		230		235		240
Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys						
	245			250		255
Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe						
	260			265		270
Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val						
	275			280		285
Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys						
	290			295		300
Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu						
	305			310		315
Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp						
	325			330		335
Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys						
	340			345		350
Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu						
	355			360		365
Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr						
	370			375		380
Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg						
	385			390		395
Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe						
	405			410		415
Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala						
	420			425		430
Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala						
	435			440		445
Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala						
	450			455		460
His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn						
	465			470		475
His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val						
	485			490		495
Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe						
	500			505		

<210> 219

<211> 430

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(430)

<223> RXN03061

<400> 219

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gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc 115
                                   Val Ser Leu Thr Phe
                                   1 5
cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
                                   10 15 20
cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct 211
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
                                   25 30 35
ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc 259
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
                                   40 45 50
acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag 307
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
                                   55 60 65
atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa 355
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
                                   70 75 80 85
gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg 403
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
                                   90 95 100
cgc ctg ccc ggc cgc tac gga cag tca 430
Arg Leu Pro Gly Arg Tyr Gly Gln Ser
                                   105 110

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<210> 220

<211> 110

<212> PRT

<213> Corynebacterium glutamicum

<400> 220

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Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
  1 5 10 15
Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
  20 25 30
Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
  35 40 45
Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala
  50 55 60
Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
  65 70 75 80
Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe

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      85              90              95
Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
      100              105              110

<210> 221
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXN03150

<400> 221
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acccaaggct gaattcctga gctcaccttg tacaagatca gtg gaa gcc cag ttc 115
              Val Glu Ala Gln Phe
              1              5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga 163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
              10              15              20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc 211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
              25              30              35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act 259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
              40              45              50

cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc 307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
              55              60              65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc 355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
              70              75              80              85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg 403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
              90              95              100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc 451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
              105              110              115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc 499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
              120              125              130

caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg 547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
              135              140              145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga 595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly

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150 155 160 165
 acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga 643
 Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
 170 175 180
 ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt 691
 Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
 185 190 195
 gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
 Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 200 205
 tat 747

<210> 222
 <211> 208
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 222
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 Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
 20 25 30
 Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
 35 40 45
 Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg
 50 55 60
 Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65 70 75 80
 Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
 85 90 95
 Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
 100 105 110
 Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
 115 120 125
 Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
 130 135 140
 Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
 145 150 155 160
 Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
 165 170 175
 Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
 180 185 190
 Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
 195 200 205

<210> 223

<211> 881

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(858)

<223> RXN01340

<400> 223

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Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro	
1 5 10 15	
cag ggc ttg gtc tca atc atc acc acc act cga gat gca gag cta tcg	96
Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser	
20 25 30	
gca gaa ctc atg gct gat cct cgc ttg gct aaa gtc acc ttc act gga	144
Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly	
35 40 45	
tca acc aac gtg gga cgc atc ctg gtc cgc caa tcc gcg gac cga ctg	192
Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu	
50 55 60	
ctg cgc acc tcc atg gaa ctc ggc gga aat gca gct ttt gtt atc gac	240
Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp	
65 70 75 80	
gaa gcc gca gac ctc gac gaa gcc gta tcc ggt gcc atc gcc gca aaa	288
Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys	
85 90 95	
ctc cgc aac gcc ggc caa gta tgc atc gca gct aac cgt ttc ttg gtt	336
Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val	
100 105 110	
cat gaa tcc cgc gct gcc gaa ttc acc tca aag ctg gcg aca gcc atg	384
His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met	
115 120 125	
cag aac act ccc att ggg ccg gtg att tct gcc cgc caa cgc gac cgg	432
Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg	
130 135 140	
atc gca gca cta gtg gat gaa gcc atc acc gac ggc gcc cgc ctc atc	480
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile	
145 150 155 160	
atc ggt ggg gag gtc ccc gac ggc tcc ggc ttc ttc tat cca gcc acc	528
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr	
165 170 175	
atc ttg gcc gat gtc cct gca cag tca cgg att gtg cat gag gaa atc	576

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Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile
      180                      185                      190

ttc gga cct gtg gcc acc att gcc act ttc acc gac ttg gcc gaa ggc 624
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly
      195                      200                      205

gtt gca caa gca aat tcc acc gaa ttc ggc ctc gca gcc tac gga ttc 672
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe
      210                      215                      220

agc aac aat gtg aaa gca aca cag tac atg gcg gaa cac ttg gaa gcc 720
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala
      225                      230                      235                      240

gga atg gtc gga atc aac aga ggc gcc atc tct gac cca gca gca cct 768
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro
      245                      250                      255

ttt ggc ggc atc gga caa tcc ggc ttc ggc aga gaa ggc gga acc gaa 816
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu
      260                      265                      270

gga atc gaa gaa tat ctc tcc gtg cgt tac ctc gct ttg ccg 858
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro
      275                      280                      285

tgacacatga gctgtccggt gaa 881

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<210> 224

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 224

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Lys Val Gly Glu Ile Ile Ala Ser Val Phe Asp Thr Phe Asn Ile Pro
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Gln Gly Leu Val Ser Ile Ile Thr Thr Thr Arg Asp Ala Glu Leu Ser
      20                      25                      30

Ala Glu Leu Met Ala Asp Pro Arg Leu Ala Lys Val Thr Phe Thr Gly
      35                      40                      45

Ser Thr Asn Val Gly Arg Ile Leu Val Arg Gln Ser Ala Asp Arg Leu
      50                      55                      60

Leu Arg Thr Ser Met Glu Leu Gly Gly Asn Ala Ala Phe Val Ile Asp
      65                      70                      75                      80

Glu Ala Ala Asp Leu Asp Glu Ala Val Ser Gly Ala Ile Ala Ala Lys
      85                      90                      95

Leu Arg Asn Ala Gly Gln Val Cys Ile Ala Ala Asn Arg Phe Leu Val
      100                      105                      110

His Glu Ser Arg Ala Ala Glu Phe Thr Ser Lys Leu Ala Thr Ala Met
      115                      120                      125

Gln Asn Thr Pro Ile Gly Pro Val Ile Ser Ala Arg Gln Arg Asp Arg

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130	135	140
Ile Ala Ala Leu Val Asp Glu Ala Ile Thr Asp Gly Ala Arg Leu Ile 145 150 155 160		
Ile Gly Gly Glu Val Pro Asp Gly Ser Gly Phe Phe Tyr Pro Ala Thr 165 170 175		
Ile Leu Ala Asp Val Pro Ala Gln Ser Arg Ile Val His Glu Glu Ile 180 185 190		
Phe Gly Pro Val Ala Thr Ile Ala Thr Phe Thr Asp Leu Ala Glu Gly 195 200 205		
Val Ala Gln Ala Asn Ser Thr Glu Phe Gly Leu Ala Ala Tyr Gly Phe 210 215 220		
Ser Asn Asn Val Lys Ala Thr Gln Tyr Met Ala Glu His Leu Glu Ala 225 230 235 240		
Gly Met Val Gly Ile Asn Arg Gly Ala Ile Ser Asp Pro Ala Ala Pro 245 250 255		
Phe Gly Gly Ile Gly Gln Ser Gly Phe Gly Arg Glu Gly Gly Thr Glu 260 265 270		
Gly Ile Glu Glu Tyr Leu Ser Val Arg Tyr Leu Ala Leu Pro 275 280 285		

<210> 225

<211> 1686

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1663)

<223> RXN01498

<400> 225

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accacacgag catcagaacg cgaaacgaag gtaaaagccc atg atc aaa cgt ctt	115
Met Ile Lys Arg Leu	
1 5	

cct tta ggt ccg ctg cct aaa gaa ctt cat cag act ctg ctt gat ctg	163
Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln Thr Leu Leu Asp Leu	
10 15 20	

acc gca aat gcc caa gat gcg gcg aaa gtg gag gtt ata gcg cca ttt	211
Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu Val Ile Ala Pro Phe	
25 30 35	

act ggc gag acc ctc gga ttt ggt ttt gat ggt gat gag caa gac gtc	259
Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly Asp Glu Gln Asp Val	
40 45 50	

gag cat gct ttt gca ctt tca agg gca gcc cag aaa aag tgg gtg cac	307
Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln Lys Lys Trp Val His	

55	60	65	
acc acg gca gtg gaa cgg aag aag atc ttc ctg aag gtt cat gat ctg			355
Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu Lys Val His Asp Leu			
70	75	80	85
gta ttg aaa aac cgt gag ctg ctc atg gac atc gtg cag ttg gaa aca			403
Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile Val Gln Leu Glu Thr			
	90	95	100
ggc aaa aat cga gca tcg gct gcc gat gag gtg ttg gac gtt gcg atc			451
Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val Leu Asp Val Ala Ile			
	105	110	115
acc acc cgc ttc tac gca aac aat gca gga aag ttt tta aat gac aag			499
Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys Phe Leu Asn Asp Lys			
	120	125	130
aaa cgc ccc ggc gcg ctt ccg atc atc acg aaa aac aca caa cag tat			547
Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys Asn Thr Gln Gln Tyr			
	135	140	145
gtg ccc aag gga gtg gtc ggg cag atc acg ccg tgg aat tac cct tta			595
Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro Trp Asn Tyr Pro Leu			
150	155	160	165
act ttg gga gta tct gat gct gtt ccg gcg ctg ctg gca gga aac gca			643
Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu Leu Ala Gly Asn Ala			
	170	175	180
gtg gtg gct aaa cct gac ctc gcg aca cct ttc tcc tgc ttg atc atg			691
Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe Ser Cys Leu Ile Met			
	185	190	195
gtg cac ctg ctc att gaa gcc ggt ctg ccg cgt gat ttg atg cag gtt			739
Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg Asp Leu Met Gln Val			
	200	205	210
gtc acc ggc cct ggc gat att gtt ggc ggt gcg att gca gct cag tgt			787
Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala Ile Ala Ala Gln Cys			
	215	220	225
gat ttc ctc atg ttc act gga tcc acg gcc acg ggc cgg atc ttg ggt			835
Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr Gly Arg Ile Leu Gly			
230	235	240	245
cgg aca atg ggt gag cgt ttg gtg ggt ttc tct gcg gaa tta ggc gga			883
Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser Ala Glu Leu Gly Gly			
	250	255	260
aag aac cct ctt att gtg gcc aag gat gca gat ctg gac aag gtg gaa			931
Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp Leu Asp Lys Val Glu			
	265	270	275
gct gag ctt ccg cag gcg tgt ttt tcc aac tcg ggg caa ttg tgt gtc			979
Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser Gly Gln Leu Cys Val			
	280	285	290
tcc act gaa cgt att tat gtc gag gaa gac gtg tac gag gag gtg att			1027
Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val Tyr Glu Glu Val Ile			
	295	300	305

gca cgg ttt agc aag gcg gcg aaa gcc atg tcc att ggt gcc gga ttt	1075
Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser Ile Gly Ala Gly Phe	
310 315 320 325	
gag tgg aaa tat gag atg ggt tcg ttg atc aat cac gcg cag ctg gat	1123
Glu Trp Lys Tyr Glu Met Gly Ser Leu Ile Asn His Ala Gln Leu Asp	
330 335 340	
cgg gtg agc acc ttt gtt gat cag gct aaa gct gcg ggc gcc acg gtg	1171
Arg Val Ser Thr Phe Val Asp Gln Ala Lys Ala Ala Gly Ala Thr Val	
345 350 355	
ctg tgc ggt ggc aag tca cgc cct gat att ggt ccc ttc ttc tat gag	1219
Leu Cys Gly Gly Lys Ser Arg Pro Asp Ile Gly Pro Phe Phe Tyr Glu	
360 365 370	
ccc acg gta ttg gcg gat gtc cca gag ggc acc cca ctg ctc acg gag	1267
Pro Thr Val Leu Ala Asp Val Pro Glu Gly Thr Pro Leu Leu Thr Glu	
375 380 385	
gaa gtc ttc ggg ccg gtg gtg ttc atc gaa aag gta gcc aca ctg gaa	1315
Glu Val Phe Gly Pro Val Val Phe Ile Glu Lys Val Ala Thr Leu Glu	
390 395 400 405	
gaa gcc gtc gat aag gca aat ggc acg ccc tac ggc ctg aat gcg tcc	1363
Glu Ala Val Asp Lys Ala Asn Gly Thr Pro Tyr Gly Leu Asn Ala Ser	
410 415 420	
gtc ttt ggg tcg tcg gaa acc ggc aat ctt gtt gca ggc cag ctg gaa	1411
Val Phe Gly Ser Ser Glu Thr Gly Asn Leu Val Ala Gly Gln Leu Glu	
425 430 435	
gct ggc ggt atc ggt att aat gat ggc tac gcc gcg acg tgg gcg agc	1459
Ala Gly Gly Ile Gly Ile Asn Asp Gly Tyr Ala Ala Thr Trp Ala Ser	
440 445 450	
gtg tcc acg cct ctg ggt ggc atg aag cag tcg ggg ctg ggg cac cgc	1507
Val Ser Thr Pro Leu Gly Gly Met Lys Gln Ser Gly Leu Gly His Arg	
455 460 465	
cat ggt gcg gag gga att aca aaa tat gcg gag atc cga aac atc gcg	1555
His Gly Ala Glu Gly Ile Thr Lys Tyr Ala Glu Ile Arg Asn Ile Ala	
470 475 480 485	
gag cag cgc tgg atg tct atg cgt ggg ccg gcc aaa atg ccg cga aag	1603
Glu Gln Arg Trp Met Ser Met Arg Gly Pro Ala Lys Met Pro Arg Lys	
490 495 500	
gtg tac tca gac acc gtg gcc aca gcg cta aag ctg ggc aaa atc ttt	1651
Val Tyr Ser Asp Thr Val Ala Thr Ala Leu Lys Leu Gly Lys Ile Phe	
505 510 515	
aaa gtt ttg ccg tagcaaaaag ccggaccctt gct	1686
Lys Val Leu Pro	
520	

<210> 226

<211> 521

<212> PRT

<213> Corynebacterium glutamicum

<400> 226

Met Ile Lys Arg Leu Pro Leu Gly Pro Leu Pro Lys Glu Leu His Gln
 1 5 10 15
 Thr Leu Leu Asp Leu Thr Ala Asn Ala Gln Asp Ala Ala Lys Val Glu
 20 25 30
 Val Ile Ala Pro Phe Thr Gly Glu Thr Leu Gly Phe Gly Phe Asp Gly
 35 40 45
 Asp Glu Gln Asp Val Glu His Ala Phe Ala Leu Ser Arg Ala Ala Gln
 50 55 60
 Lys Lys Trp Val His Thr Thr Ala Val Glu Arg Lys Lys Ile Phe Leu
 65 70 75 80
 Lys Val His Asp Leu Val Leu Lys Asn Arg Glu Leu Leu Met Asp Ile
 85 90 95
 Val Gln Leu Glu Thr Gly Lys Asn Arg Ala Ser Ala Ala Asp Glu Val
 100 105 110
 Leu Asp Val Ala Ile Thr Thr Arg Phe Tyr Ala Asn Asn Ala Gly Lys
 115 120 125
 Phe Leu Asn Asp Lys Lys Arg Pro Gly Ala Leu Pro Ile Ile Thr Lys
 130 135 140
 Asn Thr Gln Gln Tyr Val Pro Lys Gly Val Val Gly Gln Ile Thr Pro
 145 150 155 160
 Trp Asn Tyr Pro Leu Thr Leu Gly Val Ser Asp Ala Val Pro Ala Leu
 165 170 175
 Leu Ala Gly Asn Ala Val Val Ala Lys Pro Asp Leu Ala Thr Pro Phe
 180 185 190
 Ser Cys Leu Ile Met Val His Leu Leu Ile Glu Ala Gly Leu Pro Arg
 195 200 205
 Asp Leu Met Gln Val Val Thr Gly Pro Gly Asp Ile Val Gly Gly Ala
 210 215 220
 Ile Ala Ala Gln Cys Asp Phe Leu Met Phe Thr Gly Ser Thr Ala Thr
 225 230 235 240
 Gly Arg Ile Leu Gly Arg Thr Met Gly Glu Arg Leu Val Gly Phe Ser
 245 250 255
 Ala Glu Leu Gly Gly Lys Asn Pro Leu Ile Val Ala Lys Asp Ala Asp
 260 265 270
 Leu Asp Lys Val Glu Ala Glu Leu Pro Gln Ala Cys Phe Ser Asn Ser
 275 280 285
 Gly Gln Leu Cys Val Ser Thr Glu Arg Ile Tyr Val Glu Glu Asp Val
 290 295 300
 Tyr Glu Glu Val Ile Ala Arg Phe Ser Lys Ala Ala Lys Ala Met Ser


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<400> 227
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acagttggtg aagtatccac aatcaacttt aggagacctt  gtg act gca aca ttt    115
                                         Val Thr Ala Thr Phe
                                         1                      5

gct gga atc gac gcc acc aaa cac ctc atc gga ggt cag tgg gtg gag    163
Ala Gly Ile Asp Ala Thr Lys His Leu Ile Gly Gly Gln Trp Val Glu

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				10				15				20				
gga	aac	tcg	gat	cga	att	tcc	acc	aat	atc	aat	cct	tac	gac	gat	tcc	211
Gly	Asn	Ser	Asp	Arg	Ile	Ser	Thr	Asn	Ile	Asn	Pro	Tyr	Asp	Asp	Ser	
25				30				35								
gta	atc	gcc	gaa	agc	aaa	caa	gct	tcc	att	gct	gat	gtt	gat	gcc	gcg	259
Val	Ile	Ala	Glu	Ser	Lys	Gln	Ala	Ser	Ile	Ala	Asp	Val	Asp	Ala	Ala	
40				45				50								
tat	gaa	gcc	gcg	aag	aag	gcc	cag	gct	gag	tgg	gca	gct	acg	ccc	gct	307
Tyr	Glu	Ala	Ala	Lys	Lys	Ala	Gln	Ala	Glu	Trp	Ala	Ala	Thr	Pro	Ala	
55				60				65								
gcg	gaa	cga	tct	gcc	atc	atc	tac	cgt	gcg	gct	gaa	ctt	ctt	gaa	gag	355
Ala	Glu	Arg	Ser	Ala	Ile	Ile	Tyr	Arg	Ala	Ala	Glu	Leu	Leu	Glu	Glu	
70				75				80				85				
cac	cgg	gag	gaa	atc	gtg	gaa	tgg	ctg	atc	aag	gaa	tcc	ggc	tcg	acg	403
His	Arg	Glu	Glu	Ile	Val	Glu	Trp	Leu	Ile	Lys	Glu	Ser	Gly	Ser	Thr	
90				95				100								
cgt	tcc	aag	gct	aat	ttg	gaa	atc	act	ttg	gca	gga	aac	atc	act	aaa	451
Arg	Ser	Lys	Ala	Asn	Leu	Glu	Ile	Thr	Leu	Ala	Gly	Asn	Ile	Thr	Lys	
105				110				115								
gaa	tcg	gct	tca	ttc	cct	ggt	cgt	gtg	cat	ggt	cga	att	tct	cct	tcg	499
Glu	Ser	Ala	Ser	Phe	Pro	Gly	Arg	Val	His	Gly	Arg	Ile	Ser	Pro	Ser	
120				125				130								
aat	act	ccg	ggc	aaa	gaa	aac	cgt	gtg	tac	cgc	gta	gcc	aag	ggc	gtt	547
Asn	Thr	Pro	Gly	Lys	Glu	Asn	Arg	Val	Tyr	Arg	Val	Ala	Lys	Gly	Val	
135				140				145								
gtc	gga	gtg	att	agt	cca	tgg	aat	ttc	cca	ctg	aac	ctc	tcg	atc	cgc	595
Val	Gly	Val	Ile	Ser	Pro	Trp	Asn	Phe	Pro	Leu	Asn	Leu	Ser	Ile	Arg	
150				155				160				165				
tcg	gtt	gct	ccg	gca	cta	gcc	gtg	ggc	aac	gcc	gta	gtg	att	aag	cct	643
Ser	Val	Ala	Pro	Ala	Leu	Ala	Val	Gly	Asn	Ala	Val	Val	Ile	Lys	Pro	
170				175				180								
gcg	agt	gat	acc	cca	gtt	act	ggt	ggt	gta	att	cct	gca	cga	atc	ttt	691
Ala	Ser	Asp	Thr	Pro	Val	Thr	Gly	Gly	Val	Ile	Pro	Ala	Arg	Ile	Phe	
185				190				195								
gag	gag	gcc	gga	gtt	cct	gca	ggc	gtg	atc	agc	acg	gtt	gcg	ggc	gca	739
Glu	Glu	Ala	Gly	Val	Pro	Ala	Gly	Val	Ile	Ser	Thr	Val	Ala	Gly	Ala	
200				205				210								
gga	tct	gaa	atc	ggt	gat	cac	ttt	gtc	acc	cac	gcc	gtg	cca	aag	ctg	787
Gly	Ser	Glu	Ile	Gly	Asp	His	Phe	Val	Thr	His	Ala	Val	Pro	Lys	Leu	
215				220				225								
att	tct	ttc	acc	ggt	tca	acc	cca	gtc	ggt	cgt	cgt	gtc	ggt	gag	ctg	835
Ile	Ser	Phe	Thr	Gly	Ser	Thr	Pro	Val	Gly	Arg	Arg	Val	Gly	Glu	Leu	
230																

aac gcg ccg ttc gtt gtg ctt gcc gac gcc gac atc gac gcc gct gcc	931
Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp Ile Asp Ala Ala Ala	
265 270 275	
cag gct gcc gca gtt ggc gct ttc cta cac cag gga cag att tgt atg	979
Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln Gly Gln Ile Cys Met	
280 285 290	
tca atc aac cga gtc att gtt gat gct gca gtt cat gat gaa ttc cta	1027
Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val His Asp Glu Phe Leu	
295 300 305	
gag aag ttc gtt gaa gca gtg aag aac att cca acc ggc gat cca agc	1075
Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro Thr Gly Asp Pro Ser	
310 315 320 325	
gca gaa gga acc ctt gtt gga cct gtc att aat gac agt cag ctc agt	1123
Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn Asp Ser Gln Leu Ser	
330 335 340	
ggg ttg aag gaa aag atc gag ttg gcc aaa aag gaa ggc gca acc gtc	1171
Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys Glu Gly Ala Thr Val	
345 350 355	
cag gtt gaa ggg cca att gaa ggc cga ctg gtt cat ccg cat gtg ttc	1219
Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val His Pro His Val Phe	
360 365 370	
tct gat gtc acc tct gac atg gaa atc gct cgt gag gaa atc ttc gga	1267
Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg Glu Glu Ile Phe Gly	
375 380 385	
cct ctc atc agc gtg ctg aag gcc gat gat gag gca cac gca gca gag	1315
Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu Ala His Ala Ala Glu	
390 395 400 405	
ctg gcc aat gct tcc gac ttt ggt ttg agc gcg gca gtg tgg tcg aag	1363
Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala Ala Val Trp Ser Lys	
410 415 420	
gat att gat cgt gca gcc cag ttt gct ctg cag att gat tcc ggc atg	1411
Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln Ile Asp Ser Gly Met	
425 430 435	
gtt cac atc aat gac ctc acc gtc aac gat gaa cca cac gtg atg ttc	1459
Val His Ile Asn Asp Leu Thr Val Asn Asp Glu Pro His Val Met Phe	
440 445 450	
ggg ggt tca aag aac tct ggc ctc ggc cgc ttc aac ggc gat tgg gcg	1507
Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe Asn Gly Asp Trp Ala	
455 460 465	
atc gag gag ttc acc aca gat cga tgg atc ggc atc aag cgc agc	1552
Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly Ile Lys Arg Ser	
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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 228

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Gly Gln Trp Val Glu Gly Asn Ser Asp Arg Ile Ser Thr Asn Ile Asn
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Pro Tyr Asp Asp Ser Val Ile Ala Glu Ser Lys Gln Ala Ser Ile Ala
 35 40 45

Asp Val Asp Ala Ala Tyr Glu Ala Ala Lys Lys Ala Gln Ala Glu Trp
 50 55 60

Ala Ala Thr Pro Ala Ala Glu Arg Ser Ala Ile Ile Tyr Arg Ala Ala
 65 70 75 80

Glu Leu Leu Glu Glu His Arg Glu Glu Ile Val Glu Trp Leu Ile Lys
 85 90 95

Glu Ser Gly Ser Thr Arg Ser Lys Ala Asn Leu Glu Ile Thr Leu Ala
 100 105 110

Gly Asn Ile Thr Lys Glu Ser Ala Ser Phe Pro Gly Arg Val His Gly
 115 120 125

Arg Ile Ser Pro Ser Asn Thr Pro Gly Lys Glu Asn Arg Val Tyr Arg
 130 135 140

Val Ala Lys Gly Val Val Gly Val Ile Ser Pro Trp Asn Phe Pro Leu
 145 150 155 160

Asn Leu Ser Ile Arg Ser Val Ala Pro Ala Leu Ala Val Gly Asn Ala
 165 170 175

Val Val Ile Lys Pro Ala Ser Asp Thr Pro Val Thr Gly Gly Val Ile
 180 185 190

Pro Ala Arg Ile Phe Glu Glu Ala Gly Val Pro Ala Gly Val Ile Ser
 195 200 205

Thr Val Ala Gly Ala Gly Ser Glu Ile Gly Asp His Phe Val Thr His
 210 215 220

Ala Val Pro Lys Leu Ile Ser Phe Thr Gly Ser Thr Pro Val Gly Arg
 225 230 235 240

Arg Val Gly Glu Leu Ala Ile Asn Gly Gly Pro Met Lys Thr Val Ala
 245 250 255

Leu Glu Leu Gly Gly Asn Ala Pro Phe Val Val Leu Ala Asp Ala Asp
 260 265 270

Ile Asp Ala Ala Ala Gln Ala Ala Ala Val Gly Ala Phe Leu His Gln
 275 280 285

Gly Gln Ile Cys Met Ser Ile Asn Arg Val Ile Val Asp Ala Ala Val
 290 295 300

His Asp Glu Phe Leu Glu Lys Phe Val Glu Ala Val Lys Asn Ile Pro
 305 310 315 320
 Thr Gly Asp Pro Ser Ala Glu Gly Thr Leu Val Gly Pro Val Ile Asn
 325 330 335
 Asp Ser Gln Leu Ser Gly Leu Lys Glu Lys Ile Glu Leu Ala Lys Lys
 340 345 350
 Glu Gly Ala Thr Val Gln Val Glu Gly Pro Ile Glu Gly Arg Leu Val
 355 360 365
 His Pro His Val Phe Ser Asp Val Thr Ser Asp Met Glu Ile Ala Arg
 370 375 380
 Glu Glu Ile Phe Gly Pro Leu Ile Ser Val Leu Lys Ala Asp Asp Glu
 385 390 395 400
 Ala His Ala Ala Glu Leu Ala Asn Ala Ser Asp Phe Gly Leu Ser Ala
 405 410 415
 Ala Val Trp Ser Lys Asp Ile Asp Arg Ala Ala Gln Phe Ala Leu Gln
 420 425 430
 Ile Asp Ser Gly Met Val His Ile Asn Asp Leu Thr Val Asn Asp Glu
 435 440 445
 Pro His Val Met Phe Gly Gly Ser Lys Asn Ser Gly Leu Gly Arg Phe
 450 455 460
 Asn Gly Asp Trp Ala Ile Glu Glu Phe Thr Thr Asp Arg Trp Ile Gly
 465 470 475 480
 Ile Lys Arg Ser

<210> 229
 <211> 2034
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(2011)
 <223> RXN00868

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 Met Ala Glu Thr Lys
 1 5
 aga atg aca gtt agc cag gca ctg gtt gaa ttc ctt ggt cac cag tgg 163
 Arg Met Thr Val Ser Gln Ala Leu Val Glu Phe Leu Gly His Gln Trp
 10 15 20
 act gtc gac ggc gat atc cgc gag cgc acc att cca ggc atg ttc gga 211
 Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile Pro Gly Met Phe Gly

25						30						35						
att	ttc	gga	cac	gga	aac	gtt	gct	ggc	att	ggc	cag	gca	ctc	aag	cag	259		
Ile	Phe	Gly	His	Gly	Asn	Val	Ala	Gly	Ile	Gly	Gln	Ala	Leu	Lys	Gln			
		40					45					50						
tac	aac	gtt	gaa	caa	cct	gag	ctc	atg	ccg	tac	tac	cag	gct	cgt	aat	307		
Tyr	Asn	Val	Glu	Gln	Pro	Glu	Leu	Met	Pro	Tyr	Tyr	Gln	Ala	Arg	Asn			
	55					60					65							
gag	cag	gcg	atg	gtg	cac	cag	tct	gtt	gga	tat	gca	cgc	atg	cac	cgc	355		
Glu	Gln	Ala	Met	Val	His	Gln	Ser	Val	Gly	Tyr	Ala	Arg	Met	His	Arg			
	70				75					80					85			
cgt	cgt	ggc	aca	tac	gca	tct	gcc	gca	tct	gtt	gga	ccc	ggc	gcg	acc	403		
Arg	Arg	Gly	Thr	Tyr	Ala	Ser	Ala	Ala	Ser	Val	Gly	Pro	Gly	Ala	Thr			
				90					95					100				
aac	ctg	tta	acc	ggg	gcg	gct	ctt	gct	acc	acc	aac	cgt	ttg	cca	gcg	451		
Asn	Leu	Leu	Thr	Gly	Ala	Ala	Leu	Ala	Thr	Thr	Asn	Arg	Leu	Pro	Ala			
			105					110					115					
ttg	ctg	ctg	cct	agt	gat	act	ttt	gcc	acc	cgc	gtg	gcg	gat	cca	gtg	499		
Leu	Leu	Leu	Pro	Ser	Asp	Thr	Phe	Ala	Thr	Arg	Val	Ala	Asp	Pro	Val			
		120					125					130						
ttg	cag	cag	ttg	gag	cag	cca	tgg	gat	atc	ggg	ctg	acg	gtt	aat	gat	547		
Leu	Gln	Gln	Leu	Glu	Gln	Pro	Trp	Asp	Ile	Gly	Leu	Thr	Val	Asn	Asp			
	135					140					145							
gct	ttc	cgc	cct	gtg	tct	aag	ttc	ttt	gat	cgg	gtg	cag	cgc	ccg	gag	595		
Ala	Phe	Arg	Pro	Val	Ser	Lys	Phe	Phe	Asp	Arg	Val	Gln	Arg	Pro	Glu			
	150				155					160					165			
cag	ttg	ttc	tct	att	gcg	ttg	gct	gcg	atg	cgt	gtg	ttg	act	gat	ccc	643		
Gln	Leu	Phe	Ser	Ile	Ala	Leu	Ala	Ala	Met	Arg	Val	Leu	Thr	Asp	Pro			
				170					175					180				
gca	gaa	acc	ggg	gcg	gtc	acc	att	gcg	ctt	cca	gaa	gat	gtg	cag	gct	691		
Ala	Glu	Thr	Gly	Ala	Val	Thr	Ile	Ala	Leu	Pro	Glu	Asp	Val	Gln	Ala			
			185					190					195					
gaa	atg	ctc	gat	gtg	ccg	gtg	gag	ttc	ttg	cag	gat	cgt	gag	tgg	cac	739		
Glu	Met	Leu	Asp	Val	Pro	Val	Glu	Phe	Leu	Gln	Asp	Arg	Glu	Trp	His			
		200					205					210						
att	agg	cgc	cca	cgt	cca	gag	cgt	gct	gcg	ttg	gct	cgt	gcg	att	gaa	787		
Ile	Arg	Arg	Pro	Arg	Pro	Glu	Arg	Ala	Ala	Leu	Ala	Arg	Ala	Ile	Glu			
	215					220					225							
gtc	atc	aaa	aac	gct	aag	aat	ccg	atg	atc	att	gct	ggg	ggc	gga	gtg	835		
Val	Ile	Lys	Asn	Ala	Lys	Asn	Pro	Met	Ile	Ile	Ala	Gly	Gly	Gly	Val			
	230				235					240					245			
ttg	tac	tcc	gat	gcg	gaa	acg	cag	ctg	cag	gca	ctt	gtg	gag	cag	act	883		
Leu	Tyr	Ser	Asp	Ala	Glu	Thr	Gln	Leu	Gln	Ala	Leu	Val	Glu	Gln	Thr			
				250					255					260				
ggc	att	ccag	gtg	ggg	acc	tcc	caa	gct	ggg	ggg	ggc	gtg	ttg	gcg	tgg	931		
Gly	Ile	Pro	Val	Gly	Thr	Ser	Gln	Ala	Gly	Gly	Gly	Val	Leu	Ala	Trp			
			265					270					275					

gat cat gca caa aac tta ggt ggt gtg ggt gcc acc gga acg ttg gct Asp His Ala Gln Asn Leu Gly Gly Val Gly Ala Thr Gly Thr Leu Ala 280 285 290	979
gcc aac cgc att gcg ggt gat gct gat gtg atc atc ggt atc ggt act Ala Asn Arg Ile Ala Gly Asp Ala Asp Val Ile Ile Gly Ile Gly Thr 295 300 305	1027
cgt tac agc gat ttc acc acc gca tct cgc act gcg ttc caa aac cct Arg Tyr Ser Asp Phe Thr Thr Ala Ser Arg Thr Ala Phe Gln Asn Pro 310 315 320 325	1075
gat gtc acc ttc atc aac atc aat gtt gct tcc ttc gat gct tac aag Asp Val Thr Phe Ile Asn Ile Asn Val Ala Ser Phe Asp Ala Tyr Lys 330 335 340	1123
cat ggc act cag ttg cct gtg att gca gat gca cgc gag gca att gtg His Gly Thr Gln Leu Pro Val Ile Ala Asp Ala Arg Glu Ala Ile Val 345 350 355	1171
gag ctt gct gaa gcc ctg cag gga ttc acc gtg gca gag gat tac gcg Glu Leu Ala Glu Ala Leu Gln Gly Phe Thr Val Ala Glu Asp Tyr Ala 360 365 370	1219
cag cgc atc gcg aag gaa aag gct gcg tgg gac gca gaa gta gat aag Gln Arg Ile Ala Lys Glu Lys Ala Ala Trp Asp Ala Glu Val Asp Lys 375 380 385	1267
tct ttt gcc ccc tcc ggt ctt gcg ctg cct gga cag ccg gag atc atc Ser Phe Ala Pro Ser Gly Leu Ala Leu Pro Gly Gln Pro Glu Ile Ile 390 395 400 405	1315
ggc gcg gtg cag gcg tcg aca agc gaa aaa gac gtc att gtg cag gcc Gly Ala Val Gln Ala Ser Thr Ser Glu Lys Asp Val Ile Val Gln Ala 410 415 420	1363
gct gga tcc ttg cct ggt gac ctg cac aag ctg tgg cgt gtg cgc gat Ala Gly Ser Leu Pro Gly Asp Leu His Lys Leu Trp Arg Val Arg Asp 425 430 435	1411
gcg ctg ggc tac cac gtg gaa tat gcg ttc tcg tgc atg ggc tat gaa Ala Leu Gly Tyr His Val Glu Tyr Ala Phe Ser Cys Met Gly Tyr Glu 440 445 450	1459
atc gcg ggc ggt atc ggc gcg aag cgt gga ctt gat gcc gca ggc gat Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu Asp Ala Ala Gly Asp 455 460 465	1507
gac cgc gac gtg gtg atc atg gtt ggt gat ggg tcc tac ctc atg ctc Asp Arg Asp Val Val Ile Met Val Gly Asp Gly Ser Tyr Leu Met Leu 470 475 480 485	1555
aac act gag ctg gtc acg gcc gtg gca gaa ggt atc aag gtg att gtg Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly Ile Lys Val Ile Val 490 495 500	1603
gtg ctc atc caa aac cac ggt tat gcc tcc atc ggc cac ctg tct gaa Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile Gly His Leu Ser Glu 505 510 515	1651

act gtc ggt tgc cag cgt ttt ggt act tgg tac cgc gaa tat gac gct 1699
 Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr Arg Glu Tyr Asp Ala
 520 525 530

gag gcg aaa aac ttc cag ggc gag cag att ctg cct gtt gac ctg gcg 1747
 Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu Pro Val Asp Leu Ala
 535 540 545

atg aat gca cgc agc tac ggc atg gat gtc att gaa gtg gaa cca agc 1795
 Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile Glu Val Glu Pro Ser
 550 555 560 565

gcg aat gcg atc gag gat ctc aaa gca gcg atg gca acc gcg aag gct 1843
 Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met Ala Thr Ala Lys Ala
 570 575 580

tcg gag aaa tcc acc ttc atc cac atc aac agc gat ccg ttg atc tac 1891
 Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser Asp Pro Leu Ile Tyr
 585 590 595

gca cca gac ggt gct ggt tgg tgg gac gtg ccg gtg tcg gag acg tcc 1939
 Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro Val Ser Glu Thr Ser
 600 605 610

act ctg gat agc acc aac gcg gct cgt gaa gat tac ctg aaa aac caa 1987
 Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp Tyr Leu Lys Asn Gln
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gcc ctc cag cgt ccg ctg ctc ggc taaaccagtt ggctaaacca aaa 2034
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 630 635

<210> 230

<211> 637

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 230

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Leu Gly His Gln Trp Thr Val Asp Gly Asp Ile Arg Glu Arg Thr Ile
20 25 30

Pro Gly Met Phe Gly Ile Phe Gly His Gly Asn Val Ala Gly Ile Gly
35 40 45

Gln Ala Leu Lys Gln Tyr Asn Val Glu Gln Pro Glu Leu Met Pro Tyr
50 55 60

Tyr Gln Ala Arg Asn Glu Gln Ala Met Val His Gln Ser Val Gly Tyr
65 70 75 80

Ala Arg Met His Arg Arg Arg Gly Thr Tyr Ala Ser Ala Ala Ser Val
85 90 95

Gly Pro Gly Ala Thr Asn Leu Leu Thr Gly Ala Ala Leu Ala Thr Thr
100 105 110

Asn Arg Leu Pro Ala Leu Leu Leu Pro Ser Asp Thr Phe Ala Thr Arg

115					120					125					
Val	Ala	Asp	Pro	Val	Leu	Gln	Gln	Leu	Glu	Gln	Pro	Trp	Asp	Ile	Gly
130					135					140					
Leu	Thr	Val	Asn	Asp	Ala	Phe	Arg	Pro	Val	Ser	Lys	Phe	Phe	Asp	Arg
145					150					155					160
Val	Gln	Arg	Pro	Glu	Gln	Leu	Phe	Ser	Ile	Ala	Leu	Ala	Ala	Met	Arg
				165					170					175	
Val	Leu	Thr	Asp	Pro	Ala	Glu	Thr	Gly	Ala	Val	Thr	Ile	Ala	Leu	Pro
			180					185						190	
Glu	Asp	Val	Gln	Ala	Glu	Met	Leu	Asp	Val	Pro	Val	Glu	Phe	Leu	Gln
		195					200					205			
Asp	Arg	Glu	Trp	His	Ile	Arg	Arg	Pro	Arg	Pro	Glu	Arg	Ala	Ala	Leu
		210				215					220				
Ala	Arg	Ala	Ile	Glu	Val	Ile	Lys	Asn	Ala	Lys	Asn	Pro	Met	Ile	Ile
225					230					235					240
Ala	Gly	Gly	Gly	Val	Leu	Tyr	Ser	Asp	Ala	Glu	Thr	Gln	Leu	Gln	Ala
				245					250					255	
Leu	Val	Glu	Gln	Thr	Gly	Ile	Pro	Val	Gly	Thr	Ser	Gln	Ala	Gly	Gly
			260					265					270		
Gly	Val	Leu	Ala	Trp	Asp	His	Ala	Gln	Asn	Leu	Gly	Gly	Val	Gly	Ala
		275					280					285			
Thr	Gly	Thr	Leu	Ala	Ala	Asn	Arg	Ile	Ala	Gly	Asp	Ala	Asp	Val	Ile
		290				295					300				
Ile	Gly	Ile	Gly	Thr	Arg	Tyr	Ser	Asp	Phe	Thr	Thr	Ala	Ser	Arg	Thr
305					310					315					320
Ala	Phe	Gln	Asn	Pro	Asp	Val	Thr	Phe	Ile	Asn	Ile	Asn	Val	Ala	Ser
			325						330					335	
Phe	Asp	Ala	Tyr	Lys	His	Gly	Thr	Gln	Leu	Pro	Val	Ile	Ala	Asp	Ala
			340					345					350		
Arg	Glu	Ala	Ile	Val	Glu	Leu	Ala	Glu	Ala	Leu	Gln	Gly	Phe	Thr	Val
		355					360					365			
Ala	Glu	Asp	Tyr	Ala	Gln	Arg	Ile	Ala	Lys	Glu	Lys	Ala	Ala	Trp	Asp
		370				375					380				
Ala	Glu	Val	Asp	Lys	Ser	Phe	Ala	Pro	Ser	Gly	Leu	Ala	Leu	Pro	Gly
385					390					395					400
Gln	Pro	Glu	Ile	Ile	Gly	Ala	Val	Gln	Ala	Ser	Thr	Ser	Glu	Lys	Asp
			405						410					415	
Val	Ile	Val	Gln	Ala	Ala	Gly	Ser	Leu	Pro	Gly	Asp	Leu	His	Lys	Leu
			420					425					430		
Trp	Arg	Val	Arg	Asp	Ala	Leu	Gly	Tyr	His	Val	Glu	Tyr	Ala	Phe	Ser
		435					440					445			

Cys Met Gly Tyr Glu Ile Ala Gly Gly Ile Gly Ala Lys Arg Gly Leu
 450 455 460
 Asp Ala Ala Gly Asp Asp Arg Asp Val Val Ile Met Val Gly Asp Gly
 465 470 475 480
 Ser Tyr Leu Met Leu Asn Thr Glu Leu Val Thr Ala Val Ala Glu Gly
 485 490 495
 Ile Lys Val Ile Val Val Leu Ile Gln Asn His Gly Tyr Ala Ser Ile
 500 505 510
 Gly His Leu Ser Glu Thr Val Gly Ser Gln Arg Phe Gly Thr Trp Tyr
 515 520 525
 Arg Glu Tyr Asp Ala Glu Ala Lys Asn Phe Gln Gly Glu Gln Ile Leu
 530 535 540
 Pro Val Asp Leu Ala Met Asn Ala Arg Ser Tyr Gly Met Asp Val Ile
 545 550 555 560
 Glu Val Glu Pro Ser Ala Asn Ala Ile Glu Asp Leu Lys Ala Ala Met
 565 570 575
 Ala Thr Ala Lys Ala Ser Glu Lys Ser Thr Phe Ile His Ile Asn Ser
 580 585 590
 Asp Pro Leu Ile Tyr Ala Pro Asp Gly Ala Gly Trp Trp Asp Val Pro
 595 600 605
 Val Ser Glu Thr Ser Thr Leu Asp Ser Thr Asn Ala Ala Arg Glu Asp
 610 615 620
 Tyr Leu Lys Asn Gln Ala Leu Gln Arg Pro Leu Leu Gly
 625 630 635

<210> 231

<211> 1142

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1119)

<223> RXN01143

<400> 231

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 Ile Pro Val Val Thr Thr Leu Met Ala Leu Gly Thr Phe Pro Glu Ser
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cac gag ctg cac atg ggt atg cca ggc atg cat ggc act gtg tcc gct 96
 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
 20 25 30

gtt ggt gca ctg cag cgc agc gac ctg ctg att gct atc ggc tcc cgc 144
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45

ttt gat gac cgc gtc acc ggt gac gtt gac acc ttc gcg cct gac gcc	192
Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala	
50 55 60	
aag atc att cac gcc gac att gat cct gcc gaa atc ggc aag atc aag	240
Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys	
65 70 75 80	
cag gtt gag gtt cca atc gtg ggc gat gcc cgc gaa gtt ctt gct cgt	288
Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg	
85 90 95	
ctg ctg gaa acc acc aag gca agc aag gca gag acc gag gac atc tcc	336
Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser	
100 105 110	
gag tgg gtt gac tac ctc aag ggc ctc aag gca cgt ttc ccg cgt ggc	384
Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly	
115 120 125	
tac gac gag cag cca ggc gat ctg ctg gca cca cag ttt gtc att gaa	432
Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu	
130 135 140	
acc ctg tcc aag gaa gtt ggc ccc gac gca att tac tgc gcc ggc gtt	480
Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val	
145 150 155 160	
ggc cag cac caa atg tgg gca gct cag ttc gtt gac ttt gaa aag cca	528
Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro	
165 170 175	
cgc acc tgg ctc aac tcc ggt gga ctg ggc acc atg ggc tac gca gtt	576
Arg Thr Trp Leu Asn Ser Gly Gly Leu Gly Thr Met Gly Tyr Ala Val	
180 185 190	
cct gcg gcc ctt gga gca aag gct ggc gca cct gac aag gaa gtc tgg	624
Pro Ala Ala Leu Gly Ala Lys Ala Gly Ala Pro Asp Lys Glu Val Trp	
195 200 205	
gct atc gac ggc gac ggc tgt ttc cag atg acc aac cag gaa ctc acc	672
Ala Ile Asp Gly Asp Gly Cys Phe Gln Met Thr Asn Gln Glu Leu Thr	
210 215 220	
acc gcc gca gtt gaa ggt ttc ccc att aag atc gca cta atc aac aac	720
Thr Ala Ala Val Glu Gly Phe Pro Ile Lys Ile Ala Leu Ile Asn Asn	
225 230 235 240	
gga aaa cct ggg gca tgg gtt cgc caa tgg cag acc cta ttc tat gaa	768
Gly Lys Pro Gly Ala Trp Val Arg Gln Trp Gln Thr Leu Phe Tyr Glu	
245 250 255	
gga cgg tac tca aat act aaa ctt cgt aac cag ggc gag tac atg ccc	816
Gly Arg Tyr Ser Asn Thr Lys Leu Arg Asn Gln Gly Glu Tyr Met Pro	
260 265 270	
gac ttt gtt acc ctt tct gag gga ctt ggc tgt gtt gcc atc cgc gtc	864
Asp Phe Val Thr Leu Ser Glu Gly Leu Gly Cys Val Ala Ile Arg Val	
275 280 285	
acc aaa gcg gag gaa gta ctg cca gcc atc caa aag gct cga gag atc	912

Thr Lys Ala Glu Glu Val Leu Pro Ala Ile Gln Lys Ala Arg Glu Ile
 290 295 300
 aac gac cgc cca gta gtc atc gac ttc atc gtc ggt gaa gac gca cag 960
 Asn Asp Arg Pro Val Val Ile Asp Phe Ile Val Gly Glu Asp Ala Gln
 305 310 315 320
 gta tgg cca atg gtg tct gct gga tca tcc aac tcc gat atc cag tac 1008
 Val Trp Pro Met Val Ser Ala Gly Ser Ser Asn Ser Asp Ile Gln Tyr
 325 330 335
 gca ctc gga ttg cgc cca ttc ttt gat ggt gat gaa tct gca gca gaa 1056
 Ala Leu Gly Leu Arg Pro Phe Phe Asp Gly Asp Glu Ser Ala Ala Glu
 340 345 350
 gat cct gcc gac att cac gaa gcc gtc agc gac att gat gcc gcc gtt 1104
 Asp Pro Ala Asp Ile His Glu Ala Val Ser Asp Ile Asp Ala Ala Val
 355 360 365
 gaa tcg acc gag gca taaggagaga cccaagatgg cta 1142
 Glu Ser Thr Glu Ala
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<210> 232

<211> 373

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 232

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 His Glu Leu His Met Gly Met Pro Gly Met His Gly Thr Val Ser Ala
 20 25 30
 Val Gly Ala Leu Gln Arg Ser Asp Leu Leu Ile Ala Ile Gly Ser Arg
 35 40 45
 Phe Asp Asp Arg Val Thr Gly Asp Val Asp Thr Phe Ala Pro Asp Ala
 50 55 60
 Lys Ile Ile His Ala Asp Ile Asp Pro Ala Glu Ile Gly Lys Ile Lys
 65 70 75 80
 Gln Val Glu Val Pro Ile Val Gly Asp Ala Arg Glu Val Leu Ala Arg
 85 90 95
 Leu Leu Glu Thr Thr Lys Ala Ser Lys Ala Glu Thr Glu Asp Ile Ser
 100 105 110
 Glu Trp Val Asp Tyr Leu Lys Gly Leu Lys Ala Arg Phe Pro Arg Gly
 115 120 125
 Tyr Asp Glu Gln Pro Gly Asp Leu Leu Ala Pro Gln Phe Val Ile Glu
 130 135 140
 Thr Leu Ser Lys Glu Val Gly Pro Asp Ala Ile Tyr Cys Ala Gly Val
 145 150 155 160
 Gly Gln His Gln Met Trp Ala Ala Gln Phe Val Asp Phe Glu Lys Pro

165										170					175				
Arg	Thr	Trp	Leu	Asn	Ser	Gly	Gly	Leu	Gly	Thr	Met	Gly	Tyr	Ala	Val				
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Pro	Ala	Ala	Leu	Gly	Ala	Lys	Ala	Gly	Ala	Pro	Asp	Lys	Glu	Val	Trp				
			195				200					205							
Ala	Ile	Asp	Gly	Asp	Gly	Cys	Phe	Gln	Met	Thr	Asn	Gln	Glu	Leu	Thr				
	210					215					220								
Thr	Ala	Ala	Val	Glu	Gly	Phe	Pro	Ile	Lys	Ile	Ala	Leu	Ile	Asn	Asn				
225					230					235				240					
Gly	Lys	Pro	Gly	Ala	Trp	Val	Arg	Gln	Trp	Gln	Thr	Leu	Phe	Tyr	Glu				
				245					250					255					
Gly	Arg	Tyr	Ser	Asn	Thr	Lys	Leu	Arg	Asn	Gln	Gly	Glu	Tyr	Met	Pro				
			260					265					270						
Asp	Phe	Val	Thr	Leu	Ser	Glu	Gly	Leu	Gly	Cys	Val	Ala	Ile	Arg	Val				
		275					280					285							
Thr	Lys	Ala	Glu	Glu	Val	Leu	Pro	Ala	Ile	Gln	Lys	Ala	Arg	Glu	Ile				
	290					295					300								
Asn	Asp	Arg	Pro	Val	Val	Ile	Asp	Phe	Ile	Val	Gly	Glu	Asp	Ala	Gln				
305					310					315					320				
Val	Trp	Pro	Met	Val	Ser	Ala	Gly	Ser	Ser	Asn	Ser	Asp	Ile	Gln	Tyr				
				325					330					335					
Ala	Leu	Gly	Leu	Arg	Pro	Phe	Phe	Asp	Gly	Asp	Glu	Ser	Ala	Ala	Glu				
			340					345					350						
Asp	Pro	Ala	Asp	Ile	His	Glu	Ala	Val	Ser	Asp	Ile	Asp	Ala	Ala	Val				
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Glu	Ser	Thr	Glu	Ala															
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<210> 233

<211> 793

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(793)

<223> RXN01146

<400> 233

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gca	att	gtt	cga	tcg	ctc	gag	gag	ctt	aac	gcc	gac	atc	gtg	ttc	ggt	163
Ala	Ile	Val	Arg	Ser	Leu	Glu	Glu	Leu	Asn	Ala	Asp	Ile	Val	Phe	Gly	

10										15					20					
att	cct	ggt	ggt	gcg	gtg	cta	ccg	gtg	tat	gac	ccg	ctc	tat	tcc	tcc	211				
Ile	Pro	Gly	Gly	Ala	Val	Leu	Pro	Val	Tyr	Asp	Pro	Leu	Tyr	Ser	Ser					
				25					30					35						
aca	aag	gtg	cgc	cac	gtc	ttg	gtg	cgc	cac	gag	cag	ggc	gca	ggc	cac	259				
Thr	Lys	Val	Arg	His	Val	Leu	Val	Arg	His	Glu	Gln	Gly	Ala	Gly	His					
				40					45					50						
gca	gca	acc	ggc	tac	gcg	cag	gtt	act	gga	cgc	gtt	ggc	gtc	tgc	att	307				
Ala	Ala	Thr	Gly	Tyr	Ala	Gln	Val	Thr	Gly	Arg	Val	Gly	Val	Cys	Ile					
				55					60					65						
gca	acc	tct	ggc	cca	gga	gca	acc	aac	ttg	gtt	acc	cca	atc	gct	gat	355				
Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	Thr	Pro	Ile	Ala	Asp					
70					75					80					85					
gca	aac	ttg	gac	tcc	gtt	ccc	atg	gtt	gcc	atc	acc	ggc	cag	gtc	gga	403				
Ala	Asn	Leu	Asp	Ser	Val	Pro	Met	Val	Ala	Ile	Thr	Gly	Gln	Val	Gly					
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agt	ggc	ctg	ctg	ggt	acc	gac	gct	ttc	cag	gaa	gcc	gat	atc	cgc	ggc	451				
Ser	Gly	Leu	Leu	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Ala	Asp	Ile	Arg	Gly					
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atc	acc	atg	cca	gtg	acc	aag	cac	aac	ttc	atg	gtc	acc	aac	cct	aac	499				
Ile	Thr	Met	Pro	Val	Thr	Lys	His	Asn	Phe	Met	Val	Thr	Asn	Pro	Asn					
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gac	att	cca	cag	gca	ttg	gct	gag	gca	ttc	cac	ctc	gcg	att	act	ggt	547				
Asp	Ile	Pro	Gln	Ala	Leu	Ala	Glu	Ala	Phe	His	Leu	Ala	Ile	Thr	Gly					
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cgc	cct	ggc	cct	gtt	ctg	gtg	gat	att	cct	aag	gat	gtc	cag	aac	gct	595				
Arg	Pro	Gly	Pro	Val	Leu	Val	Asp	Ile	Pro	Lys	Asp	Val	Gln	Asn	Ala					
150					155					160					165					
gaa	ttg	gat	ttc	gtc	tgg	cca	cca	aag	atc	gac	ctg	cca	ggc	tac	cgc	643				
Glu	Leu	Asp	Phe	Val	Trp	Pro	Pro	Lys	Ile	Asp	Leu	Pro	Gly	Tyr	Arg					
				170					175					180						
cca	gtt	tca	aca	cca	cat	gct	cgc	cag	atc	gag	cag	gca	gtc	aag	ctg	691				
Pro	Val	Ser	Thr	Pro	His	Ala	Arg	Gln	Ile	Glu	Gln	Ala	Val	Lys	Leu					
				185					190					195						
atc	ggt	gag	gcc	aag	aag	ccc	gtc	ctt	tac	gtt	ggt	ggt	ggc	gta	atc	739				
Ile	Gly	Glu	Ala	Lys	Lys	Pro	Val	Leu	Tyr	Val	Gly	Gly	Gly	Val	Ile					
				200					205					210						
aag	gct	gac	gca	cac	gaa	gag	ctt	cgt	gcg	ttc	gct	gag	tac	acc	ggc	787				
Lys	Ala	Asp	Ala	His	Glu	Glu	Leu	Arg	Ala	Phe	Ala	Glu	Tyr	Thr	Gly					
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atc	cca														793					
Ile	Pro																			
230																				

<210> 234

<211> 231

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 234

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Pro Leu Tyr Ser Ser Thr Lys Val Arg His Val Leu Val Arg His Glu
          35           40           45
Gln Gly Ala Gly His Ala Ala Thr Gly Tyr Ala Gln Val Thr Gly Arg
          50           55           60
Val Gly Val Cys Ile Ala Thr Ser Gly Pro Gly Ala Thr Asn Leu Val
          65           70           75           80
Thr Pro Ile Ala Asp Ala Asn Leu Asp Ser Val Pro Met Val Ala Ile
          85           90           95
Thr Gly Gln Val Gly Ser Gly Leu Leu Gly Thr Asp Ala Phe Gln Glu
          100          105          110
Ala Asp Ile Arg Gly Ile Thr Met Pro Val Thr Lys His Asn Phe Met
          115          120          125
Val Thr Asn Pro Asn Asp Ile Pro Gln Ala Leu Ala Glu Ala Phe His
          130          135          140
Leu Ala Ile Thr Gly Arg Pro Gly Pro Val Leu Val Asp Ile Pro Lys
          145          150          155          160
Asp Val Gln Asn Ala Glu Leu Asp Phe Val Trp Pro Pro Lys Ile Asp
          165          170          175
Leu Pro Gly Tyr Arg Pro Val Ser Thr Pro His Ala Arg Gln Ile Glu
          180          185          190
Gln Ala Val Lys Leu Ile Gly Glu Ala Lys Lys Pro Val Leu Tyr Val
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Gly Gly Gly Val Ile Lys Ala Asp Ala His Glu Glu Leu Arg Ala Phe
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Ala Glu Tyr Thr Gly Ile Pro
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<210> 235

<211> 639

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(616)

<223> RXN01144

<400> 235

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                                         Met Ala Asn Ser Asp
                                         1 5

gtc acc cgc cac atc ctg tcc gta ctc gtt cag gac gta gac gga atc 163
Val Thr Arg His Ile Leu Ser Val Leu Val Gln Asp Val Asp Gly Ile
                        10 15 20

att tcc cgc gta tca ggt atg ttc acc cga cgc gca ttc aac ctc gtg 211
Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg Ala Phe Asn Leu Val
                        25 30 35

ttc ctc gtg tct gca aag acc gaa aca cac ggc atc aac cgc atc acg 259
Phe Leu Val Ser Ala Lys Thr Glu Thr His Gly Ile Asn Arg Ile Thr
                        40 45 50

gtt gtt gtc gac gcc gac gag ctc aac att gag cag atc acc aag cag 307
Val Val Val Asp Ala Asp Glu Leu Asn Ile Glu Gln Ile Thr Lys Gln
                        55 60 65

ctc aac aag ctg atc ccc gtg ctc aaa gtc gtg cga ctt gat gaa gag 355
Leu Asn Lys Leu Ile Pro Val Leu Lys Val Val Arg Leu Asp Glu Glu
                        70 75 80 85

acc act atc gcc cgc gca atc atg ctg gtt aag gtc tct gcg gac agc 403
Thr Thr Ile Ala Arg Ala Ile Met Leu Val Lys Val Ser Ala Asp Ser
                        90 95 100

acc aac cgt ccg cag atc gtc gac gcc gcg aac atc ttc cgc gcc cga 451
Thr Asn Arg Pro Gln Ile Val Asp Ala Ala Asn Ile Phe Arg Ala Arg
                        105 110 115

gtc gtc gac gtg gct cca gac tct gtg gtt att gaa tcc aca ggc acc 499
Val Val Asp Val Ala Pro Asp Ser Val Val Ile Glu Ser Thr Gly Thr
                        120 125 130

cca ggc aag ctc cgc gca ctg ctt gac gtg atg gaa cca ttc gga atc 547
Pro Gly Lys Leu Arg Ala Leu Leu Asp Val Met Glu Pro Phe Gly Ile
                        135 140 145

cgc gaa ctg atc caa tcc gga cag att gca ctc aac cgc ggt ccg aag 595
Arg Glu Leu Ile Gln Ser Gly Gln Ile Ala Leu Asn Arg Gly Pro Lys
                        150 155 160 165

acc atg gct ccg gcc aag atc taaacagcaa ttaatctgat tgc 639
Thr Met Ala Pro Ala Lys Ile
                        170

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<210> 236

<211> 172

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 236

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Met Ala Asn Ser Asp Val Thr Arg His Ile Leu Ser Val Leu Val Gln
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Asp Val Asp Gly Ile Ile Ser Arg Val Ser Gly Met Phe Thr Arg Arg

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20					25					30					
Ala	Phe	Asn	Leu	Val	Phe	Leu	Val	Ser	Ala	Lys	Thr	Glu	Thr	His	Gly
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Ile	Asn	Arg	Ile	Thr	Val	Val	Val	Asp	Ala	Asp	Glu	Leu	Asn	Ile	Glu
	50					55					60				
Gln	Ile	Thr	Lys	Gln	Leu	Asn	Lys	Leu	Ile	Pro	Val	Leu	Lys	Val	Val
	65					70					75				80
Arg	Leu	Asp	Glu	Glu	Thr	Thr	Ile	Ala	Arg	Ala	Ile	Met	Leu	Val	Lys
				85					90					95	
Val	Ser	Ala	Asp	Ser	Thr	Asn	Arg	Pro	Gln	Ile	Val	Asp	Ala	Ala	Asn
			100					105					110		
Ile	Phe	Arg	Ala	Arg	Val	Val	Asp	Val	Ala	Pro	Asp	Ser	Val	Val	Ile
		115					120					125			
Glu	Ser	Thr	Gly	Thr	Pro	Gly	Lys	Leu	Arg	Ala	Leu	Leu	Asp	Val	Met
		130				135					140				
Glu	Pro	Phe	Gly	Ile	Arg	Glu	Leu	Ile	Gln	Ser	Gly	Gln	Ile	Ala	Leu
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Asn	Arg	Gly	Pro	Lys	Thr	Met	Ala	Pro	Ala	Lys	Ile				
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<211> 897

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(874)

<223> RXA02474

<400> 237

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				Met	Ser	Lys	Val	Ala	
				1				5	

atg	gtt	acc	ggt	ggt	gca	caa	ggc	atc	ggt	cgt	gga	att	tca	gag	aag	163
Met	Val	Thr	Gly	Gly	Ala	Gln	Gly	Ile	Gly	Arg	Gly	Ile	Ser	Glu	Lys	
			10					15						20		

ctg	gca	gca	gat	ggt	ttc	gat	att	gcc	gta	gcc	gac	ctg	cca	caa	cag	211
Leu	Ala	Ala	Asp	Gly	Phe	Asp	Ile	Ala	Val	Ala	Asp	Leu	Pro	Gln	Gln	
			25					30						35		

gaa	gaa	caa	gct	gca	gag	acc	atc	aag	ttg	att	gaa	gct	gca	ggt	caa	259
Glu	Glu	Gln	Ala	Ala	Glu	Thr	Ile	Lys	Leu	Ile	Glu	Ala	Ala	Gly	Gln	
		40					45					50				

aag	gct	gta	ttc	gtt	gga	tta	gat	gtc	acc	gat	aag	gct	aat	ttc	gac	307
Lys	Ala	Val	Phe	Val	Gly	Leu	Asp	Val	Thr	Asp	Lys	Ala	Asn	Phe	Asp	

55	60	65	
agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta			355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu			
70	75	80	85
gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc			403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr			
	90	95	100
gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt			451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe			
	105	110	115
ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa			499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys			
	120	125	130
ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca			547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro			
	135	140	145
atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc			595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr			
	150	155	160
cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc			643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala			
	170	175	180
tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc			691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala			
	185	190	195
gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag			739
Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu			
	200	205	210
tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta			787
Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val			
	215	220	225
gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc			835
Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr			
	230	235	240
gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc			884
Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn			
	250	255	
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<210> 238

<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 238

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Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
 20 25 30
 Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
 35 40 45
 Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
 50 55 60
 Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65 70 75 80
 Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
 85 90 95
 Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
 100 105 110
 Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
 115 120 125
 Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
 130 135 140
 Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
 145 150 155 160
 Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
 165 170 175
 His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
 180 185 190
 Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
 195 200 205
 Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
 210 215 220
 Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
 225 230 235 240
 Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
 245 250 255

Tyr Asn

<210> 239

<211> 876

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(853)

<223> RXA02453

<400> 239

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Met Lys Ser Ile Phe
1 5
att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt 163
Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
10 15 20
ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc 211
Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
25 30 35
tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc 259
Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
40 45 50
gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc 307
Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
55 60 65
acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg 355
Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
70 75 80 85
ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac 403
Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
90 95 100
gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg 451
Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
105 110 115
cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg 499
Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
120 125 130
tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc 547
Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
135 140 145
gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att 595
Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
150 155 160 165
cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac 643
Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
170 175 180
ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg 691
Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
185 190 195
gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct ccg 739
Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
200 205 210
tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg 787
Trp Ala Lys Gly Lys Val His Gly Val Ser Lys Leu Asp Lys Ala
215 220 225

ctg tat ctc atg aaa tct ctg tgc cct gat cgg gta gcg atg tgt ttt 835
 Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
 230 235 240 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc 876
 Ala Arg Leu Ile Ala Gly
 250

<210> 240

<211> 251

<212> PRT

<213> Corynebacterium glutamicum

<400> 240

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 20 25 30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
 35 40 45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
 50 55 60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65 70 75 80

Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
 85 90 95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
 100 105 110

His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
 115 120 125

Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
 130 135 140

Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
 145 150 155 160

Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
 165 170 175

Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
 180 185 190

Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
 195 200 205

His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
 210 215 220

Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
 225 230 235 240

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				Met	Pro	Lys	Tyr	Ile								5	
				1													
gcc	atg	cag	gta	tcc	gaa	tcc	ggt	gca	ccg	tta	gcc	gcg	aat	ctc	gtg	163	
Ala	Met	Gln	Val	Ser	Glu	Ser	Gly	Ala	Pro	Leu	Ala	Ala	Asn	Leu	Val		
				10				15				20					
caa	cct	gct	ccg	ttg	aaa	tcg	agg	gaa	gtc	cgc	gtg	gaa	atc	gct	gct	211	
Gln	Pro	Ala	Pro	Leu	Lys	Ser	Arg	Glu	Val	Arg	Val	Glu	Ile	Ala	Ala		
				25				30				35					
agt	ggt	gtg	tgc	cat	gca	gat	att	ggc	acg	gca	gca	gca	tcg	ggg	aag	259	
Ser	Gly	Val	Cys	His	Ala	Asp	Ile	Gly	Thr	Ala	Ala	Ala	Ser	Gly	Lys		
				40				45				50					
cac	act	gtt	ttt	cct	gtt	acc	cct	ggt	cat	gag	att	gca	gga	acc	atc	307	
His	Thr	Val	Phe	Pro	Val	Thr	Pro	Gly	His	Glu	Ile	Ala	Gly	Thr	Ile		
				55				60				65					
gcg	gaa	att	ggt	gaa	aac	gta	tct	cgg	tgg	acg	gtt	ggt	gat	cgc	gtt	355	
Ala	Glu	Ile	Gly	Glu	Asn	Val	Ser	Arg	Trp	Thr	Val	Gly	Asp	Arg	Val		
				70				75				80				85	
gca	atc	ggt	tgg	ttt	ggt	ggc	aat	tgc	ggt	gac	tgc	gct	ttt	tgt	cgt	403	
Ala	Ile	Gly	Trp	Phe	Gly	Gly	Asn	Cys	Gly	Asp	Cys	Ala	Phe	Cys	Arg		
				90				95				100					
gca	ggt	gat	cct	gtg	cat	tgc	aga	gag	cgg	aag	att	cct	ggc	gtt	tct	451	
Ala	Gly	Asp	Pro	Val	His	Cys	Arg	Glu	Arg	Lys	Ile	Pro	Gly	Val	Ser		
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tat	gcg	ggt	ggt	tgg	gca	cag	aat	att	gtt	gtt	cca	gcg	gag	gct	ctt	499	
Tyr	Ala	Gly	Gly	Trp	Ala	Gln	Asn	Ile	Val	Val	Pro	Ala	Glu	Ala	Leu		
				120				125				130					
gct	gcg	att	cca	gat	ggc	atg	gac	ttt	tac	gag	ccc	gcc	ccg	atg	ggc	547	
Ala	Ala	Ile	Pro	Asp	Gly	Met	Asp	Phe	Tyr	Glu	Pro	Ala	Pro	Met	Gly		
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tgc	gca	ggt	gtg	aca	aca	ttc	aat	gcg	ttg	cga	aac	ctg	aag	ctg	gat	595	
Cys	Ala	Gly	Val	Thr	Thr	Phe	Asn	Ala	Leu	Arg	Asn	Leu	Lys	Leu	Asp		
				150				155				160				165	

ccc ggt gcg gct gtc gcg gtc ttt gga atc ggc ggt tta gtg cgc cta 643
 Pro Gly Ala Ala Val Ala Val Phe Gly Ile Gly Gly Leu Val Arg Leu
 170 175 180

gct att cag ttt gct gcg aaa atg ggt tat cga acc atc acc atc gcc 691
 Ala Ile Gln Phe Ala Ala Lys Met Gly Tyr Arg Thr Ile Thr Ile Ala
 185 190 195

cgc ggt tta gag cgt gag gag cta gct agg caa ctt ggc gcc aac cac 739
 Arg Gly Leu Glu Arg Glu Glu Leu Ala Arg Gln Leu Gly Ala Asn His
 200 205 210

tac atc gat agc aat gat ctg cac cct ggc cag gcg tta ttt gaa ctt 787
 Tyr Ile Asp Ser Asn Asp Leu His Pro Gly Gln Ala Leu Phe Glu Leu
 215 220 225

ggc ggg gct gac ttg atc ttg tct act gcg tcc acc acg gag cct ctt 835
 Gly Gly Ala Asp Leu Ile Leu Ser Thr Ala Ser Thr Thr Glu Pro Leu
 230 235 240 245

tcg gag ttg tct acc ggt ctt tct att ggc ggg cag cta acc att atc 883
 Ser Glu Leu Ser Thr Gly Leu Ser Ile Gly Gly Gln Leu Thr Ile Ile
 250 255 260

gga gtt gat ggg gga gat atc acc gtt tcg gca gcc caa ttg atg atg 931
 Gly Val Asp Gly Gly Asp Ile Thr Val Ser Ala Ala Gln Leu Met Met
 265 270 275

aac cgt cag atc atc aca ggt cac ctc act gga agt gcg aat gac acg 979
 Asn Arg Gln Ile Ile Thr Gly His Leu Thr Gly Ser Ala Asn Asp Thr
 280 285 290

gaa cag act atg aaa ttt gct cat ctc cat ggc gtg aaa ccg ctt att 1027
 Glu Gln Thr Met Lys Phe Ala His Leu His Gly Val Lys Pro Leu Ile
 295 300 305

gaa cgg atg cct ctc gat caa gcc aac gag gct att gca cgt att tca 1075
 Glu Arg Met Pro Leu Asp Gln Ala Asn Glu Ala Ile Ala Arg Ile Ser
 310 315 320 325

gct ggt aaa cca cgt ttc cgt att gtc ttg gag ccg aat tca 1117
 Ala Gly Lys Pro Arg Phe Arg Ile Val Leu Glu Pro Asn Ser
 330 335

taatgccaac agcaagccca att 1140

<210> 242

<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 242

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 20 25 30

Val Glu Ile Ala Ala Ser Gly Val Cys His Ala Asp Ile Gly Thr Ala
 35 40 45

$\langle 210 \rangle$	243
$\langle 211 \rangle$	1665

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1642)

<223> RXA02737

<400> 243

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acacatcttt cattaaagaa aggatcgtga cactaccatc gtg agc aca aac acg 115
                               Val Ser Thr Asn Thr
                               1 5
acc ccc tcc agc tgg aca aac cca ctg cgc gac ccg cag gat aaa cga 163
Thr Pro Ser Ser Trp Thr Asn Pro Leu Arg Asp Pro Gln Asp Lys Arg
                               10 15 20
ctc ccc cgc atc gct ggc cct tcc ggc atg gtg atc ttc ggt gtc act 211
Leu Pro Arg Ile Ala Gly Pro Ser Gly Met Val Ile Phe Gly Val Thr
                               25 30 35
ggc gac ttg gct cga aag aag ctg ctc ccc gcc att tat gat cta gca 259
Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala Ile Tyr Asp Leu Ala
                               40 45 50
aac cgc gga ttg ctg ccc cca gga ttc tcg ttg gta ggt tac ggc cgc 307
Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu Val Gly Tyr Gly Arg
                               55 60 65
cgc gaa tgg tcc aaa gaa gac ttt gaa aaa tac gta cgc gat gcc gca 355
Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr Val Arg Asp Ala Ala
                               70 75 80 85
agt gct ggt gct cgt acg gaa ttc cgt gaa aat gtt tgg gag cgc ctc 403
Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn Val Trp Glu Arg Leu
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gcc gag ggt atg gaa ttt gtt cgc ggc aac ttt gat gat gat gca gct 451
Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe Asp Asp Asp Ala Ala
                               105 110 115
ttc gac aac ctc gct gca aca ctc aag cgc atc gac aaa acc cgc ggc 499
Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile Asp Lys Thr Arg Gly
                               120 125 130
acc gcc ggc aac tgg gct tac tac ctg tcc att cca cca gat tcc ttc 547
Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile Pro Pro Asp Ser Phe
                               135 140 145
aca gcg gtc tgc cac cag ctg gag cgt tcc ggc atg gct gaa tcc acc 595
Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly Met Ala Glu Ser Thr
                               150 155 160 165
gaa gaa gca tgg cgc cgc gtg atc atc gag aag cct ttc ggc cac aac 643
Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys Pro Phe Gly His Asn
                               170 175 180
ctc gaa tcc gca cac gag ctc aac cag ctg gtc aac gca gtc ttc cca 691
Leu Glu Ser Ala His Glu Leu Asn Gln Leu Val Asn Ala Val Phe Pro

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Glu Ser Ser Val Phe Arg Ile Asp His Tyr Leu Gly Lys Glu Thr Val												
200	205				210							
caa aac atc ctg gct ctg cgt ttt gct aac cag ctg ttt gag cca ctg	787											
Gln Asn Ile Leu Ala Leu Arg Phe Ala Asn Gln Leu Phe Glu Pro Leu												
215	220				225							
tgg aac tcc aac tac gtt gac cac gtc cag atc acc atg gct gaa gat	835											
Trp Asn Ser Asn Tyr Val Asp His Val Gln Ile Thr Met Ala Glu Asp												
230	235				240				245			
att ggc ttg ggt gga cgt gct ggt tac tac gac ggc atc ggc gca gcc	883											
Ile Gly Leu Gly Gly Arg Ala Gly Tyr Tyr Asp Gly Ile Gly Ala Ala												
250	255				260							
cgc gac gtc atc cag aac cac ctg atc cag ctc ttg gct ctg gtt gcc	931											
Arg Asp Val Ile Gln Asn His Leu Ile Gln Leu Leu Ala Leu Val Ala												
265	270				275							
atg gaa gaa cca att tct ttc gtg cca gcg cag ctg cag gca gaa aag	979											
Met Glu Glu Pro Ile Ser Phe Val Pro Ala Gln Leu Gln Ala Glu Lys												
280	285				290							
atc aag gtg ctc tct gcg aca aag ccg tgc tac cca ttg gat aaa acc	1027											
Ile Lys Val Leu Ser Ala Thr Lys Pro Cys Tyr Pro Leu Asp Lys Thr												
295	300				305							
tcc gct cgt ggt cag tac gct gcc ggt tgg cag ggc tct gag tta gtc	1075											
Ser Ala Arg Gly Gln Tyr Ala Ala Gly Trp Gln Gly Ser Glu Leu Val												
310	315				320				325			
aag gga ctt cgc gaa gaa gat ggc ttc aac cct gag tcc acc act gag	1123											
Lys Gly Leu Arg Glu Glu Asp Gly Phe Asn Pro Glu Ser Thr Thr Glu												
330	335				340							
act ttt gcg gct tgt acc tta gag atc acg tct cgt cgc tgg gct ggt	1171											
Thr Phe Ala Ala Cys Thr Leu Glu Ile Thr Ser Arg Arg Trp Ala Gly												
345	350				355							
gtg ccg ttc tac ctg cgc acc ggt aag cgt ctt ggt cgc cgt gtt act	1219											
Val Pro Phe Tyr Leu Arg Thr Gly Lys Arg Leu Gly Arg Arg Val Thr												
360	365				370							
gag att gcc gtg gtg ttt aaa gac gca cca cac cag cct ttc gac ggc	1267											
Glu Ile Ala Val Val Phe Lys Asp Ala Pro His Gln Pro Phe Asp Gly												
375	380				385							
gac atg act gta tcc ctt ggc caa aac gcc atc gtg att cgc gtg cag	1315											
Asp Met Thr Val Ser Leu Gly Gln Asn Ala Ile Val Ile Arg Val Gln												
390	395				400				405			
cct gat gaa ggt gtg ctc atc cgc ttc ggt tcc aag gtt cca ggt tct	1363											
Pro Asp Glu Gly Val Leu Ile Arg Phe Gly Ser Lys Val Pro Gly Ser												
410	415				420							
gcc atg gaa gtc cgt gac gtc aac atg gac ttc tcc tac tca gaa tcc	1411											
Ala Met Glu Val Arg Asp Val Asn Met Asp Phe Ser Tyr Ser Glu Ser												
425	430				435							

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ttc act gaa gaa tca cct gaa gca tac gag cgc ctc att ttg gat gcg 1459
Phe Thr Glu Glu Ser Pro Glu Ala Tyr Glu Arg Leu Ile Leu Asp Ala
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ctg tta gat gaa tcc agc ctc ttc cct acc aac gag gaa gtg gaa ctg 1507
Leu Leu Asp Glu Ser Ser Leu Phe Pro Thr Asn Glu Glu Val Glu Leu
      455                      460                      465

agc tgg aag att ctg gat cca att ctt gaa gca tgg gat gcc gat gga 1555
Ser Trp Lys Ile Leu Asp Pro Ile Leu Glu Ala Trp Asp Ala Asp Gly
      470                      475                      480                      485

gaa cca gag gat tac cca gcg ggt acg tgg ggt cca aag agc gct gat 1603
Glu Pro Glu Asp Tyr Pro Ala Gly Thr Trp Gly Pro Lys Ser Ala Asp
      490                      495                      500

gaa atg ctt tcc cgc aac ggt cac acc tgg cgc agg cca taatttaggg 1652
Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg Arg Pro
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<210> 244

<211> 514

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 244

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Ile Phe Gly Val Thr Gly Asp Leu Ala Arg Lys Lys Leu Leu Pro Ala
      35                      40                      45

Ile Tyr Asp Leu Ala Asn Arg Gly Leu Leu Pro Pro Gly Phe Ser Leu
      50                      55                      60

Val Gly Tyr Gly Arg Arg Glu Trp Ser Lys Glu Asp Phe Glu Lys Tyr
      65                      70                      75                      80

Val Arg Asp Ala Ala Ser Ala Gly Ala Arg Thr Glu Phe Arg Glu Asn
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Val Trp Glu Arg Leu Ala Glu Gly Met Glu Phe Val Arg Gly Asn Phe
      100                      105                      110

Asp Asp Asp Ala Ala Phe Asp Asn Leu Ala Ala Thr Leu Lys Arg Ile
      115                      120                      125

Asp Lys Thr Arg Gly Thr Ala Gly Asn Trp Ala Tyr Tyr Leu Ser Ile
      130                      135                      140

Pro Pro Asp Ser Phe Thr Ala Val Cys His Gln Leu Glu Arg Ser Gly
      145                      150                      155                      160

Met Ala Glu Ser Thr Glu Glu Ala Trp Arg Arg Val Ile Ile Glu Lys

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165																170																175															
Pro	Phe	Gly	His	Asn	Leu	Glu	Ser	Ala	His	Glu	Leu	Asn	Gln	Leu	Val																																
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Asn	Ala	Val	Phe	Pro	Glu	Ser	Ser	Val	Phe	Arg	Ile	Asp	His	Tyr	Leu																																
		195						200						205																																	
Gly	Lys	Glu	Thr	Val	Gln	Asn	Ile	Leu	Ala	Leu	Arg	Phe	Ala	Asn	Gln																																
		210						215						220																																	
Leu	Phe	Glu	Pro	Leu	Trp	Asn	Ser	Asn	Tyr	Val	Asp	His	Val	Gln	Ile																																
225							230						235																																		
Thr	Met	Ala	Glu	Asp	Ile	Gly	Leu	Gly	Gly	Arg	Ala	Gly	Tyr	Tyr	Asp																																
			245								250			255																																	
Gly	Ile	Gly	Ala	Ala	Arg	Asp	Val	Ile	Gln	Asn	His	Leu	Ile	Gln	Leu																																
			260								265			270																																	
Leu	Ala	Leu	Val	Ala	Met	Glu	Glu	Pro	Ile	Ser	Phe	Val	Pro	Ala	Gln																																
		275								280			285																																		
Leu	Gln	Ala	Glu	Lys	Ile	Lys	Val	Leu	Ser	Ala	Thr	Lys	Pro	Cys	Tyr																																
290							295						300																																		
Pro	Leu	Asp	Lys	Thr	Ser	Ala	Arg	Gly	Gln	Tyr	Ala	Ala	Gly	Trp	Gln																																
305							310						315			320																															
Gly	Ser	Glu	Leu	Val	Lys	Gly	Leu	Arg	Glu	Glu	Asp	Gly	Phe	Asn	Pro																																
			325								330			335																																	
Glu	Ser	Thr	Thr	Glu	Thr	Phe	Ala	Ala	Cys	Thr	Leu	Glu	Ile	Thr	Ser																																
			340								345			350																																	
Arg	Arg	Trp	Ala	Gly	Val	Pro	Phe	Tyr	Leu	Arg	Thr	Gly	Lys	Arg	Leu																																
		355								360			365																																		
Gly	Arg	Arg	Val	Thr	Glu	Ile	Ala	Val	Val	Phe	Lys	Asp	Ala	Pro	His																																
370							375						380																																		
Gln	Pro	Phe	Asp	Gly	Asp	Met	Thr	Val	Ser	Leu	Gly	Gln	Asn	Ala	Ile																																
385							390						395																																		
Val	Ile	Arg	Val	Gln	Pro	Asp	Glu	Gly	Val	Leu	Ile	Arg	Phe	Gly	Ser																																
			405								410			415																																	
Lys	Val	Pro	Gly	Ser	Ala	Met	Glu	Val	Arg	Asp	Val	Asn	Met	Asp	Phe																																
		420								425			430																																		
Ser	Tyr	Ser	Glu	Ser	Phe	Thr	Glu	Glu	Ser	Pro	Glu	Ala	Tyr	Glu	Arg																																
435							440						445																																		
Leu	Ile	Leu	Asp	Ala	Leu	Leu	Asp	Glu	Ser	Ser	Leu	Phe	Pro	Thr	Asn																																
450							455						460																																		
Glu	Glu	Val	Glu	Leu	Ser	Trp	Lys	Ile	Leu	Asp	Pro	Ile	Leu	Glu	Ala																																
465							470						475																																		
Trp	Asp	Ala	Asp	Gly	Glu	Pro	Glu	Asp	Tyr	Pro	Ala	Gly	Thr	Trp	Gly																																
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Pro Lys Ser Ala Asp Glu Met Leu Ser Arg Asn Gly His Thr Trp Arg
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Arg Pro

<210> 245

<211> 1203

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1180)

<223> RXA02738

<400> 245

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cacagttcaa gaacaattct ttttaaggaaa atttagtttc atg tct cac att gat 115
 Met Ser His Ile Asp
 1 5

gat ctt gca cag ctc ggc act tcc act tgg ctc gac gac ctc tcc cgc 163
 Asp Leu Ala Gln Leu Gly Thr Ser Thr Trp Leu Asp Asp Leu Ser Arg
 10 15 20

gag cgc att act tcc ggc aat ctc agc cag gtt att gag gaa aag tct 211
 Glu Arg Ile Thr Ser Gly Asn Leu Ser Gln Val Ile Glu Glu Lys Ser
 25 30 35

gta gtc ggt gtc acc acc aac cca gct att ttc gca gca gca atg tcc 259
 Val Val Gly Val Thr Thr Asn Pro Ala Ile Phe Ala Ala Ala Met Ser
 40 45 50

aag ggc gat tcc tac gac gct cag atc gca gag ctc aag gcc gct ggc 307
 Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu Leu Lys Ala Ala Gly
 55 60 65

gca tct gtt gac cag gct gtt tac gcc atg agc atc gac gac gtt cgc 355
 Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser Ile Asp Asp Val Arg
 70 75 80 85

aat gct tgt gat ctg ttc acc ggc atc ttc gag tcc tcc aac ggc tac 403
 Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu Ser Ser Asn Gly Tyr
 90 95 100

gac ggc cgc gtg tcc atc gag gtt gac cca cgt atc tct gct gac cgc 451
 Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg Ile Ser Ala Asp Arg
 105 110 115

gac gca acc ctg gct cag gcc aag gag ctg tgg gca aag gtt gat cgt 499
 Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp Ala Lys Val Asp Arg
 120 125 130

cca aac gtc atg atc aag atc cct gca acc cca ggt tct ttg cca gca 547
 Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro Gly Ser Leu Pro Ala
 135 140 145

atc acc gac gct ttg gct gag ggc atc agc gtt aac gtc acc ttg atc 595
 Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val Asn Val Thr Leu Ile
 150 155 160 165

ttc tcc gtt gct cgc tac cgc gag gtc atc gct gcg ttc atc gag ggc 643
 Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala Ala Phe Ile Glu Gly
 170 175 180

atc aag cag gct gct gca aac ggc cac gac gtc tcc aag atc cac tct 691
 Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val Ser Lys Ile His Ser
 185 190 195

gtg gct tcc ttc ttc gtc tcc cgc gtc gac gtt gag atc gac aag cgc 739
 Val Ala Ser Phe Phe Val Ser Arg Val Asp Val Glu Ile Asp Lys Arg
 200 205 210

ctc gag gca atc gga tcc gat gag gct ttg gct ctg cgc ggc aag gca 787
 Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala Leu Arg Gly Lys Ala
 215 220 225

ggc gtt gcc aac gct cag cgc gct tac gct gtg tac aag gag ctt ttc 835
 Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val Tyr Lys Glu Leu Phe
 230 235 240 245

gac gcc gcc gag ctg cct gaa ggt gcc aac act cag cgc cca ctg tgg 883
 Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr Gln Arg Pro Leu Trp
 250 255 260

gca tcc acc ggc gtg aag aac cct gcg tac gct gca act ctt tac gtt 931
 Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala Ala Thr Leu Tyr Val
 265 270 275

tcc gag ctg gct ggt cca aac acc gtc aac acc atg cca gaa ggc acc 979
 Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr Met Pro Glu Gly Thr
 280 285 290

atc gac gcg gtt ctg gag cag ggc aac ctg cac ggt gac acc ctg tcc 1027
 Ile Asp Ala Val Leu Glu Gln Gly Asn Leu His Gly Asp Thr Leu Ser
 295 300 305

aac tcc gcg gca gaa gct gac gct gtg ttc tcc cag ctt gag gct ctg 1075
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 310 315 320 325

ggc gtt gac ttg gca gat gtc ttc cag gtc ctg gag acc gag ggt gtg 1123
 Gly Val Asp Leu Ala Asp Val Phe Gln Val Leu Glu Thr Glu Gly Val
 330 335 340

gac aag ttc gtt gct tct tgg agc gaa ctg ctt gag tcc atg gaa gct 1171
 Asp Lys Phe Val Ala Ser Trp Ser Glu Leu Leu Glu Ser Met Glu Ala
 345 350 355

cgc ctg aag tagaatcagc acgctgcac agt 1203
 Arg Leu Lys
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<210> 246

<211> 360

<212> PRT

<213> Corynebacterium glutamicum

<400> 246

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 35 40 45
 Ala Ala Ala Met Ser Lys Gly Asp Ser Tyr Asp Ala Gln Ile Ala Glu
 50 55 60
 Leu Lys Ala Ala Gly Ala Ser Val Asp Gln Ala Val Tyr Ala Met Ser
 65 70 75 80
 Ile Asp Asp Val Arg Asn Ala Cys Asp Leu Phe Thr Gly Ile Phe Glu
 85 90 95
 Ser Ser Asn Gly Tyr Asp Gly Arg Val Ser Ile Glu Val Asp Pro Arg
 100 105 110
 Ile Ser Ala Asp Arg Asp Ala Thr Leu Ala Gln Ala Lys Glu Leu Trp
 115 120 125
 Ala Lys Val Asp Arg Pro Asn Val Met Ile Lys Ile Pro Ala Thr Pro
 130 135 140
 Gly Ser Leu Pro Ala Ile Thr Asp Ala Leu Ala Glu Gly Ile Ser Val
 145 150 155 160
 Asn Val Thr Leu Ile Phe Ser Val Ala Arg Tyr Arg Glu Val Ile Ala
 165 170 175
 Ala Phe Ile Glu Gly Ile Lys Gln Ala Ala Ala Asn Gly His Asp Val
 180 185 190
 Ser Lys Ile His Ser Val Ala Ser Phe Phe Val Ser Arg Val Asp Val
 195 200 205
 Glu Ile Asp Lys Arg Leu Glu Ala Ile Gly Ser Asp Glu Ala Leu Ala
 210 215 220
 Leu Arg Gly Lys Ala Gly Val Ala Asn Ala Gln Arg Ala Tyr Ala Val
 225 230 235 240
 Tyr Lys Glu Leu Phe Asp Ala Ala Glu Leu Pro Glu Gly Ala Asn Thr
 245 250 255
 Gln Arg Pro Leu Trp Ala Ser Thr Gly Val Lys Asn Pro Ala Tyr Ala
 260 265 270
 Ala Thr Leu Tyr Val Ser Glu Leu Ala Gly Pro Asn Thr Val Asn Thr
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 Gly Asp Thr Leu Ser Asn Ser Ala Ala Glu Ala Asp Ala Val Phe Ser
 305 310 315 320

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Leu Thr Thr Leu Thr 5															
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Leu Ser Pro Glu Leu Gln Ala Leu Thr Val Arg Asn Tyr Pro Ser Asp 20															
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Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr Val Arg Val Leu Ala 35															
25 30															
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Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His Pro Gly Thr Ala Met 50															
40 45															
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Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln Arg Val Met Asn Val 65															
55 60 65															
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Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp Arg Phe Val Leu Ser 85															
70 75 80															
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Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln Leu Tyr Leu Gly Gly 100															
90 95															
ttc ggc ctt gag atg gat gac ctg aag gct ctg cgc acc tgg gat tcc 451															
Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu Arg Thr Trp Asp Ser 115															
105 110															
ttg acc cca gga cac cct gag tac cgc cac acc aag ggc gtt gag atc 499															
Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr Lys Gly Val Glu Ile 130															
120 125															
acc act ggc cct ctt ggc cag ggt ctt gca tct gca gtt ggt atg gcc 547															

Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Leu	Ala	Ser	Ala	Val	Gly	Met	Ala		
135						140					145						
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Met	Ala	Ala	Arg	Arg	Glu	Arg	Gly	Leu	Phe	Asp	Pro	Thr	Ala	Ala	Glu		
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Gly	Glu	Ser	Pro	Phe	Asp	His	His	Ile	Tyr	Val	Ile	Ala	Ser	Asp	Gly		
				170					175					180			
gac	ctg	cag	gaa	ggc	gtc	acc	tct	gag	gca	tcc	tcc	atc	gct	ggc	acc	691	
Asp	Leu	Gln	Glu	Gly	Val	Thr	Ser	Glu	Ala	Ser	Ser	Ile	Ala	Gly	Thr		
			185					190					195				
cag	cag	ctg	ggc	aac	ctc	atc	gtg	ttc	tgg	gat	gac	aac	cgc	atc	tcc	739	
Gln	Gln	Leu	Gly	Asn	Leu	Ile	Val	Phe	Trp	Asp	Asp	Asn	Arg	Ile	Ser		
		200					205					210					
atc	gaa	gac	aac	act	gag	atc	gct	ttc	aac	gag	gac	gtt	gtt	gct	cgt	787	
Ile	Glu	Asp	Asn	Thr	Glu	Ile	Ala	Phe	Asn	Glu	Asp	Val	Val	Ala	Arg		
	215					220					225						
tac	aag	gct	tac	ggc	tgg	cag	acc	att	gag	gtt	gag	gct	ggc	gag	gac	835	
Tyr	Lys	Ala	Tyr	Gly	Trp	Gln	Thr	Ile	Glu	Val	Glu	Ala	Gly	Glu	Asp		
230				235					240					245			
gtt	gca	gca	atc	gaa	gct	gca	gtg	gct	gag	gct	aag	aag	gac	acc	aag	883	
Val	Ala	Ala	Ile	Glu	Ala	Ala	Val	Ala	Glu	Ala	Lys	Lys	Asp	Thr	Lys		
				250					255					260			
cga	cct	acc	ttc	atc	cgc	gtt	cgc	acc	atc	atc	ggc	ttc	cca	gct	cca	931	
Arg	Pro	Thr	Phe	Ile	Arg	Val	Arg	Thr	Ile	Ile	Gly	Phe	Pro	Ala	Pro		
			265					270					275				
act	atg	atg	aac	acc	ggc	gct	gtg	cac	ggc	gct	gct	ctt	ggc	gca	gct	979	
Thr	Met	Met	Asn	Thr	Gly	Ala	Val	His	Gly	Ala	Ala	Leu	Gly	Ala	Ala		
		280					285					290					
gag	gtt	gca	gca	acc	aag	act	gag	ctt	gga	ttc	gat	cct	gag	gct	cac	1027	
Glu	Val	Ala	Ala	Thr	Lys	Thr	Glu	Leu	Gly	Phe	Asp	Pro	Glu	Ala	His		
	295					300					305						
ttc	gcg	atc	gac	gat	gag	gtt	atc	gct	cac	acc	cgc	tcc	ctc	gca	gag	1075	
Phe	Ala	Ile	Asp	Asp	Glu	Val	Ile	Ala	His	Thr	Arg	Ser	Leu	Ala	Glu		
310					315					320					325		
cgc	gct	gca	cag	aag	aag	gct	gca	tgg	cag	gtc	aag	ttc	gat	gag	tgg	1123	
Arg	Ala	Ala	Gln	Lys	Lys	Ala	Ala	Trp	Gln	Val	Lys	Phe	Asp	Glu	Trp		
				330					335					340			
gca	gct	gcc	aac	cct	gag	aac	aag	gct	ctg	ttc	gat	cgc	ctg	aac	tcc	1171	
Ala	Ala	Ala	Asn	Pro	Glu	Asn	Lys	Ala	Leu	Phe	Asp	Arg	Leu	Asn	Ser		
			345					350					355				
cgt	gag	ctt	cca	gcg	ggc	tac	gct	gac	gag	ctc	cca	aca	tgg	gat	gca	1219	
Arg	Glu	Leu	Pro	Ala	Gly	Tyr	Ala	Asp	Glu	Leu	Pro	Thr	Trp	Asp	Ala		
		360				365						370					
gat	gag	aag	ggc	gtc	gca	act	cgt	aag	gct	tcc	gag	gct	gca	ctt	cag	1267	
Asp	Glu	Lys	Gly	Val	Ala	Thr	Arg	Lys	Ala	Ser	Glu	Ala	Ala	Leu	Gln		

375	380	385	
gca ctg ggc aag acc ctt cct gag ctg tgg ggc ggt tcc gct gac ctc Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly Gly Ser Ala Asp Leu 390 395 400 405			1315
gca ggt tcc aac aac acc gtg atc aag ggc tcc cct tcc ttc ggc cct Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser Pro Ser Phe Gly Pro 410 415 420			1363
gag tcc atc tcc acc gag acc tgg tct gct gag cct tac ggc cgt aac Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu Pro Tyr Gly Arg Asn 425 430 435			1411
ctg cac ttc ggt atc cgt gag cac gct atg gga tcc atc ctc aac ggc Leu His Phe Gly Ile Arg Glu His Ala Met Gly Ser Ile Leu Asn Gly 440 445 450			1459
att tcc ctc cac ggt ggc acc cgc cca tac ggc gga acc ttc ctc atc Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly Gly Thr Phe Leu Ile 455 460 465			1507
ttc tcc gac tac atg cgt cct gca gtt cgt ctt gca gct ctc atg gag Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu Ala Ala Leu Met Glu 470 475 480 485			1555
acc gac gct tac tac gtc tgg acc cac gac tcc atc ggt ctg ggc gaa Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser Ile Gly Leu Gly Glu 490 495 500			1603
gat ggc cca acc cac cag cct gtt gaa acc ttg gct gca ctg cgc gcc Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu Ala Ala Leu Arg Ala 505 510 515			1651
atc cca ggt ctg tcc gtc ctg cgt cct gca gat gcg aac gag acc gcc Ile Pro Gly Leu Ser Val Leu Arg Pro Ala Asp Ala Asn Glu Thr Ala 520 525 530			1699
cag gct tgg gct gca gca ctt gag tac aag gaa ggc cct aag ggt ctt Gln Ala Trp Ala Ala Ala Leu Glu Tyr Lys Glu Gly Pro Lys Gly Leu 535 540 545			1747
gca ctg acc cgc cag aac gtt cct gtt ctg gaa ggc acc aag gag aag Ala Leu Thr Arg Gln Asn Val Pro Val Leu Glu Gly Thr Lys Glu Lys 550 555 560 565			1795
gct gct gaa ggc gtt cgc cgc ggt ggc tac gtc ctg gtt gag ggt tcc Ala Ala Glu Gly Val Arg Arg Gly Gly Tyr Val Leu Val Glu Gly Ser 570 575 580			1843
aag gaa acc cca gat gtg atc ctc atg ggc tcc ggc tcc gag gtt cag Lys Glu Thr Pro Asp Val Ile Leu Met Gly Ser Gly Ser Glu Val Gln 585 590 595			1891
ctt gca gtt aac gct gcg aag gct ctg gaa gct gag ggc gtt gca gct Leu Ala Val Asn Ala Ala Lys Ala Leu Glu Ala Glu Gly Val Ala Ala 600 605 610			1939
cgc gtt gtt tcc gtt cct tgc atg gat tgg ttc cag gag cag gac gca Arg Val Val Ser Val Pro Cys Met Asp Trp Phe Gln Glu Gln Asp Ala 615 620 625			1987

gag tac atc gag tcc gtt ctg cct gca gct gtg acc gct cgt gtg tct 2035
 Glu Tyr Ile Glu Ser Val Leu Pro Ala Ala Val Thr Ala Arg Val Ser
 630 635 640 645

gtt gaa gct ggc atc gca atg cct tgg tac cgc ttc ttg ggc acc cag 2083
 Val Glu Ala Gly Ile Ala Met Pro Trp Tyr Arg Phe Leu Gly Thr Gln
 650 655 660

ggc cgt gct gtc tcc ctt gag cac ttc ggt gct tct gcg gat tac cag 2131
 Gly Arg Ala Val Ser Leu Glu His Phe Gly Ala Ser Ala Asp Tyr Gln
 665 670 675

acc ctg ttt gag aag ttc ggc atc acc acc gat gca gtc gtg gca gcg 2179
 Thr Leu Phe Glu Lys Phe Gly Ile Thr Thr Asp Ala Val Val Ala Ala
 680 685 690

gcc aag gac tcc att aac ggt taattgccct gctgttttta gct 2223
 Ala Lys Asp Ser Ile Asn Gly
 695 700

<210> 248

<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 248

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Asn Tyr Pro Ser Asp Trp Ser Asp Val Asp Thr Lys Ala Val Asp Thr
 20 25 30

Val Arg Val Leu Ala Ala Asp Ala Val Glu Asn Cys Gly Ser Gly His
 35 40 45

Pro Gly Thr Ala Met Ser Leu Ala Pro Leu Ala Tyr Thr Leu Tyr Gln
 50 55 60

Arg Val Met Asn Val Asp Pro Gln Asp Thr Asn Trp Ala Gly Arg Asp
 65 70 75 80

Arg Phe Val Leu Ser Cys Gly His Ser Ser Leu Thr Gln Tyr Ile Gln
 85 90 95

Leu Tyr Leu Gly Gly Phe Gly Leu Glu Met Asp Asp Leu Lys Ala Leu
 100 105 110

Arg Thr Trp Asp Ser Leu Thr Pro Gly His Pro Glu Tyr Arg His Thr
 115 120 125

Lys Gly Val Glu Ile Thr Thr Gly Pro Leu Gly Gln Gly Leu Ala Ser
 130 135 140

Ala Val Gly Met Ala Met Ala Ala Arg Arg Glu Arg Gly Leu Phe Asp
 145 150 155 160

Pro Thr Ala Ala Glu Gly Glu Ser Pro Phe Asp His His Ile Tyr Val
 165 170 175

Ile Ala Ser Asp Gly Asp Leu Gln Glu Gly Val Thr Ser Glu Ala Ser
 180 185 190
 Ser Ile Ala Gly Thr Gln Gln Leu Gly Asn Leu Ile Val Phe Trp Asp
 195 200 205
 Asp Asn Arg Ile Ser Ile Glu Asp Asn Thr Glu Ile Ala Phe Asn Glu
 210 215 220
 Asp Val Val Ala Arg Tyr Lys Ala Tyr Gly Trp Gln Thr Ile Glu Val
 225 230 235 240
 Glu Ala Gly Glu Asp Val Ala Ala Ile Glu Ala Ala Val Ala Glu Ala
 245 250 255
 Lys Lys Asp Thr Lys Arg Pro Thr Phe Ile Arg Val Arg Thr Ile Ile
 260 265 270
 Gly Phe Pro Ala Pro Thr Met Met Asn Thr Gly Ala Val His Gly Ala
 275 280 285
 Ala Leu Gly Ala Ala Glu Val Ala Ala Thr Lys Thr Glu Leu Gly Phe
 290 295 300
 Asp Pro Glu Ala His Phe Ala Ile Asp Asp Glu Val Ile Ala His Thr
 305 310 315 320
 Arg Ser Leu Ala Glu Arg Ala Ala Gln Lys Lys Ala Ala Trp Gln Val
 325 330 335
 Lys Phe Asp Glu Trp Ala Ala Ala Asn Pro Glu Asn Lys Ala Leu Phe
 340 345 350
 Asp Arg Leu Asn Ser Arg Glu Leu Pro Ala Gly Tyr Ala Asp Glu Leu
 355 360 365
 Pro Thr Trp Asp Ala Asp Glu Lys Gly Val Ala Thr Arg Lys Ala Ser
 370 375 380
 Glu Ala Ala Leu Gln Ala Leu Gly Lys Thr Leu Pro Glu Leu Trp Gly
 385 390 395 400
 Gly Ser Ala Asp Leu Ala Gly Ser Asn Asn Thr Val Ile Lys Gly Ser
 405 410 415
 Pro Ser Phe Gly Pro Glu Ser Ile Ser Thr Glu Thr Trp Ser Ala Glu
 420 425 430
 Pro Tyr Gly Arg Asn Leu His Phe Gly Ile Arg Glu His Ala Met Gly
 435 440 445
 Ser Ile Leu Asn Gly Ile Ser Leu His Gly Gly Thr Arg Pro Tyr Gly
 450 455 460
 Gly Thr Phe Leu Ile Phe Ser Asp Tyr Met Arg Pro Ala Val Arg Leu
 465 470 475 480
 Ala Ala Leu Met Glu Thr Asp Ala Tyr Tyr Val Trp Thr His Asp Ser
 485 490 495
 Ile Gly Leu Gly Glu Asp Gly Pro Thr His Gln Pro Val Glu Thr Leu

500										505					510						
Ala	Ala	Leu	Arg	Ala	Ile	Pro	Gly	Leu	Ser	Val	Leu	Arg	Pro	Ala	Asp						
		515					520					525									
Ala	Asn	Glu	Thr	Ala	Gln	Ala	Trp	Ala	Ala	Ala	Leu	Glu	Tyr	Lys	Glu						
	530					535					540										
Gly	Pro	Lys	Gly	Leu	Ala	Leu	Thr	Arg	Gln	Asn	Val	Pro	Val	Leu	Glu						
545					550					555					560						
Gly	Thr	Lys	Glu	Lys	Ala	Ala	Glu	Gly	Val	Arg	Arg	Gly	Gly	Tyr	Val						
				565					570					575							
Leu	Val	Glu	Gly	Ser	Lys	Glu	Thr	Pro	Asp	Val	Ile	Leu	Met	Gly	Ser						
			580					585					590								
Gly	Ser	Glu	Val	Gln	Leu	Ala	Val	Asn	Ala	Ala	Lys	Ala	Leu	Glu	Ala						
		595					600					605									
Glu	Gly	Val	Ala	Ala	Arg	Val	Val	Ser	Val	Pro	Cys	Met	Asp	Trp	Phe						
	610					615					620										
Gln	Glu	Gln	Asp	Ala	Glu	Tyr	Ile	Glu	Ser	Val	Leu	Pro	Ala	Ala	Val						
625					630					635					640						
Thr	Ala	Arg	Val	Ser	Val	Glu	Ala	Gly	Ile	Ala	Met	Pro	Trp	Tyr	Arg						
				645					650					655							
Phe	Leu	Gly	Thr	Gln	Gly	Arg	Ala	Val	Ser	Leu	Glu	His	Phe	Gly	Ala						
			660					665					670								
Ser	Ala	Asp	Tyr	Gln	Thr	Leu	Phe	Glu	Lys	Phe	Gly	Ile	Thr	Thr	Asp						
		675					680					685									
Ala	Val	Val	Ala	Ala	Ala	Lys	Asp	Ser	Ile	Asn	Gly										
	690					695					700										

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<211> 793

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (48)..(770)

<223> RXA00965

<400> 249

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															Met	Thr	Thr
															1		
ttc	cac	gat	ctt	ccg	ctg	gag	gag	cgg	ctg	aca	ctg	gcc	agg	ttg	ggc	104	
Phe	His	Asp	Leu	Pro	Leu	Glu	Glu	Arg	Leu	Thr	Leu	Ala	Arg	Leu	Gly		
	5					10					15						
aca	tcc	cac	tac	tcc	cgt	cag	ctc	tcc	ctc	gtg	gac	aac	gct	gag	ttc	152	
Thr	Ser	His	Tyr	Ser	Arg	Gln	Leu	Ser	Leu	Val	Asp	Asn	Ala	Glu	Phe		
	20				25					30				35			

ggc gag cat tcc ctg cta gaa ggg tgg act cgt tcc cac ctc att gcc 200
 Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His Leu Ile Ala
 40 45 50

cac gtg gca tac aac gcc atc gca ctg tgc aac ctc atg cac tgg gca 248
 His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met His Trp Ala
 55 60 65

aat act ggt gag gaa acc cca atg tac gtg tgc cca gaa gcg cgc aac 296
 Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu Ala Arg Asn
 70 75 80

gag gaa att gcc tac ggt tcc acg ctc aat ccc gat gcg ttg cgt aac 344
 Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala Leu Arg Asn
 85 90 95

ctg cat gaa cac tcc gtc gca cgc ctg gac gtg gct tgg cgt gaa acg 392
 Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp Arg Glu Thr
 100 105 110 115

tct gaa gat gct tgg tca cac gag gtt ctg aca gct cag gga cgc act 440
 Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln Gly Arg Thr
 120 125 130

gtc cca gct agt gaa aca ttg tgg atg cgt tcc cgc gaa gtc tgg atc 488
 Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu Val Trp Ile
 135 140 145

cac gca gtt gac ctc ggt gca gtg gca acc ttt ggc gac atc cca gag 536
 His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp Ile Pro Glu
 150 155 160

gtc atc ctg cgc acc tta gct gca gaa atc aca caa aag tgg aca agc 584
 Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys Trp Thr Ser
 165 170 175

caa gga gcc ggc gag gga ctt gtg ctt ctc gac gag ccc tcc agc act 632
 Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro Ser Ser Thr
 180 185 190 195

cgc tac ccc gcc gcc cca ggg cag gac gag gta gta gtg tcc ggt agc 680
 Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val Ser Gly Ser
 200 205 210

ctt gca ggc att gtt cgc tac gcc gct ggc cgc ggt tcc gat gga gtc 728
 Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser Asp Gly Val
 215 220 225

act tct tcc act gga gag gtt cca gag cca ccg cgc tgg ctg 770
 Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp Leu
 230 235 240

tagtttccac acattcttaa atg 793

<210> 250

<211> 241

<212> PRT

<213> Corynebacterium glutamicum

<400> 250

Met Thr Thr Phe His Asp Leu Pro Leu Glu Glu Arg Leu Thr Leu Ala
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Arg Leu Gly Thr Ser His Tyr Ser Arg Gln Leu Ser Leu Val Asp Asn
 20 25 30

Ala Glu Phe Gly Glu His Ser Leu Leu Glu Gly Trp Thr Arg Ser His
 35 40 45

Leu Ile Ala His Val Ala Tyr Asn Ala Ile Ala Leu Cys Asn Leu Met
 50 55 60

His Trp Ala Asn Thr Gly Glu Glu Thr Pro Met Tyr Val Ser Pro Glu
 65 70 75 80

Ala Arg Asn Glu Glu Ile Ala Tyr Gly Ser Thr Leu Asn Pro Asp Ala
 85 90 95

Leu Arg Asn Leu His Glu His Ser Val Ala Arg Leu Asp Val Ala Trp
 100 105 110

Arg Glu Thr Ser Glu Asp Ala Trp Ser His Glu Val Leu Thr Ala Gln
 115 120 125

Gly Arg Thr Val Pro Ala Ser Glu Thr Leu Trp Met Arg Ser Arg Glu
 130 135 140

Val Trp Ile His Ala Val Asp Leu Gly Ala Val Ala Thr Phe Gly Asp
 145 150 155 160

Ile Pro Glu Val Ile Leu Arg Thr Leu Ala Ala Glu Ile Thr Gln Lys
 165 170 175

Trp Thr Ser Gln Gly Ala Gly Glu Gly Leu Val Leu Leu Asp Glu Pro
 180 185 190

Ser Ser Thr Arg Tyr Pro Ala Ala Pro Gly Gln Asp Glu Val Val Val
 195 200 205

Ser Gly Ser Leu Ala Gly Ile Val Arg Tyr Ala Ala Gly Arg Gly Ser
 210 215 220

Asp Gly Val Thr Ser Ser Thr Gly Glu Val Pro Glu Pro Pro Arg Trp
 225 230 235 240

Leu

<210> 251

<211> 1575

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1552)

<223> RXN00999

<400> 251

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ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat																115
Met Thr Asn Gly Asp																5
aat ctc gca cag atc ggc gtt gta ggc cta gca gta atg ggc tca aac																163
Asn Leu Ala Gln Ile Gly Val Val Gly Leu Ala Val Met Gly Ser Asn																20
ctc gcc cgc aac ttc gcc cgc aac ggc aac act gtc gct gtc tac aac																211
Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr Val Ala Val Tyr Asn																35
cgc agc act gac aaa acc gac aag ctc atc gcc gat cac ggc tcc gaa																259
Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala Asp His Gly Ser Glu																40
ggc aac ttc atc cct tct gca acc gtc gaa gag ttc gta gca tcc ctg																307
Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu Phe Val Ala Ser Leu																55
gaa aag cca cgc cgc gcc atc atc atg gtt cag gct ggt aac gcc acc																355
Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln Ala Gly Asn Ala Thr																70
gac gca gtc atc aac cag ctg gca gat gcc atg gac gaa ggc gac atc																403
Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met Asp Glu Gly Asp Ile																90
atc atc gac ggc ggc aac gcc ctc tac acc gac acc att cgt cgc gag																451
Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp Thr Ile Arg Arg Glu																105
aag gaa atc tcc gca cgc ggt ctc cac ttc gtc ggt gct ggt atc tcc																499
Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val Gly Ala Gly Ile Ser																120
ggc ggc gaa gaa ggc gca ctc aac ggc cca tcc atc atg cct ggt ggc																547
Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser Ile Met Pro Gly Gly																135
cca gca aag tcc tac gag tcc ctc gga cca ctg ctt gag tcc atc gct																595
Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu Leu Glu Ser Ile Ala																150
gcc aac gtt gac ggc acc cca tgt gtc acc cac atc ggc cca gac ggc																643
Ala Asn Val Asp Gly Thr Pro Cys Val Thr His Ile Gly Pro Asp Gly																170
gcc ggc cac ttc gtc aag atg gtc cac aac ggc atc gag tac gcc gac																691
Ala Gly His Phe Val Lys Met Val His Asn Gly Ile Glu Tyr Ala Asp																185
atg cag gtc atc ggc gag gca tac cac ctt ctc cgc tac gca gca ggc																739
Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu Arg Tyr Ala Ala Gly																200
atg cag ccagct gaa atc gct gag gtt ttc aag gaa tgg aac gca ggc																787
Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys Glu Trp Asn Ala Gly																215

gac ctg gat tcc tac ctc atc gaa atc acc gca gag gtt ctc tcc cag Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala Glu Val Leu Ser Gln 230 235 240 245	835
gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp 265 270 275	931
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala 280 285 290	979
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro 295 300 305	1027
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln 310 315 320 325	1075
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn 345 350 355	1171
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys 360 365 370	1219
atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala 375 380 385	1267
aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu 390 395 400 405	1315
ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val Ile Val Thr Ala Thr 410 415 420	1363
cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr 425 430 435	1411
gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln 440 445 450	1459
cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly 455 460 465	1507

tcc ttc cac acc gag tgg tcc ggc gac cgc tcc gag gtt gaa gct 1552
 Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser Glu Val Glu Ala
 470 475 480

taaaggctct ccttttaaca caa 1575

<210> 252

<211> 484

<212> PRT

<213> Corynebacterium glutamicum

<400> 252

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 1 5 10 15

Val Met Gly Ser Asn Leu Ala Arg Asn Phe Ala Arg Asn Gly Asn Thr
 20 25 30

Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160

Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205

Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220

Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240

Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270
 Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285
 Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460
 Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg Ser
 465 470 475 480
 Glu Val Glu Ala

<210> 253

<211> 1537

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1537)

<223> FRXA00999

<400> 253

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 ttgctgacac cgggctatgc cgtcaagtac gatcaataac atg act aat gga gat 115
 Met Thr Asn Gly Asp

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aat	ctc	gca	cag	atc	ggc	gtt	gta	ggc	cta	gca	gta	atg	ggc	tca	aac	163	
Asn	Leu	Ala	Gln	Ile	Gly	Val	Val	Gly	Leu	Ala	Val	Met	Gly	Ser	Asn		
				10					15					20			
ctc	gcc	cgc	aac	ttc	gcc	cgc	aac	ggc	aac	act	gtc	gct	gtc	tac	aac	211	
Leu	Ala	Arg	Asn	Phe	Ala	Arg	Asn	Gly	Asn	Thr	Val	Ala	Val	Tyr	Asn		
				25					30					35			
cgc	agc	act	gac	aaa	acc	gac	aag	ctc	atc	gcc	gat	cac	ggc	tcc	gaa	259	
Arg	Ser	Thr	Asp	Lys	Thr	Asp	Lys	Leu	Ile	Ala	Asp	His	Gly	Ser	Glu		
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ggc	aac	ttc	atc	cct	tct	gca	acc	gtc	gaa	gag	ttc	gta	gca	tcc	ctg	307	
Gly	Asn	Phe	Ile	Pro	Ser	Ala	Thr	Val	Glu	Glu	Phe	Val	Ala	Ser	Leu		
				55					60					65			
gaa	aag	cca	cgc	cgc	gcc	atc	atc	atg	gtt	cag	gct	ggg	aac	gcc	acc	355	
Glu	Lys	Pro	Arg	Arg	Ala	Ile	Ile	Met	Val	Gln	Ala	Gly	Asn	Ala	Thr		
				70					75					80			
gac	gca	gtc	atc	aac	cag	ctg	gca	gat	gcc	atg	gac	gaa	ggc	gac	atc	403	
Asp	Ala	Val	Ile	Asn	Gln	Leu	Ala	Asp	Ala	Met	Asp	Glu	Gly	Asp	Ile		
				90					95					100			
atc	atc	gac	ggc	ggc	aac	gcc	ctc	tac	acc	gac	acc	att	cgt	cgc	gag	451	
Ile	Ile	Asp	Gly	Gly	Asn	Ala	Leu	Tyr	Thr	Asp	Thr	Ile	Arg	Arg	Glu		
				105					110					115			
aag	gaa	atc	tcc	gca	cgc	ggg	ctc	cac	ttc	gtc	ggg	gct	ggg	atc	tcc	499	
Lys	Glu	Ile	Ser	Ala	Arg	Gly	Leu	His	Phe	Val	Gly	Ala	Gly	Ile	Ser		
				120					125					130			
ggc	ggc	gaa	gaa	ggc	gca	ctc	aac	ggc	cca	tcc	atc	atg	cct	ggg	ggc	547	
Gly	Gly	Glu	Glu	Gly	Ala	Leu	Asn	Gly	Pro	Ser	Ile	Met	Pro	Gly	Gly		
				135					140					145			
cca	gca	aag	tcc	tac	gag	tcc	ctc	gga	cca	ctg	ctt	gag	tcc	atc	gct	595	
Pro	Ala	Lys	Ser	Tyr	Glu	Ser	Leu	Gly	Pro	Leu	Leu	Glu	Ser	Ile	Ala		
				150					155					160			
gcc	aac	gtt	gac	ggc	acc	cca	tgt	gtc	acc	cac	atc	ggc	cca	gac	ggc	643	
Ala	Asn	Val	Asp	Gly	Thr	Pro	Cys	Val	Thr	His	Ile	Gly	Pro	Asp	Gly		
				170					175					180			
gcc	ggc	cac	ttc	gtc	aag	atg	gtc	cac	aac	ggc	atc	gag	tac	gcc	gac	691	
Ala	Gly	His	Phe	Val	Lys	Met	Val	His	Asn	Gly	Ile	Glu	Tyr	Ala	Asp		
				185					190					195			
atg	cag	gtc	atc	ggc	gag	gca	tac	cac	ctt	ctc	cgc	tac	gca	gca	ggc	739	
Met	Gln	Val	Ile	Gly	Glu	Ala	Tyr	His	Leu	Leu	Arg	Tyr	Ala	Ala	Gly		
				200					205					210			
atg	cag	cca	gct	gaa	atc	gct	gag	gtt	ttc	aag	gaa	tgg	aac	gca	ggc	787	
Met	Gln	Pro	Ala	Glu	Ile	Ala	Glu	Val	Phe	Lys	Glu	Trp	Asn	Ala	Gly		
				215					220					225			
gac	ctg	gat	tcc	tac	ctc	atc	gaa	atc	acc	gca	gag	gtt	ctc	tcc	cag	835	
Asp	Leu	Asp	Ser	Tyr	Leu	Ile	Glu	Ile	Thr	Ala	Glu	Val	Leu	Ser	Gln		
				230					235					240			
														245			

gtg gat gct gaa acc ggc aag cca cta atc gac gtc atc gtt gac gct Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp Val Ile Val Asp Ala 250 255 260	883
gca ggt cag aag ggc acc gga cgt tgg acc gtc aag gct gct ctt gat Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val Lys Ala Ala Leu Asp 265 270 275	931
ctg ggt att gct acc acc ggc atc ggc gaa gct gtt ttc gca cgt gca Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala Val Phe Ala Arg Ala 280 285 290	979
ctc tcc ggc gca acc agc cag cgc gct gca gca cag ggc aac cta cct Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala Gln Gly Asn Leu Pro 295 300 305	1027
gca ggt gtc ctc acc gat ctg gaa gca ctt ggc gtg gac aag gca cag Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly Val Asp Lys Ala Gln 310 315 320 325	1075
ttc gtc gaa gac gtt cgc cgt gca ctg tac gca tcc aag ctt gtt gct Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala Ser Lys Leu Val Ala 330 335 340	1123
tac gca cag ggc ttc gac gag atc aag gct ggc tcc gac gag aac aac Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly Ser Asp Glu Asn Asn 345 350 355	1171
tgg gac gtt gac cct cgc gac ctc gct acc atc tgg cgc ggc ggc tgc Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile Trp Arg Gly Gly Cys 360 365 370	1219
atc att cgc gct aag ttc ctc aac cgc atc gtc gaa gca tac gat gca Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val Glu Ala Tyr Asp Ala 375 380 385	1267
aac gct gaa ctt gag tcc ctg ctg ctc gat cct tac ttc aag agc gag Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro Tyr Phe Lys Ser Glu 390 395 400 405	1315
ctc ggc gac ctc atc gat tca tgg cgt cgc gtg att gtc acc gcc acc Leu Gly Asp Leu Ile Asp Ser Trp Arg Val Ile Val Thr Ala Thr 410 415 420	1363
cag ctt ggc ctg cca atc cca gtg ttc gct tcc tcc ctg tcc tac tac Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser Ser Leu Ser Tyr Tyr 425 430 435	1411
gac agc ctg cgt gca gag cgt ctg cca gca gcc ctg atc caa gga cag Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala Leu Ile Gln Gly Gln 440 445 450	1459
cgc gac ttc ttc ggt gcg cac acc tac aag cgc atc gac aag gat ggc Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg Ile Asp Lys Asp Gly 455 460 465	1507
tcc ttc cac acc gag tgg tcc ggc gac cgc Ser Phe His Thr Glu Trp Ser Gly Asp Arg 470 475	1537

<210> 254

<211> 479

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 254

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Val Ala Val Tyr Asn Arg Ser Thr Asp Lys Thr Asp Lys Leu Ile Ala
 35 40 45

Asp His Gly Ser Glu Gly Asn Phe Ile Pro Ser Ala Thr Val Glu Glu
 50 55 60

Phe Val Ala Ser Leu Glu Lys Pro Arg Arg Ala Ile Ile Met Val Gln
 65 70 75 80

Ala Gly Asn Ala Thr Asp Ala Val Ile Asn Gln Leu Ala Asp Ala Met
 85 90 95

Asp Glu Gly Asp Ile Ile Ile Asp Gly Gly Asn Ala Leu Tyr Thr Asp
 100 105 110

Thr Ile Arg Arg Glu Lys Glu Ile Ser Ala Arg Gly Leu His Phe Val
 115 120 125

Gly Ala Gly Ile Ser Gly Gly Glu Glu Gly Ala Leu Asn Gly Pro Ser
 130 135 140

Ile Met Pro Gly Gly Pro Ala Lys Ser Tyr Glu Ser Leu Gly Pro Leu
 145 150 155 160

Leu Glu Ser Ile Ala Ala Asn Val Asp Gly Thr Pro Cys Val Thr His
 165 170 175

Ile Gly Pro Asp Gly Ala Gly His Phe Val Lys Met Val His Asn Gly
 180 185 190

Ile Glu Tyr Ala Asp Met Gln Val Ile Gly Glu Ala Tyr His Leu Leu
 195 200 205

Arg Tyr Ala Ala Gly Met Gln Pro Ala Glu Ile Ala Glu Val Phe Lys
 210 215 220

Glu Trp Asn Ala Gly Asp Leu Asp Ser Tyr Leu Ile Glu Ile Thr Ala
 225 230 235 240

Glu Val Leu Ser Gln Val Asp Ala Glu Thr Gly Lys Pro Leu Ile Asp
 245 250 255

Val Ile Val Asp Ala Ala Gly Gln Lys Gly Thr Gly Arg Trp Thr Val
 260 265 270

Lys Ala Ala Leu Asp Leu Gly Ile Ala Thr Thr Gly Ile Gly Glu Ala
 275 280 285

Val Phe Ala Arg Ala Leu Ser Gly Ala Thr Ser Gln Arg Ala Ala Ala
 290 295 300
 Gln Gly Asn Leu Pro Ala Gly Val Leu Thr Asp Leu Glu Ala Leu Gly
 305 310 315 320
 Val Asp Lys Ala Gln Phe Val Glu Asp Val Arg Arg Ala Leu Tyr Ala
 325 330 335
 Ser Lys Leu Val Ala Tyr Ala Gln Gly Phe Asp Glu Ile Lys Ala Gly
 340 345 350
 Ser Asp Glu Asn Asn Trp Asp Val Asp Pro Arg Asp Leu Ala Thr Ile
 355 360 365
 Trp Arg Gly Gly Cys Ile Ile Arg Ala Lys Phe Leu Asn Arg Ile Val
 370 375 380
 Glu Ala Tyr Asp Ala Asn Ala Glu Leu Glu Ser Leu Leu Leu Asp Pro
 385 390 395 400
 Tyr Phe Lys Ser Glu Leu Gly Asp Leu Ile Asp Ser Trp Arg Arg Val
 405 410 415
 Ile Val Thr Ala Thr Gln Leu Gly Leu Pro Ile Pro Val Phe Ala Ser
 420 425 430
 Ser Leu Ser Tyr Tyr Asp Ser Leu Arg Ala Glu Arg Leu Pro Ala Ala
 435 440 445
 Leu Ile Gln Gly Gln Arg Asp Phe Phe Gly Ala His Thr Tyr Lys Arg
 450 455 460
 Ile Asp Lys Asp Gly Ser Phe His Thr Glu Trp Ser Gly Asp Arg
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<210> 255

<211> 1326

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1303)

<223> RXN02596

<400> 255

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 gaaatttcgg caacgccgaa tgtaagtttag tgtcgaatgc atg acg gaa tcg aaa 115
 Met Thr Glu Ser Lys
 1 5
 aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
 Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
 10 15 20
 gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
 Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
 25 30 35

cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag	259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu	
40 45 50	
acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc	307
Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser	
55 60 65	
aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc	355
Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly	
70 75 80 85	
tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc	403
Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe	
90 95 100	
ccg atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc	451
Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser	
105 110 115	
cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat	499
Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp	
120 125 130	
tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt	547
Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly	
135 140 145	
cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg	595
Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp	
150 155 160 165	
cag act gat cca aag aac ctc cca gcc ggc aac atc acc cgc ctg cca	643
Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn Ile Thr Arg Leu Pro	
170 175 180	
gtt cgc tac aac ttc aac aac cgc tat ttc aac gac acc tac gaa ggc	691
Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn Asp Thr Tyr Glu Gly	
185 190 195	
ctt ccc aca gac ggc tac gcg gca tgg ttg gaa aag atg gca gag cat	739
Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu Lys Met Ala Glu His	
200 205 210	
gag ctt atc gac gtc cgc ctc gac acc gac tgg ttc gac gtt cgc gat	787
Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp Phe Asp Val Arg Asp	
215 220 225	
gac ctc cgc gca agc aac ccc gac gca cct gtg gtc tac acc ggc cca	835
Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val Val Tyr Thr Gly Pro	
230 235 240 245	
ctc gac ctc tac ttc aac tac gca gag ggc aag ctg gga tgg cgc acc	883
Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys Leu Gly Trp Arg Thr	
250 255 260	
ctc gac ttt gaa acc gaa gta gta gaa acc ggt gac ttc caa gga acc	931
Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly Asp Phe Gln Gly Thr	
265 270 275	

cca gtg atg aac tac aac gat gcg gac gta cct ttc acc cgc atc cac 979
 Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro Phe Thr Arg Ile His
 280 285 290

gag ttc cgt cac ttc cac cca gag cgt gat gac agt tac ccc aag gat 1027
 Glu Phe Arg His Phe His Pro Glu Arg Asp Asp Ser Tyr Pro Lys Asp
 295 300 305

aag acc gtc atc atg cgc gag ttc tcc cgt ttc gca gat aac gag gat 1075
 Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe Ala Asp Asn Glu Asp
 310 315 320 325

gag cct tat tac cca atc aac act cca gac gac cga gac atg ctg aag 1123
 Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp Arg Asp Met Leu Lys
 330 335 340

cag tac cgc ctt ctg gct gct gaa gag gct gct aat aat aag gtg ctg 1171
 Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala Asn Asn Lys Val Leu
 345 350 355

ttc ggc ggt cga ctg ggc acg tac cag tac ctc gac atg cac atg gct 1219
 Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu Asp Met His Met Ala
 360 365 370

atc ggt tct gcg ctg agc atg ttt gac aac aag ctg gtg ccg ttc ttt 1267
 Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys Leu Val Pro Phe Phe
 375 380 385

gaa gaa ggc aca ccg cta gag cag gaa cgc gga cac taaaaggaag 1313
 Glu Glu Gly Thr Pro Leu Glu Gln Glu Arg Gly His
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ggcatctccc aca 1326

<210> 256
 <211> 401
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 256
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 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125
 Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140
 Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160
 Thr Ala Lys Gln Trp Gln Thr Asp Pro Lys Asn Leu Pro Ala Gly Asn
 165 170 175
 Ile Thr Arg Leu Pro Val Arg Tyr Asn Phe Asn Asn Arg Tyr Phe Asn
 180 185 190
 Asp Thr Tyr Glu Gly Leu Pro Thr Asp Gly Tyr Ala Ala Trp Leu Glu
 195 200 205
 Lys Met Ala Glu His Glu Leu Ile Asp Val Arg Leu Asp Thr Asp Trp
 210 215 220
 Phe Asp Val Arg Asp Asp Leu Arg Ala Ser Asn Pro Asp Ala Pro Val
 225 230 235 240
 Val Tyr Thr Gly Pro Leu Asp Leu Tyr Phe Asn Tyr Ala Glu Gly Lys
 245 250 255
 Leu Gly Trp Arg Thr Leu Asp Phe Glu Thr Glu Val Val Glu Thr Gly
 260 265 270
 Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp Val Pro
 275 280 285
 Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg Asp Asp
 290 295 300
 Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser Arg Phe
 305 310 315 320
 Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro Asp Asp
 325 330 335
 Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu Ala Ala
 340 345 350
 Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln Tyr Leu
 355 360 365
 Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp Asn Lys
 370 375 380
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His

<210> 257

<211> 512

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(489)

<223> FRXA02596

<400> 257

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Gly	Lys	Leu	Gly	Trp	Arg	Thr	Leu	Asp	Phe	Glu	Thr	Glu	Val	Val	Glu	
		20						25					30			
acc	ggt	gac	ttc	caa	gga	acc	cca	gtg	atg	aac	tac	aac	gat	gcg	gac	144
Thr	Gly	Asp	Phe	Gln	Gly	Thr	Pro	Val	Met	Asn	Tyr	Asn	Asp	Ala	Asp	
		35					40					45				
gta	cct	ttc	acc	cgc	atc	cac	gag	ttc	cgt	cac	ttc	cac	cca	gag	cgt	192
Val	Pro	Phe	Thr	Arg	Ile	His	Glu	Phe	Arg	His	Phe	His	Pro	Glu	Arg	
	50					55					60					
gat	gac	agt	tac	ccc	aag	gat	aag	acc	gtc	atc	atg	cgc	gag	ttc	tcc	240
Asp	Asp	Ser	Tyr	Pro	Lys	Asp	Lys	Thr	Val	Ile	Met	Arg	Glu	Phe	Ser	
65					70					75					80	
cgt	ttc	gca	gat	aac	gag	gat	gag	cct	tat	tac	cca	atc	aac	act	cca	288
Arg	Phe	Ala	Asp	Asn	Glu	Asp	Glu	Pro	Tyr	Tyr	Pro	Ile	Asn	Thr	Pro	
				85				90						95		
gac	gac	cga	gac	atg	ctg	aag	cag	tac	cgc	ctt	ctg	gct	gct	gaa	gag	336
Asp	Asp	Arg	Asp	Met	Leu	Lys	Gln	Tyr	Arg	Leu	Leu	Ala	Ala	Glu	Glu	
		100					105						110			
gct	gct	aat	aat	aag	gtg	ctg	ttc	ggc	ggt	cga	ctg	ggc	acg	tac	cag	384
Ala	Ala	Asn	Asn	Lys	Val	Leu	Phe	Gly	Gly	Arg	Leu	Gly	Thr	Tyr	Gln	
		115					120					125				
tac	ctc	gac	atg	cac	atg	gct	atc	ggt	tct	gcg	ctg	agc	atg	ttt	gac	432
Tyr	Leu	Asp	Met	His	Met	Ala	Ile	Gly	Ser	Ala	Leu	Ser	Met	Phe	Asp	
	130					135					140					
aac	aag	ctg	gtg	ccg	ttc	ttt	gaa	gaa	ggc	aca	ccg	cta	gag	cag	gaa	480
Asn	Lys	Leu	Val	Pro	Phe	Phe	Glu	Glu	Gly	Thr	Pro	Leu	Glu	Gln	Glu	
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Arg	Gly	His														

<210> 258

<211> 163

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 258

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Thr Gly Asp Phe Gln Gly Thr Pro Val Met Asn Tyr Asn Asp Ala Asp	35	40	45
Val Pro Phe Thr Arg Ile His Glu Phe Arg His Phe His Pro Glu Arg	50	55	60
Asp Asp Ser Tyr Pro Lys Asp Lys Thr Val Ile Met Arg Glu Phe Ser	65	70	75
Arg Phe Ala Asp Asn Glu Asp Glu Pro Tyr Tyr Pro Ile Asn Thr Pro	85	90	95
Asp Asp Arg Asp Met Leu Lys Gln Tyr Arg Leu Leu Ala Ala Glu Glu	100	105	110
Ala Ala Asn Asn Lys Val Leu Phe Gly Gly Arg Leu Gly Thr Tyr Gln	115	120	125
Tyr Leu Asp Met His Met Ala Ile Gly Ser Ala Leu Ser Met Phe Asp	130	135	140
Asn Lys Leu Val Pro Phe Phe Glu Glu Gly Thr Pro Leu Glu Gln Glu	145	150	155
Arg Gly His			

<210> 259

<211> 598

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(598)

<223> FRXA02642

<400> 259

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               Met Thr Glu Ser Lys
               1 5
aat tac gac tta atc gtt gta ggc tcc ggc ctc ttc ggg ctc acc gtg 163
Asn Tyr Asp Leu Ile Val Val Gly Ser Gly Leu Phe Gly Leu Thr Val
               10 15 20
gct gag cgt gca gct agc cag ctg ggt aag aaa gtc ctc atc gtt gaa 211
Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys Val Leu Ile Val Glu
               25 30 35
cgc cgc tcg cac ctc ggt ggc aat gct tac tct gaa gca gaa cca gag 259
Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser Glu Ala Glu Pro Glu
               40 45 50

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acc ggc att gaa atc cac aaa tac ggc gcg cac ctc ttc cac acc tcc 307
 Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His Leu Phe His Thr Ser
 55 60 65

aac aca cgc gtg tgg gaa tac gtc aac cag ttc acc agt ttc acc ggc 355
 Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe Thr Ser Phe Thr Gly
 70 75 80 85

tac cag cac cgc gtc ttc gca atg cac aac ggc acc gcc tac caa ttc 403
 Tyr Gln His Arg Val Phe Ala Met His Asn Gly Thr Ala Tyr Gln Phe
 90 95 100

ccc atg gga ctg ggc ctg att aac cag ttc ttc ggc aag tac tac agc 451
 Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe Gly Lys Tyr Tyr Ser
 105 110 115

cca gat gaa gcc cgt gag ctc atc aag gaa cag tct gca gaa atc gat 499
 Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln Ser Ala Glu Ile Asp
 120 125 130

tcc tcc gac gcc acc aac ctc gaa gaa aag gcc att tcc ctc att ggt 547
 Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala Ile Ser Leu Ile Gly
 135 140 145

cgc cca ctt tac gag gca ttc atc cgc gac tac acc gca aag cag tgg 595
 Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr Thr Ala Lys Gln Trp
 150 155 160 165

cag 598
 Gln

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 <213> Corynebacterium glutamicum

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Phe Gly Leu Thr Val Ala Glu Arg Ala Ala Ser Gln Leu Gly Lys Lys
 20 25 30

Val Leu Ile Val Glu Arg Arg Ser His Leu Gly Gly Asn Ala Tyr Ser
 35 40 45

Glu Ala Glu Pro Glu Thr Gly Ile Glu Ile His Lys Tyr Gly Ala His
 50 55 60

Leu Phe His Thr Ser Asn Thr Arg Val Trp Glu Tyr Val Asn Gln Phe
 65 70 75 80

Thr Ser Phe Thr Gly Tyr Gln His Arg Val Phe Ala Met His Asn Gly
 85 90 95

Thr Ala Tyr Gln Phe Pro Met Gly Leu Gly Leu Ile Asn Gln Phe Phe
 100 105 110

Gly Lys Tyr Tyr Ser Pro Asp Glu Ala Arg Glu Leu Ile Lys Glu Gln
 115 120 125

Ser Ala Glu Ile Asp Ser Ser Asp Ala Thr Asn Leu Glu Glu Lys Ala
 130 135 140

Ile Ser Leu Ile Gly Arg Pro Leu Tyr Glu Ala Phe Ile Arg Asp Tyr
 145 150 155 160

Thr Ala Lys Gln Trp Gln
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<210> 261
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(645)
 <223> RXA02572

<400> 261

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Val Asp Ala Ile Gly His Asp Asp Arg Ile Gly Arg Lys Phe Leu Gly	
20 25 30	
gcg ggc ctg gga ttc ggt ggc ggt tgt ttg cct aaa gac atc cgc gct	144
Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala	
35 40 45	
ttc atg gca cgc gcg ggc gaa ttg ggt gct gac cag gca tta acg ttc	192
Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe	
50 55 60	
ttg cgt gag gtc gat tcc atc aat atg cgt cgt cgc gac cgt gtg gtg	240
Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val	
65 70 75 80	
cag ctg gcc aaa gag atg tgt ggc ggt tcg ctg ctg ggc aag cgg gtt	288
Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val	
85 90 95	
aca gtg ctc ggc gcc gca ttc aaa ccc aac tcg gac gat gtc cgc gat	336
Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp	
100 105 110	
tct ccg gcg ctg tcg gtc gcg ggt tcg ctg tcg ctc cag ggt gcg gcg	384
Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala	
115 120 125	
gtc tcg gtc tac gac ccg gaa gct atg gac aac gct cga cgc gtc ttc	432
Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe	
130 135 140	
ccg acg ctc agc tat gcg tcc agc act aaa gag gcg ctt atc gac gcc	480

Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160

cac ctc gtc gtt ctt gcc act gaa tgg caa gaa ttc cgc gac ctt gac 528
 His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175

ccc gaa gtg gcg gga ggg gtc gtc gag aag cgc gct att att gat ggc 576
 Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190

cga aac gtc ctc gat gtt gcc aaa tgg aag gcc gcc ggt tgg gaa atg 624
 Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
 195 200 205

gaa gcg ctc ggc cgc aac ctt tagtgcggtg gatcaggcgg ggc 668
 Glu Ala Leu Gly Arg Asn Leu
 210 215

<210> 262

<211> 215

<212> PRT

<213> Corynebacterium glutamicum

<400> 262

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 20 25 30

Ala Gly Leu Gly Phe Gly Gly Gly Cys Leu Pro Lys Asp Ile Arg Ala
 35 40 45

Phe Met Ala Arg Ala Gly Glu Leu Gly Ala Asp Gln Ala Leu Thr Phe
 50 55 60

Leu Arg Glu Val Asp Ser Ile Asn Met Arg Arg Arg Asp Arg Val Val
 65 70 75 80

Gln Leu Ala Lys Glu Met Cys Gly Gly Ser Leu Leu Gly Lys Arg Val
 85 90 95

Thr Val Leu Gly Ala Ala Phe Lys Pro Asn Ser Asp Asp Val Arg Asp
 100 105 110

Ser Pro Ala Leu Ser Val Ala Gly Ser Leu Ser Leu Gln Gly Ala Ala
 115 120 125

Val Ser Val Tyr Asp Pro Glu Ala Met Asp Asn Ala Arg Arg Val Phe
 130 135 140

Pro Thr Leu Ser Tyr Ala Ser Ser Thr Lys Glu Ala Leu Ile Asp Ala
 145 150 155 160

His Leu Val Val Leu Ala Thr Glu Trp Gln Glu Phe Arg Asp Leu Asp
 165 170 175

Pro Glu Val Ala Gly Gly Val Val Glu Lys Arg Ala Ile Ile Asp Gly
 180 185 190

Arg Asn Val Leu Asp Val Ala Lys Trp Lys Ala Ala Gly Trp Glu Met
 195 200 205

Glu Ala Leu Gly Arg Asn Leu
 210 215

<210> 263

<211> 1224

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1201)

<223> RXA02485

<400> 263

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tacgcgttgc catgaggata agactaccgt tagtgggggtg ttg gat tca tcg cta 115
 Leu Asp Ser Ser Leu
 1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163
 Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val
 10 15 20

act ttc gcc gat ctg acg acc ctc cgc atc ggc gga aaa ccc cgc agc 211
 Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly Gly Lys Pro Arg Ser
 25 30 35

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg 259
 Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu
 40 45 50

ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat 307
 Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn
 55 60 65

ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa 355
 Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu
 70 75 80 85

acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat 403
 Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp
 90 95 100

gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc 451
 Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly
 105 110 115

ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc 499
 Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala
 120 125 130

acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta 547
 Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val
 135 140 145

ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg 595
 Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp
 150 155 160 165

gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa 643
 Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys
 170 175 180

ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc 691
 Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr
 185 190 195

gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta 739
 Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu
 200 205 210

gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc 787
 Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val
 215 220 225

cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa 835
 Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu
 230 235 240 245

cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca 883
 His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro
 250 255 260

atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa 931
 Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu
 265 270 275

ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc 979
 Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
 280 285 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc 1027
 Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
 295 300 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc 1075
 Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
 310 315 320 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa 1123
 Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
 330 335 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa 1171
 Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
 345 350 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg 1221
 Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
 360 365

gca 1224

<210> 264

<211> 367

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 264

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Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
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Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
          35           40           45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
 50           55           60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65           70           75           80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
          85           90           95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
          100          105          110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
          115          120          125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
          130          135          140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
145           150           155           160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
          165          170          175

Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
          180          185          190

Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
          195          200          205

Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
210           215           220

Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
225           230           235           240

Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
          245           250           255

Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
          260           265           270

Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
          275          280           285

Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
290           295           300

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Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
305 310 315 320

Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
325 330 335

Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val
340 345 350

Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
355 360 365

<210> 265

<211> 1124

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1101)

<223> RXA01216

<400> 265

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acc gct gtc acc gtg ttg acc atg cgt ctg gat gac ccc acc ggc tac 96
Thr Ala Val Thr Val Leu Thr Met Arg Leu Asp Asp Pro Thr Gly Tyr
20 25 30

ggc cgc atc gtg cgc aac gaa gaa ggc gaa gtc acc gcc atc gtt gag 144
Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu
35 40 45

caa aaa gat gct tca gca gaa gtc caa gcc atc gat gag gtc aac tcc 192
Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser
50 55 60

ggt gtc ttt gct ttc gac gcc gcc atc ttg cgt tcc gca ctg gct gaa 240
Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
65 70 75 80

ctg aag tcc gac aac gct cag ggc gag ctg tac ctg acc gac gtt ttg 288
Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu
85 90 95

ggc att gct cgt ggc gag ggc cac cca gtg cgc gcc cac acc gcc gcc 336
Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
100 105 110

gat gct cgt gaa ctc gcc ggc gtc aac gat cgt gtg cag ctc gca gaa 384
Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu
115 120 125

gcc ggc gcc gaa cta aac cgt cgc acc gtc atc gcc gct atg cgt ggt 432
Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
130 135 140

ggc gca acc atc gtt gat cca gca acc acc tgg atc gat gtg gag gtt 480

Gly 145	Ala	Thr	Ile	Val	Asp 150	Pro	Ala	Thr	Thr	Trp 155	Ile	Asp	Val	Glu	Val 160	
tct	atc	gga	cgc	gac	gtg	atc	atc	cac	cct	ggc	acc	cag	ctc	aag	ggc	528
Ser	Ile	Gly	Arg	Asp 165	Val	Ile	Ile	His	Pro 170	Gly	Thr	Gln	Leu	Lys 175	Gly	
gaa	act	gtc	atc	gga	gac	cgc	gtt	gaa	gtt	ggc	cca	gac	acc	acc	ttg	576
Glu	Thr	Val	Ile 180	Gly	Asp	Arg	Val	Glu 185	Val	Gly	Pro	Asp	Thr	Thr	Leu	
acc	aac	atg	acc	atc	ggc	gac	ggc	gca	tcc	gta	atc	cgc	acc	cac	ggc	624
Thr	Asn	Met 195	Thr	Ile	Gly	Asp	Gly 200	Ala	Ser	Val	Ile	Arg	Thr	His	Gly	
ttc	gac	tcc	acc	atc	ggc	gaa	aac	gcc	acc	gtt	ggc	ccc	ttc	acc	tac	672
Phe	Asp	Ser	Thr	Ile	Gly	Glu 215	Asn	Ala	Thr	Val	Gly 220	Pro	Phe	Thr	Tyr	
atc	cgc	cca	gga	acc	aca	ctg	gga	cca	gaa	ggc	aag	ctc	ggc	ggc	ttc	720
Ile	Arg	Pro	Gly	Thr	Thr 230	Leu	Gly	Pro	Glu	Gly 235	Lys	Leu	Gly	Gly	Phe 240	
gta	gaa	acc	aag	aag	gcc	aca	atc	ggc	cgt	ggc	tcc	aag	gtt	cca	cac	768
Val	Glu	Thr	Lys	Lys 245	Ala	Thr	Ile	Gly	Arg 250	Gly	Ser	Lys	Val	Pro 255	His	
ctc	acc	tat	gtc	ggc	gac	gcc	acc	atc	ggc	gag	gaa	tcc	aac	atc	gga	816
Leu	Thr	Tyr	Val 260	Gly	Asp	Ala	Thr	Ile 265	Gly	Glu	Glu	Ser	Asn	Ile	Gly 270	
gcc	tcc	tct	gtc	ttc	gtg	aac	tac	gac	ggc	gaa	aac	aag	cac	cac	acc	864
Ala	Ser	Ser 275	Val	Phe	Val	Asn	Tyr 280	Asp	Gly	Glu	Asn	Lys	His	His	Thr 285	
acc	atc	ggc	agc	cac	gtt	cgc	act	ggc	tct	gac	acc	atg	ttt	atc	gct	912
Thr	Ile	Gly	Ser	His	Val	Arg	Thr 295	Gly	Ser	Asp	Thr	Met	Phe	Ile	Ala 300	
cca	gtg	acc	gtg	ggc	gac	gga	gcg	tat	tcc	gga	gcc	ggc	aca	gta	att	960
Pro	Val	Thr	Val	Gly	Asp 310	Gly	Ala	Tyr	Ser	Gly 315	Ala	Gly	Thr	Val	Ile 320	
aaa	gac	gat	gtt	ccg	cca	gga	gcc	ctt	gcc	gtg	tcc	ggc	gga	cgc	caa	1008
Lys	Asp	Asp	Val	Pro	Pro	Gly	Ala	Leu 325	Ala	Val	Ser	Gly	Gly	Arg	Gln 335	
cga	aac	atc	gaa	ggc	tggt	gtg	caa	aag	aag	cgc	cct	gga	acc	gct	gca	1056
Arg	Asn	Ile	Glu	Gly	Trp	Val	Gln 340	Lys	Lys	Arg	Pro	Gly	Thr	Ala	Ala 350	
gca	caa	gcc	gca	gaa	gcc	gcc	caa	aac	gtc	cac	aac	cag	gaa	ggc		1101
Ala	Gln	Ala	Ala	Glu	Ala	Ala	Gln 355	Asn	Val	His	Asn	Gln	Glu	Gly		
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<210> 266
 <211> 367
 <212> PRT

<213> Corynebacterium glutamicum

<400> 266

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 Gly Arg Ile Val Arg Asn Glu Glu Gly Glu Val Thr Ala Ile Val Glu
 35 40 45
 Gln Lys Asp Ala Ser Ala Glu Val Gln Ala Ile Asp Glu Val Asn Ser
 50 55 60
 Gly Val Phe Ala Phe Asp Ala Ala Ile Leu Arg Ser Ala Leu Ala Glu
 65 70 75 80
 Leu Lys Ser Asp Asn Ala Gln Gly Glu Leu Tyr Leu Thr Asp Val Leu
 85 90 95
 Gly Ile Ala Arg Gly Glu Gly His Pro Val Arg Ala His Thr Ala Ala
 100 105 110
 Asp Ala Arg Glu Leu Ala Gly Val Asn Asp Arg Val Gln Leu Ala Glu
 115 120 125
 Ala Gly Ala Glu Leu Asn Arg Arg Thr Val Ile Ala Ala Met Arg Gly
 130 135 140
 Gly Ala Thr Ile Val Asp Pro Ala Thr Thr Trp Ile Asp Val Glu Val
 145 150 155 160
 Ser Ile Gly Arg Asp Val Ile Ile His Pro Gly Thr Gln Leu Lys Gly
 165 170 175
 Glu Thr Val Ile Gly Asp Arg Val Glu Val Gly Pro Asp Thr Thr Leu
 180 185 190
 Thr Asn Met Thr Ile Gly Asp Gly Ala Ser Val Ile Arg Thr His Gly
 195 200 205
 Phe Asp Ser Thr Ile Gly Glu Asn Ala Thr Val Gly Pro Phe Thr Tyr
 210 215 220
 Ile Arg Pro Gly Thr Thr Leu Gly Pro Glu Gly Lys Leu Gly Gly Phe
 225 230 235 240
 Val Glu Thr Lys Lys Ala Thr Ile Gly Arg Gly Ser Lys Val Pro His
 245 250 255
 Leu Thr Tyr Val Gly Asp Ala Thr Ile Gly Glu Glu Ser Asn Ile Gly
 260 265 270
 Ala Ser Ser Val Phe Val Asn Tyr Asp Gly Glu Asn Lys His His Thr
 275 280 285
 Thr Ile Gly Ser His Val Arg Thr Gly Ser Asp Thr Met Phe Ile Ala
 290 295 300
 Pro Val Thr Val Gly Asp Gly Ala Tyr Ser Gly Ala Gly Thr Val Ile

<400> 267															
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Met Gly Thr Arg Phe 1 5															
ctt cct gca acg aag aca att cca aag gag ctt ctt cct gta gtt gat 163															
Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu Leu Pro Val Val Asp 10 15 20															
acc ccg ggt att gaa ctt gtt gcc aaa gag gct gct gat ctt ggt gca 211															
Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala Ala Asp Leu Gly Ala 25 30 35															
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Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys Asp Gly Ile Leu Lys 40 45 50															
cac ttc gag gag ttc cct gag ctt gag gca act ctt gag gct cgc ggt 307															
His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr Leu Glu Ala Arg Gly 55 60 65															
aag act gat caa ctg aat aaa gtt cga gca gct cga gaa ttg att gca 355															
Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala Arg Glu Leu Ile Ala 70 75 80 85															
aca gtt cca gtg gtt caa gaa aag cca ttg ggg ctt ggt cac gct gtt 403															
Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly Leu Gly His Ala Val 90 95 100															
ggc ctt gct gag tct gtg ctc gat gat gat gaa gat gtt gtg gct gtc 451															
Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu Asp Val Val Ala Val 105 110 115															
atg ctg cca gac gat ttg gtg ctg cca ttt ggt gtg acc gag aga atg 499															
Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly Val Thr Glu Arg Met 120 125 130															

gca gaa gtt cgc gct aag ttt ggc gga tct gtt ctt gca gca att gag 547
 Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val Leu Ala Ala Ile Glu
 135 140 145

gtg gct gaa gat gaa gtc tca aat tac gga gta ttt aag ctc ggt gaa 595
 Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val Phe Lys Leu Gly Glu
 150 155 160 165

ctc gat gca gag tcc gaa agt gaa ggc att agg cgt gtt gta gga atg 643
 Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg Arg Val Val Gly Met
 170 175 180

gtt gaa aag cct gcg cct gaa gat gca cca tca agg ttt gcc gca acg 691
 Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser Arg Phe Ala Ala Thr
 185 190 195

ggc cgt tat cta ctt gat cga gct att ttt gat gca ctg cgt cga att 739
 Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp Ala Leu Arg Arg Ile
 200 205 210

gag cct ggt gct ggt gga gaa ctg caa tta aca gat gcc atc gca tta 787
 Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr Asp Ala Ile Ala Leu
 215 220 225

ttg atc gaa gaa ggc cat ccg gta cac att gtg gtt cat gaa gga aag 835
 Leu Ile Glu Glu Gly His Pro Val His Ile Val Val His Glu Gly Lys
 230 235 240 245

cgc cat gac ctt ggt aat cca gct ggg tac att cct gct gtt gtg tac 883
 Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile Pro Ala Val Val Tyr
 250 255 260

ttc gga ctt cgt cat gca gag tac ggt tcc aag att cac cgt gcg gtg 931
 Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys Ile His Arg Ala Val
 265 270 275

aag gaa ata ctc gct gag ttt gaa tct taaaaaggaa accgccttcc 978
 Lys Glu Ile Leu Ala Glu Phe Glu Ser
 280 285

aca 981

<210> 268

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 268

Met Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Ile Pro Lys Glu Leu
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Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Val Ala Lys Glu Ala
 20 25 30

Ala Asp Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
 35 40 45

Asp Gly Ile Leu Lys His Phe Glu Glu Phe Pro Glu Leu Glu Ala Thr
 50 55 60

Leu Glu Ala Arg Gly Lys Thr Asp Gln Leu Asn Lys Val Arg Ala Ala
 65 70 75 80
 Arg Glu Leu Ile Ala Thr Val Pro Val Val Gln Glu Lys Pro Leu Gly
 85 90 95
 Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
 100 105 110
 Asp Val Val Ala Val Met Leu Pro Asp Asp Leu Val Leu Pro Phe Gly
 115 120 125
 Val Thr Glu Arg Met Ala Glu Val Arg Ala Lys Phe Gly Gly Ser Val
 130 135 140
 Leu Ala Ala Ile Glu Val Ala Glu Asp Glu Val Ser Asn Tyr Gly Val
 145 150 155 160
 Phe Lys Leu Gly Glu Leu Asp Ala Glu Ser Glu Ser Glu Gly Ile Arg
 165 170 175
 Arg Val Val Gly Met Val Glu Lys Pro Ala Pro Glu Asp Ala Pro Ser
 180 185 190
 Arg Phe Ala Ala Thr Gly Arg Tyr Leu Leu Asp Arg Ala Ile Phe Asp
 195 200 205
 Ala Leu Arg Arg Ile Glu Pro Gly Ala Gly Gly Glu Leu Gln Leu Thr
 210 215 220
 Asp Ala Ile Ala Leu Leu Ile Glu Glu Gly His Pro Val His Ile Val
 225 230 235 240
 Val His Glu Gly Lys Arg His Asp Leu Gly Asn Pro Ala Gly Tyr Ile
 245 250 255
 Pro Ala Val Val Tyr Phe Gly Leu Arg His Ala Glu Tyr Gly Ser Lys
 260 265 270
 Ile His Arg Ala Val Lys Glu Ile Leu Ala Glu Phe Glu Ser
 275 280 285

<210> 269
 <211> 526
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(526)
 <223> RXA02028

<400> 269
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 tacgacgatt ggggttgcgg gggcaggtac tcttggttcc atg agt ttg cct atc 115
 Met Ser Leu Pro Ile
 1 5
 gat gag cac gtg aac gcg gtt aaa acc gtc gta gtg cct gct gca gga 163


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Asp Glu His Val Asn Ala Val Lys Thr Val Val Val Pro Ala Ala Gly
      10                      15                      20

ctg gga acc cga ttc ctt ccg gcc acc aaa acc gta ccc aag gag ttg 211
Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr Val Pro Lys Glu Leu
      25                      30                      35

ctg ccg gtt gtc gat acc cca ggt att gag ctg att gct gct gag gct 259
Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu Ile Ala Ala Glu Ala
      40                      45                      50

gcc gaa ctt ggt gcg acc agg ctg gcg atc atc act gcg cca aac aaa 307
Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile Thr Ala Pro Asn Lys
      55                      60                      65

gct ggg gta ctt gca cac ttt gag cgt tct tct gaa ttg gaa gaa acg 355
Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser Glu Leu Glu Glu Thr
      70                      75                      80                      85

ctg atg gag cgt ggc aag act gac cag gtg gag ata atc cgc cgc gcc 403
Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu Ile Ile Arg Arg Ala
      90                      95                      100

gcc gat tta atc aag gca gtt cca gta acc cag gac aag ccg ctg ggg 451
Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln Asp Lys Pro Leu Gly
      105                      110                      115

cta ggt cat gct gtt ggt ttg gct gag tct gtg ttg gat gat gat gaa 499
Leu Gly His Ala Val Gly Leu Ala Glu Ser Val Leu Asp Asp Asp Glu
      120                      125                      130

gat gtc gta gcg gtg atg ttg ccg cac
Asp Val Val Ala Val Met Leu Pro His
      135                      140

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<210> 270

<211> 142

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 270

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Met Ser Leu Pro Ile Asp Glu His Val Asn Ala Val Lys Thr Val Val
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Val Pro Ala Ala Gly Leu Gly Thr Arg Phe Leu Pro Ala Thr Lys Thr
      20                      25                      30

Val Pro Lys Glu Leu Leu Pro Val Val Asp Thr Pro Gly Ile Glu Leu
      35                      40                      45

Ile Ala Ala Glu Ala Ala Glu Leu Gly Ala Thr Arg Leu Ala Ile Ile
      50                      55                      60

Thr Ala Pro Asn Lys Ala Gly Val Leu Ala His Phe Glu Arg Ser Ser
      65                      70                      75                      80

Glu Leu Glu Glu Thr Leu Met Glu Arg Gly Lys Thr Asp Gln Val Glu
      85                      90                      95

Ile Ile Arg Arg Ala Ala Asp Leu Ile Lys Ala Val Pro Val Thr Gln

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100      105      110
Asp Lys Pro Leu Gly Leu Gly His Ala Val Gly Leu Ala Glu Ser Val
    115              120              125

Leu Asp Asp Asp Glu Asp Val Val Ala Val Met Leu Pro His
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<210> 271
<211> 1284
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1261)
<223> RXA01262

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aaacttgctg tatcaataaa acacgaaaag gaatactttt atg aaa att gcc gtc 115
                               Met Lys Ile Ala Val
                                1                    5

gca ggg ctg gga tat gtt ggg ctt tca aat gca gct ctg ctg tct aaa 163
Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala Ala Leu Leu Ser Lys
               10                     15                20

aat cat aaa gtt gtt gca gtt gac att gat gaa gaa cga gtg aaa cta 211
Asn His Lys Val Val Ala Val Asp Ile Asp Glu Glu Arg Val Lys Leu
             25                     30                35

gtt caa gaa ttt cgt tcg cca att gtc gat agc gat ctg gaa gaa tat 259
Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser Asp Leu Glu Glu Tyr
            40                     45                50

ctg tcc act aag cct caa aac tta act gcc aca acg gac gcc gaa gcc 307
Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr Thr Asp Ala Glu Ala
          55                     60                65

gct tac aaa ggc gca gat ttt att gtt att gca acg cca act aat tac 355
Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala Thr Pro Thr Asn Tyr
   70                      75                 80                85

gac cca gag tca aac ttt ttt gat act tcc agc gtt gag tcc gta att 403
Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser Val Glu Ser Val Ile
           90                     95                100

gag ata gtc ctt aag gtt tct cct gga tcc aca atc gta att aaa tcg 451
Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr Ile Val Ile Lys Ser
         105                     110                115

act atc cct gtt ggt ttt aca tcg gaa cta cgc att aag cat cca gaa 499
Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg Ile Lys His Pro Glu
        120                     125                130

gct tcg att att ttt tca cct gag ttc ctg cgt gaa ggc cga gca ttc 547
Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg Glu Gly Arg Ala Phe
       135                     140                145
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tac gac aat ctc tac cca tcc aga gtt gtc gtt ggt gat cgc agt cct	595
Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val Gly Asp Arg Ser Pro	
150 155 160 165	
ctg ggg gaa gaa ttt gcg act ctg tta gct gag ggg gca aaa gaa aag	643
Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu Gly Ala Lys Glu Lys	
170 175 180	
cct ccg att cta ctt acg gac tca act gag gca gag gcg att aaa tta	691
Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala Glu Ala Ile Lys Leu	
185 190 195	
ttt tct aat aca tat ctt gca ctg cga gtt gct ttt ttc aac gaa ctg	739
Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala Phe Phe Asn Glu Leu	
200 205 210	
gat act tat gcg tct gtt cga agc ttg gat act aag cag att att gaa	787
Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr Lys Gln Ile Ile Glu	
215 220 225	
ggg gta ggg ctc gat cca cgt att gga tct cat tac aat aat cct tca	835
Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His Tyr Asn Asn Pro Ser	
230 235 240 245	
ttt gga tat ggc gga tat tgt ctt ccg aaa gat acg aaa cag ctt ctc	883
Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp Thr Lys Gln Leu Leu	
250 255 260	
gcc aac tat aag gat gtc ccg cag aat cta atc tct gca gta gtc caa	931
Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile Ser Ala Val Val Gln	
265 270 275	
gca aat aag act cgt aag gac ttt att gca gag gat atc ctc agt aaa	979
Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu Asp Ile Leu Ser Lys	
280 285 290	
tca cct act gta gtt gga att tac cgc ctt gta atg aag tct gga tca	1027
Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val Met Lys Ser Gly Ser	
295 300 305	
gat aac ttt cgt tct tct tct att caa gga gtc atg aaa cga att aag	1075
Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val Met Lys Arg Ile Lys	
310 315 320 325	
gcc aag gga atc gaa att gta gta ttt gaa ccg aat ctc gga gaa gaa	1123
Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro Asn Leu Gly Glu Glu	
330 335 340	
act ttc tac aat tcg aag atc ctt aat gac atc gaa gag ttt aag gat	1171
Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile Glu Glu Phe Lys Asp	
345 350 355	
tac tgc gac atc att att gca aat cgt cca acc gat gag ctt tct gat	1219
Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr Asp Glu Leu Ser Asp	
360 365 370	
gta cca gaa aaa gtt tat aca cgt gat att ttc cag cgt gac	1261
Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe Gln Arg Asp	
375 380 385	

taagtggaaa gaatcttttg ttg

1284

<210> 272

<211> 387

<212> PRT

<213> Corynebacterium glutamicum

<400> 272

Met Lys Ile Ala Val Ala Gly Leu Gly Tyr Val Gly Leu Ser Asn Ala
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Ala Leu Leu Ser Lys Asn His Lys Val Val Ala Val Asp Ile Asp Glu
 20 25 30

Glu Arg Val Lys Leu Val Gln Glu Phe Arg Ser Pro Ile Val Asp Ser
 35 40 45

Asp Leu Glu Glu Tyr Leu Ser Thr Lys Pro Gln Asn Leu Thr Ala Thr
 50 55 60

Thr Asp Ala Glu Ala Ala Tyr Lys Gly Ala Asp Phe Ile Val Ile Ala
 65 70 75 80

Thr Pro Thr Asn Tyr Asp Pro Glu Ser Asn Phe Phe Asp Thr Ser Ser
 85 90 95

Val Glu Ser Val Ile Glu Ile Val Leu Lys Val Ser Pro Gly Ser Thr
 100 105 110

Ile Val Ile Lys Ser Thr Ile Pro Val Gly Phe Thr Ser Glu Leu Arg
 115 120 125

Ile Lys His Pro Glu Ala Ser Ile Ile Phe Ser Pro Glu Phe Leu Arg
 130 135 140

Glu Gly Arg Ala Phe Tyr Asp Asn Leu Tyr Pro Ser Arg Val Val Val
 145 150 155 160

Gly Asp Arg Ser Pro Leu Gly Glu Glu Phe Ala Thr Leu Leu Ala Glu
 165 170 175

Gly Ala Lys Glu Lys Pro Pro Ile Leu Leu Thr Asp Ser Thr Glu Ala
 180 185 190

Glu Ala Ile Lys Leu Phe Ser Asn Thr Tyr Leu Ala Leu Arg Val Ala
 195 200 205

Phe Phe Asn Glu Leu Asp Thr Tyr Ala Ser Val Arg Ser Leu Asp Thr
 210 215 220

Lys Gln Ile Ile Glu Gly Val Gly Leu Asp Pro Arg Ile Gly Ser His
 225 230 235 240

Tyr Asn Asn Pro Ser Phe Gly Tyr Gly Gly Tyr Cys Leu Pro Lys Asp
 245 250 255

Thr Lys Gln Leu Leu Ala Asn Tyr Lys Asp Val Pro Gln Asn Leu Ile
 260 265 270

Ser Ala Val Val Gln Ala Asn Lys Thr Arg Lys Asp Phe Ile Ala Glu

275	280	285
Asp Ile Leu Ser Lys Ser Pro Thr Val Val Gly Ile Tyr Arg Leu Val		
290	295	300
Met Lys Ser Gly Ser Asp Asn Phe Arg Ser Ser Ser Ile Gln Gly Val		
305	310	315
Met Lys Arg Ile Lys Ala Lys Gly Ile Glu Ile Val Val Phe Glu Pro		
325	330	335
Asn Leu Gly Glu Glu Thr Phe Tyr Asn Ser Lys Ile Leu Asn Asp Ile		
340	345	350
Glu Glu Phe Lys Asp Tyr Cys Asp Ile Ile Ile Ala Asn Arg Pro Thr		
355	360	365
Asp Glu Leu Ser Asp Val Pro Glu Lys Val Tyr Thr Arg Asp Ile Phe		
370	375	380
Gln Arg Asp		
385		

<210> 273
 <211> 1209
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1186)
 <223> RXA01377

<400> 273
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 ccccttaaag acaccctaaa caccgagtga ataggaacac atg act tta act gac 115
 Met Thr Leu Thr Asp
 1 5
 aac agc aaa aac gtt gat gct gtc atc ttg gtc ggt ggc aaa ggt acc 163
 Asn Ser Lys Asn Val Asp Ala Val Ile Leu Val Gly Gly Lys Gly Thr
 10 15 20
 cga ctg cgc ccc ctg acc gtc aat act cca aag cca atg ctg cca act 211
 Arg Leu Arg Pro Leu Thr Val Asn Thr Pro Lys Pro Met Leu Pro Thr
 25 30 35
 gct ggc cac cca ttc ttg acc cac ctt ttg gcc cgc atc aag gcc gca 259
 Ala Gly His Pro Phe Leu Thr His Leu Leu Ala Arg Ile Lys Ala Ala
 40 45 50
 ggc atc aca cac gtc gtg ctg gga acg tca ttc aaa gct gaa gtc ttc 307
 Gly Ile Thr His Val Val Leu Gly Thr Ser Phe Lys Ala Glu Val Phe
 55 60 65
 gag gaa tac ttc gga gat ggc tcc gaa atg ggc ttg gaa att gaa tat 355
 Glu Glu Tyr Phe Gly Asp Gly Ser Glu Met Gly Leu Glu Ile Glu Tyr
 70 75 80 85

gtc gtc gag gat cag cct ttg ggc act ggt ggt ggc atc cga aac gtc	403
Val Val Glu Asp Gln Pro Leu Gly Thr Gly Gly Gly Ile Arg Asn Val	
90 95 100	
tac gac aag ctg cgt cac gat act gcg att gtg ttc aac ggc gat gtg	451
Tyr Asp Lys Leu Arg His Asp Thr Ala Ile Val Phe Asn Gly Asp Val	
105 110 115	
ctc tcc ggt gcg gat ctc aac agc att ctg gac acc cac cgc gaa aag	499
Leu Ser Gly Ala Asp Leu Asn Ser Ile Leu Asp Thr His Arg Glu Lys	
120 125 130	
gac gca gat ctg acc atg cat ctc gtg cgc gta gct aac cct cgt gcg	547
Asp Ala Asp Leu Thr Met His Leu Val Arg Val Ala Asn Pro Arg Ala	
135 140 145	
ttt ggt tgc gtc ccc acc gat gag gat ggt cgc gtc agc gaa ttc ctt	595
Phe Gly Cys Val Pro Thr Asp Glu Asp Gly Arg Val Ser Glu Phe Leu	
150 155 160 165	
gaa aag acc gaa gat cca cca acc gat cag atc aac gcc ggc tgc tac	643
Glu Lys Thr Glu Asp Pro Pro Thr Asp Gln Ile Asn Ala Gly Cys Tyr	
170 175 180	
gtg ttc aag aag gaa ctc atc gag cag atc ccg gca ggc cga gca gtt	691
Val Phe Lys Lys Glu Leu Ile Glu Gln Ile Pro Ala Gly Arg Ala Val	
185 190 195	
tcc gtc gag cgc gaa acc ttc cct cag ctg ttg gaa gaa ggc aag cga	739
Ser Val Glu Arg Glu Thr Phe Pro Gln Leu Leu Glu Glu Gly Lys Arg	
200 205 210	
gtc ttc ggc cac gtc gac gct tcc tac tgg cgc gac atg ggc acc cca	787
Val Phe Gly His Val Asp Ala Ser Tyr Trp Arg Asp Met Gly Thr Pro	
215 220 225	
agc gac ttc gtc cgc ggc tcg gct gac ctg gtc cgc ggc att gcg tac	835
Ser Asp Phe Val Arg Gly Ser Ala Asp Leu Val Arg Gly Ile Ala Tyr	
230 235 240 245	
tcc cca ttg ctc gaa ggc aaa aca gga gag tcg ctt gtc gac gcc tcc	883
Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser Leu Val Asp Ala Ser	
250 255 260	
gcc ggc gtt cgc gac ggc gtc ctg ctg ctc ggc gga acc gta gtc ggc	931
Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly Gly Thr Val Val Gly	
265 270 275	
cgc ggc act gag atc ggt gcc ggc tgc cgc gtt gac aac act gtt att	979
Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val Asp Asn Thr Val Ile	
280 285 290	
ttc gac ggc gtc acc att gaa cca ggt gcg gtc att gaa aat tcc atc	1027
Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val Ile Glu Asn Ser Ile	
295 300 305	
att tcc tcg gga gca cgc atc ggt gct aat gcg cac atc tcc ggt tgc	1075
Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala His Ile Ser Gly Cys	
310 315 320 325	
atc att ggc gag ggc gca cag gtt ggt gct cgg tgt gaa ctc aac gca	1123

<210> 274
<211> 362
<212> PRT
<213> Corynebacterium glutamicum

<400> 274																
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Gly	Gly	Lys	Gly	Thr	Arg	Leu	Arg	Pro	Leu	Thr	Val	Asn	Thr	Pro	Lys	
			20					25					30			
Pro	Met	Leu	Pro	Thr	Ala	Gly	His	Pro	Phe	Leu	Thr	His	Leu	Leu	Ala	
		35					40					45				
Arg	Ile	Lys	Ala	Ala	Gly	Ile	Thr	His	Val	Val	Leu	Gly	Thr	Ser	Phe	
	50					55					60					
Lys	Ala	Glu	Val	Phe	Glu	Glu	Tyr	Phe	Gly	Asp	Gly	Ser	Glu	Met	Gly	
65					70					75					80	
Leu	Glu	Ile	Glu	Tyr	Val	Val	Glu	Asp	Gln	Pro	Leu	Gly	Thr	Gly	Gly	
				85					90					95		
Gly	Ile	Arg	Asn	Val	Tyr	Asp	Lys	Leu	Arg	His	Asp	Thr	Ala	Ile	Val	
			100					105					110			
Phe	Asn	Gly	Asp	Val	Leu	Ser	Gly	Ala	Asp	Leu	Asn	Ser	Ile	Leu	Asp	
		115					120					125				
Thr	His	Arg	Glu	Lys	Asp	Ala	Asp	Leu	Thr	Met	His	Leu	Val	Arg	Val	
	130					135					140					
Ala	Asn	Pro	Arg	Ala	Phe	Gly	Cys	Val	Pro	Thr	Asp	Glu	Asp	Gly	Arg	
145					150					155					160	
Val	Ser	Glu	Phe	Leu	Glu	Lys	Thr	Glu	Asp	Pro	Pro	Thr	Asp	Gln	Ile	
				165					170					175		
Asn	Ala	Gly	Cys	Tyr	Val	Phe	Lys	Lys	Glu	Leu	Ile	Glu	Gln	Ile	Pro	
			180					185					190			
Ala	Gly	Arg	Ala	Val	Ser	Val	Glu	Arg	Glu	Thr	Phe	Pro	Gln	Leu	Leu	
		195					200					205				
Glu	Glu	Gly	Lys	Arg	Val	Phe	Gly	His	Val	Asp	Ala	Ser	Tyr	Trp	Arg	
	210					215					220					
Asp	Met	Gly	Thr	Pro	Ser	Asp	Phe	Val	Arg	Gly	Ser	Ala	Asp	Leu	Val	

225	230	235	240
Arg Gly Ile Ala Tyr Ser Pro Leu Leu Glu Gly Lys Thr Gly Glu Ser	245	250	255
Leu Val Asp Ala Ser Ala Gly Val Arg Asp Gly Val Leu Leu Leu Gly	260	265	270
Gly Thr Val Val Gly Arg Gly Thr Glu Ile Gly Ala Gly Cys Arg Val	275	280	285
Asp Asn Thr Val Ile Phe Asp Gly Val Thr Ile Glu Pro Gly Ala Val	290	295	300
Ile Glu Asn Ser Ile Ile Ser Ser Gly Ala Arg Ile Gly Ala Asn Ala	305	310	315
His Ile Ser Gly Cys Ile Ile Gly Glu Gly Ala Gln Val Gly Ala Arg	325	330	335
Cys Glu Leu Asn Ala Gly Met Arg Val Phe Pro Gly Val Val Ile Pro	340	345	350
Asp Ser Gly Ile Arg Phe Ser Ser Asp Gln	355	360	

<210> 275

<211> 1350

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1327)

<223> RXA02063

<400> 275

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ttgttaccca gctttcatgc gggatagtta ttttgcttt	atg gtt aag ggt gtg	115
	Met Val Lys Gly Val	
	1 5	

aag ggt aga cca aat gtt cta gca atc gtt ctc gca ggt ggc gag ggc	163
Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu Ala Gly Gly Glu Gly	
10 15 20	

aaa cga ctt ttt ccg ttg acg gag gac cga gct aag cct gcg gtc cca	211
Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala Lys Pro Ala Val Pro	
25 30 35	

ttc ggc gga act tac aga ttg atc gac ttt gtt ttg tcg aac ctg gtg	259
Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val Leu Ser Asn Leu Val	
40 45 50	

aac tcc gga ttc ctc aag atc gcg gta ctg act cag tac aag tcg cat	307
Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr Gln Tyr Lys Ser His	
55 60 65	

tca ttg gat agg cat att tca ttg tcg tgg aac gtg tct ggt cca acg	355
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Ser 70	Leu	Asp	Arg	His	Ile 75	Ser	Leu	Ser	Trp	Asn 80	Val	Ser	Gly	Pro	Thr 85	
ggg Gly	cag Gln	tac Tyr	att Ile	gct Ala	tct Ser	ggt Val	cct Pro	gcg Ala	cag Gln	cag Gln	cgc Arg	ctg Leu	ggc Gly	aag Lys	cga Arg	403
tgg Trp	ttc Phe	act Thr	ggt Gly	tcc Ser	gcg Ala	gat Asp	gca Ala	att Ile	ttg Leu	cag Gln	tct Ser	ctg Leu	aac Asn	ttg Leu	atc Ile	451
tct Ser	gat Asp	gag Glu	aaa Lys	ccg Pro	gat Asp	tat Tyr	gtc Val	atc Ile	ggt Val	ttc Phe	ggc Gly	gcg Ala	gac Asp	cac His	gtg Val	499
tat Tyr	cg Arg	atg Met	gac Asp	cca Pro	agc Ser	cag Gln	atg Met	cta Leu	gat Asp	gag Glu	cac His	att Ile	gca Ala	tct Ser	ggt Gly	547
cg Arg	gcg Ala	gtg Val	tct Ser	gtg Val	gca Ala	ggt Gly	att Ile	cg Arg	ggt Val	cca Pro	cgt Arg	gag Glu	gaa Glu	gca Ala	act Thr	595
gcg Ala	ttt Phe	ggt Gly	tgc Cys	atc Ile	cag Gln	tcc Ser	gat Asp	gtc Val	gac Asp	ggc Gly	aac Asn	ata Ile	acc Thr	gag Glu	ttc Phe	643
ttg Leu	gaa Glu	aag Lys	cca Pro	gct Ala	gac Asp	cct Pro	ccg Pro	gga Gly	acc Thr	cct Pro	gat Asp	gat Asp	cct Pro	gac Asp	atg Met	691
act Thr	tac Tyr	gcg Ala	tcg Ser	atg Met	ggt Gly	aac Asn	tac Tyr	att Ile	ttc Phe	acc Thr	act Thr	gaa Glu	gcc Ala	ctg Leu	atc Ile	739
cag Gln	gcg Ala	ctg Leu	aaa Lys	gat Asp	gat Asp	gaa Glu	aac Asn	aac Asn	gag Glu	aac Asn	agt Ser	gat Asp	cat His	gac Asp	atg Met	787
ggc Gly	gga Gly	gac Asp	atc Ile	att Ile	ccg Pro	tac Tyr	ttc Phe	gtc Val	tct Ser	cg Arg	aac Asn	gat Asp	gcg Ala	cat His	gtt Val	835
tat Tyr	gat Asp	ttc Phe	tcc Ser	gga Gly	aac Asn	att Ile	ggt Val	cct Pro	ggc Gly	gca Ala	act Thr	gag Glu	cgt Arg	gac Asp	aag Lys	883
ggc Gly	tac Tyr	tgg Trp	cg Arg	gac Asp	gtc Val	ggt Gly	acc Thr	att Ile	gat Asp	gcg Ala	ttc Phe	tac Tyr	gag Glu	tgc Cys	cac His	931
atg Met	gac Asp	ctg Leu	att Ile	tcc Ser	gtg Val	cac His	cca Pro	atc Ile	ttc Phe	aac Asn	ctg Leu	tat Tyr	aac Asn	tct Ser	gag Glu	979
tgg Trp	cca Pro	atc Ile	cac His	acg Thr	acc Thr	tct Ser	gaa Glu	ggt Gly	aac Asn	ttg Leu	cct Pro	ccg Pro	gct Ala	aag Lys	ttc Phe	1027
gtt Val	cg Arg	ggc Gly	ggt Gly	atc Ile	gcg Ala	cag Gln	tcg Ser	tcg Ser	atg Met	gtg Val	tct Ser	tca Ser	ggt Gly	tcc Ser	atc Ile	1075

310	315	320	325	
att tct gct ggg act gtt cgc aac tcc gtg ctg tcc aac aac gtt gtc				1123
Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu Ser Asn Asn Val Val	330	335	340	
gtc gaa gag ggc gca acg gtg gaa ggt gca gtg ctg atg cca ggc gtg				1171
Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val Leu Met Pro Gly Val	345	350	355	
cgc atc ggt aag ggt gct gtt gtc cgc cat gcg att ctg gac aag aac				1219
Arg Ile Gly Lys Gly Ala Val Val Arg His Ala Ile Leu Asp Lys Asn	360	365	370	
gtg gtt gtc cgc gac gga gag ctc atc ggt gtc gac caa gtg cgc gat				1267
Val Val Val Arg Asp Gly Glu Leu Ile Gly Val Asp Gln Val Arg Asp	375	380	385	
gcg cag cgc ttc aag gtg agc gcc ggc ggc gtc gtg gtt gtc ggt aag				1315
Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val Val Val Val Gly Lys	390	395	400	405
aac cag gta gtc taaacgggaa agggacctta aaa				1350
Asn Gln Val Val				

<210> 276

<211> 409

<212> PRT

<213> Corynebacterium glutamicum

<400> 276

Met Val Lys Gly Val Lys Gly Arg Pro Asn Val Leu Ala Ile Val Leu	1	5	10	15
Ala Gly Gly Glu Gly Lys Arg Leu Phe Pro Leu Thr Glu Asp Arg Ala	20	25	30	
Lys Pro Ala Val Pro Phe Gly Gly Thr Tyr Arg Leu Ile Asp Phe Val	35	40	45	
Leu Ser Asn Leu Val Asn Ser Gly Phe Leu Lys Ile Ala Val Leu Thr	50	55	60	
Gln Tyr Lys Ser His Ser Leu Asp Arg His Ile Ser Leu Ser Trp Asn	65	70	75	80
Val Ser Gly Pro Thr Gly Gln Tyr Ile Ala Ser Val Pro Ala Gln Gln	85	90	95	
Arg Leu Gly Lys Arg Trp Phe Thr Gly Ser Ala Asp Ala Ile Leu Gln	100	105	110	
Ser Leu Asn Leu Ile Ser Asp Glu Lys Pro Asp Tyr Val Ile Val Phe	115	120	125	
Gly Ala Asp His Val Tyr Arg Met Asp Pro Ser Gln Met Leu Asp Glu	130	135	140	
His Ile Ala Ser Gly Arg Ala Val Ser Val Ala Gly Ile Arg Val Pro				

```

145                150                155                160
Arg Glu Glu Ala Thr Ala Phe Gly Cys Ile Gln Ser Asp Val Asp Gly
      165                170                175
Asn Ile Thr Glu Phe Leu Glu Lys Pro Ala Asp Pro Pro Gly Thr Pro
      180                185                190
Asp Asp Pro Asp Met Thr Tyr Ala Ser Met Gly Asn Tyr Ile Phe Thr
      195                200                205
Thr Glu Ala Leu Ile Gln Ala Leu Lys Asp Asp Glu Asn Asn Glu Asn
      210                215                220
Ser Asp His Asp Met Gly Gly Asp Ile Ile Pro Tyr Phe Val Ser Arg
      225                230                235                240
Asn Asp Ala His Val Tyr Asp Phe Ser Gly Asn Ile Val Pro Gly Ala
      245                250                255
Thr Glu Arg Asp Lys Gly Tyr Trp Arg Asp Val Gly Thr Ile Asp Ala
      260                265                270
Phe Tyr Glu Cys His Met Asp Leu Ile Ser Val His Pro Ile Phe Asn
      275                280                285
Leu Tyr Asn Ser Glu Trp Pro Ile His Thr Thr Ser Glu Gly Asn Leu
      290                295                300
Pro Pro Ala Lys Phe Val Arg Gly Gly Ile Ala Gln Ser Ser Met Val
      305                310                315                320
Ser Ser Gly Ser Ile Ile Ser Ala Gly Thr Val Arg Asn Ser Val Leu
      325                330                335
Ser Asn Asn Val Val Val Glu Glu Gly Ala Thr Val Glu Gly Ala Val
      340                345                350
Leu Met Pro Gly Val Arg Ile Gly Lys Gly Ala Val Val Arg His Ala
      355                360                365
Ile Leu Asp Lys Asn Val Val Val Arg Asp Gly Glu Leu Ile Gly Val
      370                375                380
Asp Gln Val Arg Asp Ala Gln Arg Phe Lys Val Ser Ala Gly Gly Val
      385                390                395                400
Val Val Val Gly Lys Asn Gln Val Val
      405

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<210> 277

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> RXN00014

<400> 277

catcaaagtg accgccggcg gcgtcgaaatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaacttttaa gcgcactaga ctaacaacac atg agc aaa tat gca 115
Met Ser Lys Tyr Ala
1 5

gac gat tta gcc tta gcc ctc gaa ctt gcc gaa ctt gcc gat tcc atc 163
Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
25 30 35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259
Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
40 45 50

cgt gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307
Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
55 60 65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355
Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
70 75 80 85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403
Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
90 95 100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451
Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile
105 110 115

tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc 499
Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly
120 125 130

gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc 547
Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser
135 140 145

cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc 595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser
150 155 160 165

ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat 643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp
170 175 180

acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc 691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu
185 190 195

gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc 739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu
200 205 210

tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag 787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys

```

      215              220              225
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta 835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val
230              235              240              245

gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa 880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys
      250              255              260

tagactcccg gggttttgctt ggt 903

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<210> 278
 <211> 260
 <212> PRT
 <213> Corynebacterium glutamicum

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<400> 278
Met Ser Lys Tyr Ala Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu
  1              5              10              15

Leu Ala Asp Ser Ile Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu
      20              25              30

Val Ser Ser Lys Pro Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala
      35              40              45

Thr Glu Glu Ala Leu Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp
      50              55              60

Ser Ile Leu Gly Glu Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg
      65              70              75              80

Gln Trp Ile Ile Asp Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly
      85              90              95

Val Pro Val Trp Ala Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro
      100             105             110

Val Ala Gly Val Ile Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala
      115             120             125

Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg
      130             135             140

Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser
      145             150             155             160

Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe
      165             170             175

Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe
      180             185             190

Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu
      195             200             205

Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr
      210             215             220

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Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His
 225 230 235 240

Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu
 245 250 255

Asp Arg Leu Lys
 260

<210> 279

<211> 903

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(880)

<223> FRXA00014

<400> 279

catcaaagtg accgccggcg gcgtcgatg gtccgttgca ggaaacgcgg aagcagttag 60

tgagatctcc gaaactttaa ggcactaga ctagcaacac atg agc aaa tat gca 115
 Met Ser Lys Tyr Ala
 1 5

gac gat tta gcc tta gcc ctc gaa ctc gcc gaa ctt gcc gat tcc atc 163
 Asp Asp Leu Ala Leu Ala Leu Glu Leu Ala Glu Leu Ala Asp Ser Ile
 10 15 20

acc ctc gac cgc ttc gaa gcc tct gac ctg gaa gta tcc tcc aag cca 211
 Thr Leu Asp Arg Phe Glu Ala Ser Asp Leu Glu Val Ser Ser Lys Pro
 25 30 35

gac atg act ccc gtc agc gat gcc gac ctg gcg acc gaa gaa gca ctc 259
 Asp Met Thr Pro Val Ser Asp Ala Asp Leu Ala Thr Glu Glu Ala Leu
 40 45 50

cgc gag aaa atc gcc acc gcc cgc ccc gcc gac tcc atc ctc ggt gaa 307
 Arg Glu Lys Ile Ala Thr Ala Arg Pro Ala Asp Ser Ile Leu Gly Glu
 55 60 65

gaa ttc ggt ggc gac gta gaa ttc agc ggc cgc cag tgg atc atc gac 355
 Glu Phe Gly Gly Asp Val Glu Phe Ser Gly Arg Gln Trp Ile Ile Asp
 70 75 80 85

ccc atc gac ggc acc aaa aac tac gtc cgc ggc gtc ccc gta tgg gca 403
 Pro Ile Asp Gly Thr Lys Asn Tyr Val Arg Gly Val Pro Val Trp Ala
 90 95 100

acc ctg atc gcg ctg ctc gac aac ggc aaa ccc gtc gca ggt gtc atc 451
 Thr Leu Ile Ala Leu Leu Asp Asn Gly Lys Pro Val Ala Gly Val Ile
 105 110 115

tcc gca ccc gca ctg gct agg cgt tgg tgg gca tcc gaa ggg gcc ggc 499
 Ser Ala Pro Ala Leu Ala Arg Arg Trp Trp Ala Ser Glu Gly Ala Gly
 120 125 130

gca tgg cgc acc ttc aac ggc agc tcc cca cgc aaa ctg tcc gtg tcc 547
 Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg Lys Leu Ser Val Ser

135	140	145	
cag gtg tcc aag ctt gac gac gcc tcc ctc tcc ttc tcc tcc ctc tcc			595
Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser Phe Ser Ser Leu Ser			
150	155	160	165
ggc tgg gcc gaa cga gat ttg cgc gat cag ttc gtc tcc cta act gat			643
Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe Val Ser Leu Thr Asp			
	170	175	180
acc acc tgg cga ctc cgc ggc tac ggc gac ttc ttc tcc tac tgc ctc			691
Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe Phe Ser Tyr Cys Leu			
	185	190	195
gtc gcc gaa ggt gcc gtc gat atc gcc gct gaa cca gaa gtc agc ctc			739
Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu Pro Glu Val Ser Leu			
	200	205	210
tgg gat ctt gct ccc ctg tcc atc ctg gtc acc gaa gcc gga gga aag			787
Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr Glu Ala Gly Gly Lys			
	215	220	225
ttc acc tca ctg gct ggc gtc gat gga cca cac ggt ggc gat gca gta			835
Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His Gly Gly Asp Ala Val			
	230	235	240
gcc acc aac ggc atc ctg cac gat gag acg ctg gat cgt tta aaa			880
Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu Asp Arg Leu Lys			
	250	255	260
tagactcccg gggttttgctt ggt			903

<210> 280

<211> 260

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 280

Met	Ser	Lys	Tyr	Ala	Asp	Asp	Leu	Ala	Leu	Ala	Leu	Glu	Leu	Ala	Glu
1				5					10					15	

Leu	Ala	Asp	Ser	Ile	Thr	Leu	Asp	Arg	Phe	Glu	Ala	Ser	Asp	Leu	Glu
		20						25					30		

Val	Ser	Ser	Lys	Pro	Asp	Met	Thr	Pro	Val	Ser	Asp	Ala	Asp	Leu	Ala
		35					40					45			

Thr	Glu	Glu	Ala	Leu	Arg	Glu	Lys	Ile	Ala	Thr	Ala	Arg	Pro	Ala	Asp
	50					55				60					

Ser	Ile	Leu	Gly	Glu	Glu	Phe	Gly	Gly	Asp	Val	Glu	Phe	Ser	Gly	Arg
65				70					75					80	

Gln	Trp	Ile	Ile	Asp	Pro	Ile	Asp	Gly	Thr	Lys	Asn	Tyr	Val	Arg	Gly
				85				90						95	

Val	Pro	Val	Trp	Ala	Thr	Leu	Ile	Ala	Leu	Leu	Asp	Asn	Gly	Lys	Pro
			100					105					110		

Val	Ala	Gly	Val	Ile	Ser	Ala	Pro	Ala	Leu	Ala	Arg	Arg	Trp	Trp	Ala
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

115	120	125
Ser Glu Gly Ala Gly Ala Trp Arg Thr Phe Asn Gly Ser Ser Pro Arg		
130	135	140
Lys Leu Ser Val Ser Gln Val Ser Lys Leu Asp Asp Ala Ser Leu Ser		
145	150	155
Phe Ser Ser Leu Ser Gly Trp Ala Glu Arg Asp Leu Arg Asp Gln Phe		
	165	170
Val Ser Leu Thr Asp Thr Thr Trp Arg Leu Arg Gly Tyr Gly Asp Phe		
	180	185
Phe Ser Tyr Cys Leu Val Ala Glu Gly Ala Val Asp Ile Ala Ala Glu		
	195	200
Pro Glu Val Ser Leu Trp Asp Leu Ala Pro Leu Ser Ile Leu Val Thr		
	210	215
Glu Ala Gly Gly Lys Phe Thr Ser Leu Ala Gly Val Asp Gly Pro His		
225	230	235
Gly Gly Asp Ala Val Ala Thr Asn Gly Ile Leu His Asp Glu Thr Leu		
	245	250
Asp Arg Leu Lys		
	260	

<210> 281
 <211> 978
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(955)
 <223> RXA01570

<400> 281
 cactgaactc cgttttggat ctcggcaaaa tcgaagccac cggatttagc gcaccgacct 60
 ggcagacccg cctcaacgac tacctcaagg aactctcaaa gtg aaa ggc atc atc 115
 Val Lys Gly Ile Ile
 1 5
 ctc gca ggt ggc tcc ggc acc cgg ctc tac ccc atc acc aag ggc atc 163
 Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro Ile Thr Lys Gly Ile
 10 15 20
 tcc aag caa ctg atg ccg att tac gac aaa ccc atg gtc tac tac cca 211
 Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro Met Val Tyr Tyr Pro
 25 30 35
 ctg acc acg ctc att cag gcc ggc atc aaa gac atc ctg att atc acc 259
 Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp Ile Leu Ile Ile Thr
 40 45 50
 acc cct gaa gac agc gcc tcc ttt gaa cgc ttg ctt ggc gac ggc tcc 307
 Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu Leu Gly Asp Gly Ser

55	60	65	
tcc tgg ggc atc aac ctc acc tac gcc gtc caa ccc tcc ccc gac gga			355
Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln Pro Ser Pro Asp Gly			
70	75	80	85
cta gcc caa gca ttc atc atc ggc gag gaa ttc atc ggt gac gac gac			403
Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe Ile Gly Asp Asp Asp			
	90	95	100
gtc gcg ttg gtg ctt ggc gat aac atc ttc gac ggc gca caa ctt ggc			451
Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp Gly Ala Gln Leu Gly			
	105	110	115
cac gca cta aag cag tgc tcc aac ccc gac ggt ggc att gtc ttt gct			499
His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly Gly Ile Val Phe Ala			
	120	125	130
tat gag gtc tcc gat cct gag cgt tat ggc gtg gtg gaa ttt gat gct			547
Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val Val Glu Phe Asp Ala			
	135	140	145
gct aat aag gcg gtg tct att gaa gaa aag ccc acc gcg cca aaa tcc			595
Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro Thr Ala Pro Lys Ser			
	150	155	160
aac ttt gcc gtg gta gga cta tat ttc tac gac aat cgc gtg gtg gac			643
Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp Asn Arg Val Val Asp			
	170	175	180
atc gcc aag tca atc aag cct tcc tcg cgt ggc gaa ctg gaa atc acc			691
Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly Glu Leu Glu Ile Thr			
	185	190	195
tcc gtt aac gat gcc tac ctc cag caa ggt gct tta act gtg cag cgc			739
Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala Leu Thr Val Gln Arg			
	200	205	210
ctg gac cgt ggc gat gtc tgg tta gat acc ggc aca atc gat tcc atg			787
Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly Thr Ile Asp Ser Met			
	215	220	225
tcc gag gcg tct tcc tat gtt gag gtc ctg caa aaa cgt acc ggc aac			835
Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln Lys Arg Thr Gly Asn			
	230	235	240
atc atc gga tcc ccc gaa gtc gct gcg tac cgc gaa ggt ttc atc aca			883
Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg Glu Gly Phe Ile Thr			
	250	255	260
gct gaa gaa ctc aca gtg ctt ggt gag gaa ctg aag aaa tca ggc tac			931
Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu Lys Lys Ser Gly Tyr			
	265	270	275
gga aac tac ctg ctg aga gct ttg taattttacgg tgtggttgag gag			978
Gly Asn Tyr Leu Leu Arg Ala Leu			
	280	285	

<210> 282

<211> 285

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 282

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Val Lys Gly Ile Ile Leu Ala Gly Gly Ser Gly Thr Arg Leu Tyr Pro
 1           5           10           15

Ile Thr Lys Gly Ile Ser Lys Gln Leu Met Pro Ile Tyr Asp Lys Pro
          20           25           30

Met Val Tyr Tyr Pro Leu Thr Thr Leu Ile Gln Ala Gly Ile Lys Asp
          35           40           45

Ile Leu Ile Ile Thr Thr Pro Glu Asp Ser Ala Ser Phe Glu Arg Leu
 50           55           60

Leu Gly Asp Gly Ser Ser Trp Gly Ile Asn Leu Thr Tyr Ala Val Gln
 65           70           75           80

Pro Ser Pro Asp Gly Leu Ala Gln Ala Phe Ile Ile Gly Glu Glu Phe
          85           90           95

Ile Gly Asp Asp Asp Val Ala Leu Val Leu Gly Asp Asn Ile Phe Asp
          100           105           110

Gly Ala Gln Leu Gly His Ala Leu Lys Gln Cys Ser Asn Pro Asp Gly
          115           120           125

Gly Ile Val Phe Ala Tyr Glu Val Ser Asp Pro Glu Arg Tyr Gly Val
          130           135           140

Val Glu Phe Asp Ala Ala Asn Lys Ala Val Ser Ile Glu Glu Lys Pro
          145           150           155           160

Thr Ala Pro Lys Ser Asn Phe Ala Val Val Gly Leu Tyr Phe Tyr Asp
          165           170           175

Asn Arg Val Val Asp Ile Ala Lys Ser Ile Lys Pro Ser Ser Arg Gly
          180           185           190

Glu Leu Glu Ile Thr Ser Val Asn Asp Ala Tyr Leu Gln Gln Gly Ala
          195           200           205

Leu Thr Val Gln Arg Leu Asp Arg Gly Asp Val Trp Leu Asp Thr Gly
          210           215           220

Thr Ile Asp Ser Met Ser Glu Ala Ser Ser Tyr Val Glu Val Leu Gln
          225           230           235           240

Lys Arg Thr Gly Asn Ile Ile Gly Ser Pro Glu Val Ala Ala Tyr Arg
          245           250           255

Glu Gly Phe Ile Thr Ala Glu Glu Leu Thr Val Leu Gly Glu Glu Leu
          260           265           270

Lys Lys Ser Gly Tyr Gly Asn Tyr Leu Leu Arg Ala Leu
          275           280           285

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<210> 283

<211> 891

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(868)

<223> RXA02666

<400> 283

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gctcggcgcgac gaggaagaga agaaggacgc attcgacgac ttcgacgatt ccgacgtgga 60
tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115
                                         Met Ser Ser Thr Arg
                                         1 5
atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu
                        10 15 20
ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
                        25 30 35
tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
                        40 45 50
atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
                        55 60 65
ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg
                        70 75 80 85
ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu
                        90 95 100
cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc 451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile
                        105 110 115
cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg 499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val
                        120 125 130
gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca 547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro
                        135 140 145
gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc 595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val
                        150 155 160 165
gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc 643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly
                        170 175 180
ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac 691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp

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                185                190                195
ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg 739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp
                200                205                210

tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa 787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys
                215                220                225

gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa 835
Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu
                230                235                240                245

gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg 888
Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
                250                255

tag 891

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<210> 284
<211> 256
<212> PRT
<213> Corynebacterium glutamicum

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<400> 284
Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly
  1             5             10             15

Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
      20             25             30

Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
      35             40             45

Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
      50             55             60

Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
      65             70             75             80

Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
      85             90             95

Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
      100            105            110

Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
      115            120            125

Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
      130            135            140

Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
      145            150            155            160

Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
      165            170            175

Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu

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180	185	190
Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala		
195	200	205
Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp		
210	215	220
Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln		
225	230	235
Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp		
245	250	255

<210> 285

<211> 1056

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1033)

<223> RXA00825

<400> 285

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cccgttcattg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60
tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
                                         Met Arg Thr Val Val
                                         1      5

acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
                        10                        15                        20

aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
                        25                        30                        35

ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val
                        40                        45                        50

gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac 307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His
                        55                        60                        65

aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac 355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His
                        70                        75                        80                        85

tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc 403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr
                        90                        95                        100

atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc 451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val

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105	110	115	
ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca			499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro			
120	125	130	
ggt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc			547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser			
135	140	145	
aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc			595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly			
150	155	160	165
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa			643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln			
170	175	180	
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt			691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu			
185	190	195	
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc			739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg			
200	205	210	
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct			787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser			
215	220	225	
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa			835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu			
230	235	240	245
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc			883
Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser			
250	255	260	
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc			931
Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg			
265	270	275	
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct			979
Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro			
280	285	290	
gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc			1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg			
295	300	305	
act cac taggggaaaa tccaccacaa atc			1056
Thr His			
310			

<210> 286

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 286

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu
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 Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn
 20 25 30
 Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly
 35 40 45
 Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu
 50 55 60
 Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80
 Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95
 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110
 Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125
 Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140
 Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160
 Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175
 Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

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ttatagtaga acgtttctagt aaaacttgga aggatgaaaa																115
Met Ser Val Lys Leu																5
1																
gcc ctc atc ggt gct gga cgc atc gga tca aat cac gca cgc ctg atc																163
Ala Leu Ile Gly Ala Gly Arg Ile Gly Ser Asn His Ala Arg Leu Ile																20
10 15																
aca aac cac gtg atc ggc tct gaa ctg gtc gcc gtc gtt gac cca act																211
Thr Asn His Val Ile Gly Ser Glu Leu Val Ala Val Val Asp Pro Thr																35
25 30																
ccc aac gca gaa acc ctc gct gat gaa ttg ggc gcc gtt gcg ttc tct																259
Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly Ala Val Ala Phe Ser																50
40 45																
aac cca gat gac gtc ctg acc cgc gat gac att gac gcg gtt ttg att																307
Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile Asp Ala Val Leu Ile																65
55 60																
gct aca cca gca cga acc cac gcg gat ctc gtg gtc aaa gca gcg gca																355
Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val Val Lys Ala Ala Ala																85
70 75 80																
gcg ggc aag cac gtg ttt gtg gaa aag ccc atg gcc gtc acc ctc gag																403
Ala Gly Lys His Val Phe Val Glu Lys Pro Met Ala Val Thr Leu Glu																100
90 95																
gac gca gat cgt gcc atc aac gca gca cgc gaa gca aac act gtc ctg																451
Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu Ala Asn Thr Val Leu																115
105 110																
cag gtg ggc ttc aat cgt cgt ttc gcg gca ggt ttc gct gca gca cgc																499
Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly Phe Ala Ala Ala Arg																130
120 125																
gca cgc att gac gca ggc gat atc ggc acc cca cag ctg ctt cgt tcc																547
Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro Gln Leu Leu Arg Ser																145
135 140																
gtg acc cgc gat cca gga cca ttc acc gct gac ccc aac aag atc cct																595
Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp Pro Asn Lys Ile Pro																165
150 155 160																
cag tgg acc atc ttc ctg gaa acc ctc atc cac gat ttc gat gcg ctg																643
Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His Asp Phe Asp Ala Leu																180
170 175																

tgc tac ctc aac cca ggc gca acc cca gtg gaa gta acc gct cac gct 691
 Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu Val Thr Ala His Ala
 185 190 195

gat tgc ctc gtc gtt cca gaa gct gct ggc act ggc ttc ctc gac acc 739
 Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr Gly Phe Leu Asp Thr
 200 205 210

gca gtg gtg act gtc cgt ttt gat aac gga gca att ggt act gca gaa 787
 Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala Ile Gly Thr Ala Glu
 215 220 225

gca agc ttc agc gca gcc tat ggt tat gac gtt cgc ggt gaa gtc ttc 835
 Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val Arg Gly Glu Val Phe
 230 235 240 245

gga tcc aag ggc atg atg acc gca ggc gac gcg cgc gca acc aac atg 883
 Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala Arg Ala Thr Asn Met
 250 255 260

act ttc tac ggc gct gag ggc atc gcg gct gcc acc tca cgc gcg gat 931
 Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala Thr Ser Arg Ala Asp
 265 270 275

acc gat ctg ctc tcc gat gct tac cga gct gaa ttc caa gct ttc gtc 979
 Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu Phe Gln Ala Phe Val
 280 285 290

gac tcc atc cgt acc aac acc cct tcc aag gtt cca ggc gaa gct gca 1027
 Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val Pro Gly Glu Ala Ala
 295 300 305

cgc acc gca cta ctc atc gca ctc ggc gcc atc cga agc gta gaa acc 1075
 Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile Arg Ser Val Glu Thr
 310 315 320 325

ggc gca acc atc aac ctt gct gaa agc atc gag gtt taacctgac 1121
 Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu Val
 330 335

ttttaaactc gca 1134

<210> 288

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 288

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His Ala Arg Leu Ile Thr Asn His Val Ile Gly Ser Glu Leu Val Ala
 20 25 30

Val Val Asp Pro Thr Pro Asn Ala Glu Thr Leu Ala Asp Glu Leu Gly
 35 40 45

Ala Val Ala Phe Ser Asn Pro Asp Asp Val Leu Thr Arg Asp Asp Ile
 50 55 60

Asp Ala Val Leu Ile Ala Thr Pro Ala Arg Thr His Ala Asp Leu Val
 65 70 75 80
 Val Lys Ala Ala Ala Gly Lys His Val Phe Val Glu Lys Pro Met
 85 90 95
 Ala Val Thr Leu Glu Asp Ala Asp Arg Ala Ile Asn Ala Ala Arg Glu
 100 105 110
 Ala Asn Thr Val Leu Gln Val Gly Phe Asn Arg Arg Phe Ala Ala Gly
 115 120 125
 Phe Ala Ala Ala Arg Ala Arg Ile Asp Ala Gly Asp Ile Gly Thr Pro
 130 135 140
 Gln Leu Leu Arg Ser Val Thr Arg Asp Pro Gly Pro Phe Thr Ala Asp
 145 150 155 160
 Pro Asn Lys Ile Pro Gln Trp Thr Ile Phe Leu Glu Thr Leu Ile His
 165 170 175
 Asp Phe Asp Ala Leu Cys Tyr Leu Asn Pro Gly Ala Thr Pro Val Glu
 180 185 190
 Val Thr Ala His Ala Asp Cys Leu Val Val Pro Glu Ala Ala Gly Thr /
 195 200 205
 Gly Phe Leu Asp Thr Ala Val Val Thr Val Arg Phe Asp Asn Gly Ala
 210 215 220
 Ile Gly Thr Ala Glu Ala Ser Phe Ser Ala Ala Tyr Gly Tyr Asp Val
 225 230 235 240
 Arg Gly Glu Val Phe Gly Ser Lys Gly Met Met Thr Ala Gly Asp Ala
 245 250 255
 Arg Ala Thr Asn Met Thr Phe Tyr Gly Ala Glu Gly Ile Ala Ala Ala
 260 265 270
 Thr Ser Arg Ala Asp Thr Asp Leu Leu Ser Asp Ala Tyr Arg Ala Glu
 275 280 285
 Phe Gln Ala Phe Val Asp Ser Ile Arg Thr Asn Thr Pro Ser Lys Val
 290 295 300
 Pro Gly Glu Ala Ala Arg Thr Ala Leu Leu Ile Ala Leu Gly Ala Ile
 305 310 315 320
 Arg Ser Val Glu Thr Gly Ala Thr Ile Asn Leu Ala Glu Ser Ile Glu
 325 330 335
 Val

<210> 289

<211> 996

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(973)

<223> RXN00013

<400> 289

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acgccacctt attcagcaca cttggccgac ggcattgcaca atg gaa ggc atg act 115
              Met Glu Gly Met Thr
              1 5

aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa 163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys
              10 15 20

acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag 211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu
              25 30 35

cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc 259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg
              40 45 50

atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat 307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp
              55 60 65

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
              70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Glu Ala
              90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
              105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
              120 125 130

gcg ctg gtc gag ggc gat cca tec gcg cca tcg cgc gtg ctt ttc ggc 547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
              135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
              150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
              170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
              185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro

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200	205	210	
gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc			787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile			
215	220	225	
gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg			835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp			
230	235	240	245
gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gca tgc			883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys			
250	255	260	
atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg			931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala			
265	270	275	
gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac			973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp			
280	285	290	
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<211> 291

<212> PRT

<213> Corynebacterium glutamicum

<400> 290

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Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp	
20 25 30	
Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly	
35 40 45	
Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys	
50 55 60	
Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala	
65 70 75 80	
Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu	
85 90 95	
Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val	
100 105 110	
Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr	
115 120 125	
Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser	
130 135 140	
Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp	
145 150 155 160	

<400> 291																
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Met Glu Gly Met Thr																115
1 5																
aat cca gag cag aca cat ccc gct gca agc ctc gaa gac atg atc aaa																163
Asn Pro Glu Gln Thr His Pro Ala Ala Ser Leu Glu Asp Met Ile Lys																
10 15 20																
acc atc aca aag acc ttc gtg att gct cac gat cag gat tct gat gag																211
Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp Gln Asp Ser Asp Glu																
25 30 35																
cat ctt gcg cag gca ctg gtg tac aac gct gga cgt ttg gca tgg cgc																259
His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly Arg Leu Ala Trp Arg																
40 45 50																
atg cgc gaa aac ggt gtg gat acg gat tac aag act tct gtg tct gat																307
Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys Thr Ser Val Ser Asp																
55 60 65																

gtg gtc acg gat gcc gat cgt gcg gcc gag gcc ttc gtc gca ggc gtt 355
Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala Phe Val Ala Gly Val
70 75 80 85

ctt gaa gcg ttg cgg cct gag gac ggc gtg ctt ggc gag gaa ggc gcg 403
Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu Gly Glu Glu Gly Ala
90 95 100

gac cgg gcg tcg aaa agc gga aaa acc tgg gtc atc gac ccg gtt gat 451
Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val Ile Asp Pro Val Asp
105 110 115

ggc acc tac aac ttc acc cag ggc tca gat tat tgg tgc tcg gcg ctc 499
Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr Trp Cys Ser Ala Leu
120 125 130

gcg ctg gtc gag ggc gat cca tcc gcg cca tcg cgc gtg ctt ttc ggc 547
Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser Arg Val Leu Phe Gly
135 140 145

gcc gta cac cgc cca gcc atg ggt tat acg tgg ttc ggt ggc ccg gga 595
Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp Phe Gly Gly Pro Gly
150 155 160 165

atc cgc acc acg ctc gac ggc aag gag cta gat ttg ctt gtc gac gcc 643
Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp Leu Leu Val Asp Ala
170 175 180

ccc ctc aat caa atc tcc ctg gcc acc tac atc cac ccg tca cgc atc 691
Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile His Pro Ser Arg Ile
185 190 195

gcg gaa cct gat att caa aag gcg tgg atg agc gtt gcc acc cac cct 739
Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser Val Ala Thr His Pro
200 205 210

gca acg ctg cgc atg ttc ggc gcc ggc tcc atc gat ttg gcc aac atc 787
Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile Asp Leu Ala Asn Ile
215 220 225

gcc gac ggc agc atg ggc gca tgg gtg cag cac agc gtc gca gat tgg 835
Ala Asp Gly Ser Met Gly Ala Trp Val Gln His Ser Val Ala Asp Trp
230 235 240 245

gac tgg cta ccc ggc cgc gca ctc atc gaa ggc gtc ggc gga gcg tgc 883
Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly Val Gly Gly Ala Cys
250 255 260

atc aaa gtg acc gcc ggc ggc gtc gaa tgg tcc gtt gca gga aac gcg 931
Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser Val Ala Gly Asn Ala
265 270 275

gaa gca gtt agt gag atc tcc gaa act tta agc gca cta gac 973
Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser Ala Leu Asp
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<210> 292

<211> 291

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 292

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Glu Asp Met Ile Lys Thr Ile Thr Lys Thr Phe Val Ile Ala His Asp
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Gln Asp Ser Asp Glu His Leu Ala Gln Ala Leu Val Tyr Asn Ala Gly
      35           40           45

Arg Leu Ala Trp Arg Met Arg Glu Asn Gly Val Asp Thr Asp Tyr Lys
 50           55           60

Thr Ser Val Ser Asp Val Val Thr Asp Ala Asp Arg Ala Ala Glu Ala
 65           70           75           80

Phe Val Ala Gly Val Leu Glu Ala Leu Arg Pro Glu Asp Gly Val Leu
      85           90           95

Gly Glu Glu Gly Ala Asp Arg Ala Ser Lys Ser Gly Lys Thr Trp Val
      100           105           110

Ile Asp Pro Val Asp Gly Thr Tyr Asn Phe Thr Gln Gly Ser Asp Tyr
      115           120           125

Trp Cys Ser Ala Leu Ala Leu Val Glu Gly Asp Pro Ser Ala Pro Ser
      130           135           140

Arg Val Leu Phe Gly Ala Val His Arg Pro Ala Met Gly Tyr Thr Trp
      145           150           155           160

Phe Gly Gly Pro Gly Ile Arg Thr Thr Leu Asp Gly Lys Glu Leu Asp
      165           170           175

Leu Leu Val Asp Ala Pro Leu Asn Gln Ile Ser Leu Ala Thr Tyr Ile
      180           185           190

His Pro Ser Arg Ile Ala Glu Pro Asp Ile Gln Lys Ala Trp Met Ser
      195           200           205

Val Ala Thr His Pro Ala Thr Leu Arg Met Phe Gly Ala Gly Ser Ile
      210           215           220

Asp Leu Ala Asn Ile Ala Asp Gly Ser Met Gly Ala Trp Val Gln His
      225           230           235           240

Ser Val Ala Asp Trp Asp Trp Leu Pro Gly Arg Ala Leu Ile Glu Gly
      245           250           255

Val Gly Gly Ala Cys Ile Lys Val Thr Ala Gly Gly Val Glu Trp Ser
      260           265           270

Val Ala Gly Asn Ala Glu Ala Val Ser Glu Ile Ser Glu Thr Leu Ser
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Ala Leu Asp
      290

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Met Asp Ala Arg Gly																5
1																
atg ttg gcc att gcg gag gcc gtt gta gat gat gcc gaa gcc ctc ttc																163
Met Leu Ala Ile Ala Glu Ala Val Val Asp Asp Ala Glu Ala Leu Phe																20
10 15																
atg cag gcc ttc gga gct gca cct gcc cat atg aaa tcc ccg ggg gat																211
Met Gln Gly Phe Gly Ala Ala Pro Ala His Met Lys Ser Pro Gly Asp																35
25 30																
ttt gcc acg gaa gtg gat atg gcc atc gaa tcc cat atg cgt tcg atg																259
Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser His Met Arg Ser Met																50
40 45																
ctg aac atg atg aca ggc att gct gtc atc ggt gaa gaa ggt ggc ggt																307
Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly Glu Glu Gly Gly Gly																65
55 60																
gcg acc tcc ggc acg cgc tgg gtg att gat ccc atc gac ggc acc gcc																355
Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro Ile Asp Gly Thr Ala																85
70 75 80																
aac ttc gcg gcg tcc aac ccg atg agc gcg atc ctg gtg tct ttg ctt																403
Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile Leu Val Ser Leu Leu																100
90 95																
gtc gac gac cag ccc gtc ctg ggt att acc tcc atg ccc atg ctg ggt																451
Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser Met Pro Met Leu Gly																115
105 110																
aaa cgc ctc acc gct ttt gaa ggt tca ccg ctg atg atc aac ggt gaa																499
Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu Met Ile Asn Gly Glu																130
120 125																
cct cag gaa cca ttg caa gaa caa tcc agt ttg gta tcc cac att ggt																547
Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu Val Ser His Ile Gly																145
135 140																
ttt agt tcc atg gcc tcc ccg cgc aat aca gcg ttt cct gtg gag ttg																595
Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala Phe Pro Val Glu Leu																165
150 155 160																
cgt cgg gat ctt ctg acc gag ctc acg gaa tcg tat ctt cgt ccc cgc																643
Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser Tyr Leu Arg Pro Arg																180
170 175																

att aca ggt tcg gtg ggt gtt gat ctc gcg ttc act gcg cag ggc att 691
 Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe Thr Ala Gln Gly Ile
 185 190 195
 ttt gga gca tgc gta tcg ttt agt cct cat gtt tgg gac aat tcc gca 739
 Phe Gly Ala Cys Val Ser Phe Ser Pro His Val Trp Asp Asn Ser Ala
 200 205 210
 ggc gtg atg ttg atg cgc gct gct ggt gca caa gtt act gac acc gaa 787
 Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln Val Thr Asp Thr Glu
 215 220 225
 ggc cat ccg tgg gca cca ggt agg gga gtc gtg gcc gga aca aaa agg 835
 Gly His Pro Trp Ala Pro Gly Arg Gly Val Val Ala Gly Thr Lys Arg
 230 235 240 245
 gct cac gat gtg ctg tta agt aag att gaa aaa gtt cgg ttg atg cat 883
 Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys Val Arg Leu Met His
 250 255 260
 gca gat gca ggt aat gac cag tcg tta aat gag gag tac aag 925
 Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu Glu Tyr Lys
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<210> 294

<211> 275

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 294

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 20 25 30
 Lys Ser Pro Gly Asp Phe Ala Thr Glu Val Asp Met Ala Ile Glu Ser
 35 40 45
 His Met Arg Ser Met Leu Asn Met Met Thr Gly Ile Ala Val Ile Gly
 50 55 60
 Glu Glu Gly Gly Gly Ala Thr Ser Gly Thr Arg Trp Val Ile Asp Pro
 65 70 75 80
 Ile Asp Gly Thr Ala Asn Phe Ala Ala Ser Asn Pro Met Ser Ala Ile
 85 90 95
 Leu Val Ser Leu Leu Val Asp Asp Gln Pro Val Leu Gly Ile Thr Ser
 100 105 110
 Met Pro Met Leu Gly Lys Arg Leu Thr Ala Phe Glu Gly Ser Pro Leu
 115 120 125
 Met Ile Asn Gly Glu Pro Gln Glu Pro Leu Gln Glu Gln Ser Ser Leu
 130 135 140

Val Ser His Ile Gly Phe Ser Ser Met Ala Ser Pro Arg Asn Thr Ala
 145 150 155 160

Phe Pro Val Glu Leu Arg Arg Asp Leu Leu Thr Glu Leu Thr Glu Ser
 165 170 175

Tyr Leu Arg Pro Arg Ile Thr Gly Ser Val Gly Val Asp Leu Ala Phe
 180 185 190

Thr Ala Gln Gly Ile Phe Gly Ala Cys Val Ser Phe Ser Pro His Val
 195 200 205

Trp Asp Asn Ser Ala Gly Val Met Leu Met Arg Ala Ala Gly Ala Gln
 210 215 220

Val Thr Asp Thr Glu Gly His Pro Trp Ala Pro Gly Arg Gly Val Val
 225 230 235 240

Ala Gly Thr Lys Arg Ala His Asp Val Leu Leu Ser Lys Ile Glu Lys
 245 250 255

Val Arg Leu Met His Ala Asp Ala Gly Asn Asp Gln Ser Leu Asn Glu
 260 265 270

Glu Tyr Lys
 275

<210> 295

<211> 576

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(576)

<223> RXN01332

<400> 295

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His Ile Ser Ala Ile Ile Glu Pro Asp Ala Ala Arg Ala Ala Ala Ala	
1 5 10 15	
gca gaa gac gcg ccg ggt gca cag gcc ttc act cgc att gaa gat gct	96
Ala Glu Asp Ala Pro Gly Ala Gln Ala Phe Thr Arg Ile Glu Asp Ala	
20 25 30	
atc gca gcc gat gct gtc gac gca gtg ctg atc gcc gta cca ggt cag	144
Ile Ala Ala Asp Ala Val Asp Ala Val Leu Ile Ala Val Pro Gly Gln	
35 40 45	
ttc cat gag cca gta ctt gtc cca gca cta gaa gca ggc ctt ccc atc	192
Phe His Glu Pro Val Leu Val Pro Ala Leu Glu Ala Gly Leu Pro Ile	
50 55 60	
ctg tgt gaa aag cca ctg acc cca gat tct gaa tcc tca ctg cgc atc	240
Leu Cys Glu Lys Pro Leu Thr Pro Asp Ser Glu Ser Ser Leu Arg Ile	
65 70 75 80	
gtc gag ctg gag cag aag ctg gac aag cca cac atc cag gtt ggt ttc	288
Val Glu Leu Glu Gln Lys Leu Asp Lys Pro His Ile Gln Val Gly Phe	

	85	90	95	
atg cgc cgc ttc gac cct gag tac aac aac ttg cgc aaa ttg gtg gaa				336
Met Arg Arg Phe Asp Pro Glu Tyr Asn Asn Leu Arg Lys Leu Val Glu				
	100	105	110	
tcc ggc gaa gct ggc gaa ctg ctc atg ctc cgc ggc ctg cac cgc aac				384
Ser Gly Glu Ala Gly Glu Leu Met Leu Arg Gly Leu His Arg Asn				
	115	120	125	
cca agt gtt ggt gag agc tac acc cag tcc atg ctg atc acc gac tcc				432
Pro Ser Val Gly Glu Ser Tyr Thr Gln Ser Met Leu Ile Thr Asp Ser				
	130	135	140	
gtc gtc cac gaa ttc gat gtc atc cca tgg ctc gca ggc tcc cga gtt				480
Val Val His Glu Phe Asp Val Ile Pro Trp Leu Ala Gly Ser Arg Val				
	145	150	155	160
gtc tcc gtt gaa gtg aag tac cca aag acc tcc tca ctg gcg cac tcc				528
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser				
	165	170	175	
ggc ctc aag gaa cca atc ctg gtg atc atg gag ctc gaa aac ggc gtg				576
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val				
	180	185	190	

<210> 296

<211> 192

<212> PRT

<213> Corynebacterium glutamicum

<400> 296

His	Ile	Ser	Ala	Ile	Ile	Glu	Pro	Asp	Ala	Ala	Arg	Ala	Ala	Ala	Ala
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Ala	Glu	Asp	Ala	Pro	Gly	Ala	Gln	Ala	Phe	Thr	Arg	Ile	Glu	Asp	Ala
			20					25					30		

Ile	Ala	Ala	Asp	Ala	Val	Asp	Ala	Val	Leu	Ile	Ala	Val	Pro	Gly	Gln
	35						40					45			

Phe	His	Glu	Pro	Val	Leu	Val	Pro	Ala	Leu	Glu	Ala	Gly	Leu	Pro	Ile
	50					55					60				

Leu	Cys	Glu	Lys	Pro	Leu	Thr	Pro	Asp	Ser	Glu	Ser	Ser	Leu	Arg	Ile
65					70					75					80

Val	Glu	Leu	Glu	Gln	Lys	Leu	Asp	Lys	Pro	His	Ile	Gln	Val	Gly	Phe
				85					90					95	

Met	Arg	Arg	Phe	Asp	Pro	Glu	Tyr	Asn	Asn	Leu	Arg	Lys	Leu	Val	Glu
			100					105					110		

Ser	Gly	Glu	Ala	Gly	Glu	Leu	Leu	Met	Leu	Arg	Gly	Leu	His	Arg	Asn
	115					120						125			

Pro	Ser	Val	Gly	Glu	Ser	Tyr	Thr	Gln	Ser	Met	Leu	Ile	Thr	Asp	Ser
	130					135					140				

Val	Val	His	Glu	Phe	Asp	Val	Ile	Pro	Trp	Leu	Ala	Gly	Ser	Arg	Val
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

145		150		155		160
Val Ser Val Glu Val Lys Tyr Pro Lys Thr Ser Ser Leu Ala His Ser						
		165		170		175
Gly Leu Lys Glu Pro Ile Leu Val Ile Met Glu Leu Glu Asn Gly Val						
		180		185		190

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(549)
 <223> FRXA01332

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ttc act cgc att gaa gat gct atc gca gcc gat gct gtc gac gca gtg	96
Phe Thr Arg Ile Glu Asp Ala Ile Ala Ala Asp Ala Val Asp Ala Val	
20 25 30	
ctg atc gcc gta cca ggt cag ttc cat gag cca gta ctt gtc cca gca	144
Leu Ile Ala Val Pro Gly Gln Phe His Glu Pro Val Leu Val Pro Ala	
35 40 45	
cta gaa gca ggc ctt ccc atc ctg tgt gaa aag cca ctg acc cca gat	192
Leu Glu Ala Gly Leu Pro Ile Leu Cys Glu Lys Pro Leu Thr Pro Asp	
50 55 60	
tct gaa tcc tca ctg cgc atc gtc gag ctg gag cag aag ctg gac aag	240
Ser Glu Ser Ser Leu Arg Ile Val Glu Leu Glu Gln Lys Leu Asp Lys	
65 70 75 80	
cca cac atc cag gtt ggt ttc atg cgc cgc ttc gac cct gag tac aac	288
Pro His Ile Gln Val Gly Phe Met Arg Arg Phe Asp Pro Glu Tyr Asn	
85 90 95	
aac ttg cgc aaa ttg gtg gaa tcc ggc gaa gct ggc gaa ctg ctc atg	336
Asn Leu Arg Lys Leu Val Glu Ser Gly Glu Ala Gly Glu Leu Leu Met	
100 105 110	
ctc cgc ggc ctg cac cgc aac cca agt gtt ggt gag agc tac acc cag	384
Leu Arg Gly Leu His Arg Asn Pro Ser Val Gly Glu Ser Tyr Thr Gln	
115 120 125	
tcc atg ctg atc acc gac tcc gtc gtc cac gaa ttc gat gtc atc cca	432
Ser Met Leu Ile Thr Asp Ser Val Val His Glu Phe Asp Val Ile Pro	
130 135 140	
tgg ctc gca ggc tcc cga gtt gtc tcc gtt gaa gtg aag tac cca aag	480
Trp Leu Ala Gly Ser Arg Val Val Ser Val Glu Val Lys Tyr Pro Lys	

atg gag ctc gaa aac ggc gtg 549
Met Glu Leu Glu Asn Gly Val
180

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<220>
<221> CDS

<222> (101)..(1105)

<223> RXA01632

<400> 299

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ccccctccac taactgatct ttgaaaggct gaaaaaactc atg act ctt cgt atc 115
                                         Met Thr Leu Arg Ile
                                         1 5

gcc ctt ttc ggc gct ggc cgc atc ggt cac gtc cac gct gcc aac att 163
Ala Leu Phe Gly Ala Gly Arg Ile Gly His Val His Ala Ala Asn Ile
                        10 15 20

gct gca aac cct gat ctt gaa ctc gtt gtt atc gcc gat cct ttc att 211
Ala Ala Asn Pro Asp Leu Glu Leu Val Ile Ala Asp Pro Phe Ile
                        25 30 35

gaa ggc gca cag cgt ttg gca gaa gcc aat ggg gca gaa gcg gtt gca 259
Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly Ala Glu Ala Val Ala
                        40 45 50

tca cca gat gag gtg ttc gcc cgc gat gat atc gat ggc atc gtg atc 307
Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile Asp Gly Ile Val Ile
                        55 60 65

ggt tca cca acc agc acc cac gtt gat ctg atc acc cgc gcc gtg gaa 355
Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile Thr Arg Ala Val Glu
                        70 75 80 85

cgt ggc att cct gca ctg tgc gaa aaa ccc att gat tta gac att gaa 403
Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile Asp Leu Asp Ile Glu
                        90 95 100

atg gtg cgt gcc tgc aaa gag aag atc ggc gac ggc gct tcc aag gtg 451
Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp Gly Ala Ser Lys Val
                        105 110 115

atg ctg ggg ttt aac cga cgc ttc gat cct tct ttc gct gcc atc aat 499
Met Leu Gly Phe Asn Arg Arg Phe Asp Pro Ser Phe Ala Ala Ile Asn
                        120 125 130

gcg cga gtg gca aac cag gag atc ggc aac ctg gag cag ttg gtg atc 547
Ala Arg Val Ala Asn Gln Glu Ile Gly Asn Leu Glu Gln Leu Val Ile
                        135 140 145

atc agc cgc gat cca gcg ccc gca ccg aag gac tac atc gca ggt tcc 595
Ile Ser Arg Asp Pro Ala Pro Ala Pro Lys Asp Tyr Ile Ala Gly Ser
                        150 155 160 165

ggt gga atc ttc cgc gat atg acc atc cac gat ctg gat atg gcg cgt 643
Gly Gly Ile Phe Arg Asp Met Thr Ile His Asp Leu Asp Met Ala Arg
                        170 175 180

ttc ttt gtg ccc aat atc gtg gaa gtg act gca acc ggc gcc aat gtt 691
Phe Phe Val Pro Asn Ile Val Glu Val Thr Ala Thr Gly Ala Asn Val
                        185 190 195

ttc agc cag gaa atc gcg gag ttc aat gac tac gac cag gtt atc gtc 739
Phe Ser Gln Glu Ile Ala Glu Phe Asn Asp Tyr Asp Gln Val Ile Val
                        200 205 210

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acg ctt cgt ggc tca aag ggc gag ttg atc aac atc gtg aac tcc cgc 787
 Thr Leu Arg Gly Ser Lys Gly Glu Leu Ile Asn Ile Val Asn Ser Arg
 215 220 225

cac tgc tcc tac ggc tac gac cag cga ctt gag gct ttc ggc tct aag 835
 His Cys Ser Tyr Gly Tyr Asp Gln Arg Leu Glu Ala Phe Gly Ser Lys
 230 235 240 245

ggc atg ctc gcc gcc gac aac atc agg ccc acc acg gtg cgc aag cac 883
 Gly Met Leu Ala Ala Asp Asn Ile Arg Pro Thr Thr Val Arg Lys His
 250 255 260

aat gcg gaa agc acc gag cag gca gat ccg att ttc aac ttc ttc ctc 931
 Asn Ala Glu Ser Thr Glu Gln Ala Asp Pro Ile Phe Asn Phe Phe Leu
 265 270 275

gag cgc tac gac gcc gct tac aag gca gag ctc gca act ttt gct caa 979
 Glu Arg Tyr Asp Ala Ala Tyr Lys Ala Glu Leu Ala Thr Phe Ala Gln
 280 285 290

gga atc cgc gac ggc caa ggc ttc tca cca aac ttc gag gac ggc gtc 1027
 Gly Ile Arg Asp Gly Gln Gly Phe Ser Pro Asn Phe Glu Asp Gly Val
 295 300 305

atc gcc ctt gaa cta gcg aat gca tgc ctt gaa tca gct caa acc ggc 1075
 Ile Ala Leu Glu Leu Ala Asn Ala Cys Leu Glu Ser Ala Gln Thr Gly
 310 315 320 325

cgc acc gtc acc ctc aac cct gcc aac gtt tagtcaacgt ctagttaatg 1125
 Arg Thr Val Thr Leu Asn Pro Ala Asn Val
 330 335

cct 1128

<210> 300
 <211> 335
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 300
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 20 25 30

Ala Asp Pro Phe Ile Glu Gly Ala Gln Arg Leu Ala Glu Ala Asn Gly
 35 40 45

Ala Glu Ala Val Ala Ser Pro Asp Glu Val Phe Ala Arg Asp Asp Ile
 50 55 60

Asp Gly Ile Val Ile Gly Ser Pro Thr Ser Thr His Val Asp Leu Ile
 65 70 75 80

Thr Arg Ala Val Glu Arg Gly Ile Pro Ala Leu Cys Glu Lys Pro Ile
 85 90 95

Asp Leu Asp Ile Glu Met Val Arg Ala Cys Lys Glu Lys Ile Gly Asp

100					105					110						
Gly	Ala	Ser	Lys	Val	Met	Leu	Gly	Phe	Asn	Arg	Arg	Phe	Asp	Pro	Ser	
115					120					125						
Phe	Ala	Ala	Ile	Asn	Ala	Arg	Val	Ala	Asn	Gln	Glu	Ile	Gly	Asn	Leu	
130					135					140						
Glu	Gln	Leu	Val	Ile	Ile	Ser	Arg	Asp	Pro	Ala	Pro	Ala	Pro	Lys	Asp	
145					150					155					160	
Tyr	Ile	Ala	Gly	Ser	Gly	Gly	Ile	Phe	Arg	Asp	Met	Thr	Ile	His	Asp	
165					170					175						
Leu	Asp	Met	Ala	Arg	Phe	Phe	Val	Pro	Asn	Ile	Val	Glu	Val	Thr	Ala	
180					185					190						
Thr	Gly	Ala	Asn	Val	Phe	Ser	Gln	Glu	Ile	Ala	Glu	Phe	Asn	Asp	Tyr	
195					200					205						
Asp	Gln	Val	Ile	Val	Thr	Leu	Arg	Gly	Ser	Lys	Gly	Glu	Leu	Ile	Asn	
210					215					220						
Ile	Val	Asn	Ser	Arg	His	Cys	Ser	Tyr	Gly	Tyr	Asp	Gln	Arg	Leu	Glu	
225					230					235					240	
Ala	Phe	Gly	Ser	Lys	Gly	Met	Leu	Ala	Ala	Asp	Asn	Ile	Arg	Pro	Thr	
245					250					255						
Thr	Val	Arg	Lys	His	Asn	Ala	Glu	Ser	Thr	Glu	Gln	Ala	Asp	Pro	Ile	
260					265					270						
Phe	Asn	Phe	Phe	Leu	Glu	Arg	Tyr	Asp	Ala	Ala	Tyr	Lys	Ala	Glu	Leu	
275					280					285						
Ala	Thr	Phe	Ala	Gln	Gly	Ile	Arg	Asp	Gly	Gln	Gly	Phe	Ser	Pro	Asn	
290					295					300						
Phe	Glu	Asp	Gly	Val	Ile	Ala	Leu	Glu	Leu	Ala	Asn	Ala	Cys	Leu	Glu	
305					310					315					320	
Ser	Ala	Gln	Thr	Gly	Arg	Thr	Val	Thr	Leu	Asn	Pro	Ala	Asn	Val		
325					330					335						

<210> 301

<211> 1206

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1183)

<223> RXA01633

<400> 301

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gtttagtcaa cgtctagtta atgcctaagg agaaaacctc atg aaa aac atc acc 115

Met Lys Asn Ile Thr

1

5

atc gga atg gtc ggc gtc ggc cgc att ggc cgc atg cac gtc gcc aac	163
Ile Gly Met Val Gly Val Gly Arg Ile Gly Arg Met His Val Ala Asn	
10 15 20	
atg ctt gcc gtt gct gaa act ttg aag gaa cgc gac ctc aac att gag	211
Met Leu Ala Val Ala Glu Thr Leu Lys Glu Arg Asp Leu Asn Ile Glu	
25 30 35	
atc gtg ctc gca gac gca atg ccc ggt ttt gcg gag cag gtg ggc gcg	259
Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala Glu Gln Val Gly Ala	
40 45 50	
gac atg ggc gtg aag gcg gcg gca agc gtc gat aag ctt att gag gac	307
Asp Met Gly Val Lys Ala Ala Ser Val Asp Lys Leu Ile Glu Asp	
55 60 65	
ggg gtg gat gcc ctt ttc att gcc acc agc acc gct ggc cac gtc gat	355
Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr Ala Gly His Val Asp	
70 75 80 85	
gtt ttg cgc aag ggc atc gcg gca aag ctg ccg atg ttc tgc gag aag	403
Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro Met Phe Cys Glu Lys	
90 95 100	
ccg atc gcg tcg gat gtg cct gag tcg ctg aac atc atc cgc gaa att	451
Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn Ile Ile Arg Glu Ile	
105 110 115	
gat gcg gct ggc gcg acg gtt cag gtc ggc cac cag cgc cgt ttt gac	499
Asp Ala Ala Gly Ala Thr Val Gln Val Gly His Gln Arg Arg Phe Asp	
120 125 130	
ctc ggt tac cag gaa gct aaa cga cgc cta gat gca ggc gac ctc ggc	547
Leu Gly Tyr Gln Glu Ala Lys Arg Arg Leu Asp Ala Gly Asp Leu Gly	
135 140 145	
tgg ctt cat tcg ctc aag gcc gta tcg agc gat gcg ttt ccg cca ccg	595
Trp Leu His Ser Leu Lys Ala Val Ser Ser Asp Ala Phe Pro Pro Pro	
150 155 160 165	
gtg tcc tac tgc gct acc tct ggt gga ctt ttc cgc gat gtg tcg ctg	643
Val Ser Tyr Cys Ala Thr Ser Gly Gly Leu Phe Arg Asp Val Ser Leu	
170 175 180	
cac gat ttc gac atc att cgc tgg ctg acc ggc cag gat att gtc gag	691
His Asp Phe Asp Ile Ile Arg Trp Leu Thr Gly Gln Asp Ile Val Glu	
185 190 195	
gtg tac gcc aag ggc agc aac aac ggc gac cca gaa atc ggc gca gtc	739
Val Tyr Ala Lys Gly Ser Asn Asn Gly Asp Pro Glu Ile Gly Ala Val	
200 205 210	
ggt gac atc gat acc gga gcg gcc cta ctc acg ctt gcc gac ggc acc	787
Gly Asp Ile Asp Thr Gly Ala Ala Leu Leu Thr Leu Ala Asp Gly Thr	
215 220 225	
ctc gcc acc gcc atc gcc act cgt tac aac ggt gca ggc cac gac gtt	835
Leu Ala Thr Ala Ile Ala Thr Arg Tyr Asn Gly Ala Gly His Asp Val	
230 235 240 245	

cgc ctc gat gtt atg ggc tct aaa gat tcc acg atc gtt ggc ctg gat 883
 Arg Leu Asp Val Met Gly Ser Lys Asp Ser Thr Ile Val Gly Leu Asp
 250 255 260

gaa aag tct gcg ttc gct tct gcg gag gag ggc atc gat ttc cca acc 931
 Glu Lys Ser Ala Phe Ala Ser Ala Glu Glu Gly Ile Asp Phe Pro Thr
 265 270 275

ggc gaa tcg cac cca acg ttt gcc gag cgc ttc gcc gac gca tac aag 979
 Gly Glu Ser His Pro Thr Phe Ala Glu Arg Phe Ala Asp Ala Tyr Lys
 280 285 290

aat gag tgc att gcg ttc gtg gag ttg atc ctg gga gag cgg gaa aac 1027
 Asn Glu Cys Ile Ala Phe Val Glu Leu Ile Leu Gly Glu Arg Glu Asn
 295 300 305

cct tgt acc cct gca gac gct gtg gct gcg gcg att gtt gcc gat gca 1075
 Pro Cys Thr Pro Ala Asp Ala Val Ala Ala Ile Val Ala Asp Ala
 310 315 320 325

gct cag ctg tcg ctg gtc act ggc gag cca gtg aag att cct act gta 1123
 Ala Gln Leu Ser Leu Val Thr Gly Glu Pro Val Lys Ile Pro Thr Val
 330 335 340

cgg gaa att ctt gaa ggt tct gcg cag cca gtt gag gtg cgt gcg ctg 1171
 Arg Glu Ile Leu Glu Gly Ser Ala Gln Pro Val Glu Val Arg Ala Leu
 345 350 355

gtt cca tct gct taaaacctta ctgcttatct aaa 1206
 Val Pro Ser Ala
 360

<210> 302

<211> 361

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 302

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 20 25 30

Asp Leu Asn Ile Glu Ile Val Leu Ala Asp Ala Met Pro Gly Phe Ala
 35 40 45

Glu Gln Val Gly Ala Asp Met Gly Val Lys Ala Ala Ala Ser Val Asp
 50 55 60

Lys Leu Ile Glu Asp Gly Val Asp Ala Leu Phe Ile Ala Thr Ser Thr
 65 70 75 80

Ala Gly His Val Asp Val Leu Arg Lys Gly Ile Ala Ala Lys Leu Pro
 85 90 95

Met Phe Cys Glu Lys Pro Ile Ala Ser Asp Val Pro Glu Ser Leu Asn
 100 105 110

Ile Ile Arg Glu Ile Asp Ala Ala Gly Ala Thr Val Gln Val Gly His

115					120					125					
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130						135					140				
Ala	Gly	Asp	Leu	Gly	Trp	Leu	His	Ser	Leu	Lys	Ala	Val	Ser	Ser	Asp
145					150					155					160
Ala	Phe	Pro	Pro	Pro	Val	Ser	Tyr	Cys	Ala	Thr	Ser	Gly	Gly	Leu	Phe
				165					170					175	
Arg	Asp	Val	Ser	Leu	His	Asp	Phe	Asp	Ile	Ile	Arg	Trp	Leu	Thr	Gly
		180						185					190		
Gln	Asp	Ile	Val	Glu	Val	Tyr	Ala	Lys	Gly	Ser	Asn	Asn	Gly	Asp	Pro
	195						200					205			
Glu	Ile	Gly	Ala	Val	Gly	Asp	Ile	Asp	Thr	Gly	Ala	Ala	Leu	Leu	Thr
210					215						220				
Leu	Ala	Asp	Gly	Thr	Leu	Ala	Thr	Ala	Ile	Ala	Thr	Arg	Tyr	Asn	Gly
225					230					235					240
Ala	Gly	His	Asp	Val	Arg	Leu	Asp	Val	Met	Gly	Ser	Lys	Asp	Ser	Thr
				245					250					255	
Ile	Val	Gly	Leu	Asp	Glu	Lys	Ser	Ala	Phe	Ala	Ser	Ala	Glu	Glu	Gly
			260					265					270		
Ile	Asp	Phe	Pro	Thr	Gly	Glu	Ser	His	Pro	Thr	Phe	Ala	Glu	Arg	Phe
		275					280					285			
Ala	Asp	Ala	Tyr	Lys	Asn	Glu	Cys	Ile	Ala	Phe	Val	Glu	Leu	Ile	Leu
	290					295					300				
Gly	Glu	Arg	Glu	Asn	Pro	Cys	Thr	Pro	Ala	Asp	Ala	Val	Ala	Ala	Ala
305					310					315					320
Ile	Val	Ala	Asp	Ala	Ala	Gln	Leu	Ser	Leu	Val	Thr	Gly	Glu	Pro	Val
			325						330					335	
Lys	Ile	Pro	Thr	Val	Arg	Glu	Ile	Leu	Glu	Gly	Ser	Ala	Gln	Pro	Val
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Glu	Val	Arg	Ala	Leu	Val	Pro	Ser	Ala							
	355						360								

<210> 303

<211> 1146

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1123)

<223> RXN01406

<400> 303

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	Met Thr Ile Arg Ile	
	1 5	
gga ctc gtt ggc tac ggt gtc ggc ggc agg ctc ttt cac acc cct tac	163	
Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu Phe His Thr Pro Tyr		
10 15 20		
atc caa gct tct acg cac tgc gaa tta gta ggc gta gtt gct cgt tcc	211	
Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly Val Val Ala Arg Ser		
25 30 35		
gaa ggc acc aaa gca gcc gtt gca gaa gat ctt cca gat gtt gcc atc	259	
Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu Pro Asp Val Ala Ile		
40 45 50		
gtg gga tgc ctg aca gaa ctc ctc gaa ctg ggc gtc gat gca gtg gtg	307	
Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly Val Asp Ala Val Val		
55 60 65		
atc tcc acc cct cca gcc acg cgc cgg gaa ctg gcc ttg gaa gca atc	355	
Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu Ala Leu Glu Ala Ile		
70 75 80 85		
aac gca ggt gtc gca gtg gtt gcc gat aaa ccg ttt gca cca tca gcc	403	
Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro Phe Ala Pro Ser Ala		
90 95 100		
gca gat gcc atg gaa ctt gtc gaa gcc gcc gaa aag gct gga gtg ctg	451	
Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu Lys Ala Gly Val Leu		
105 110 115		
ctc aac gtc ttc cac aac agg cgc aac gac acc cac att gtc acg gca	499	
Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr His Ile Val Thr Ala		
120 125 130		
ctg gga atc caa gaa gaa ctt ggt gcg atg cgt gga ctg gac ctg cga	547	
Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg Gly Leu Asp Leu Arg		
135 140 145		
cta gac ctg atc gaa cct gat tcc ttg gag gca ggt cct gaa ggt ggt	595	
Leu Asp Leu Ile Glu Pro Asp Ser Leu Glu Ala Gly Pro Glu Gly Gly		
150 155 160 165		
ttg ctg cgc gat ctg ggc tca cac gta gtc gat cag acc ctg gtt ctc	643	
Leu Leu Arg Asp Leu Gly Ser His Val Val Asp Gln Thr Leu Val Leu		
170 175 180		
atg ggg ccg gct acc tct gtc acc gcc caa ctt gga tcc atc gac ctt	691	
Met Gly Pro Ala Thr Ser Val Thr Ala Gln Leu Gly Ser Ile Asp Leu		
185 190 195		
cca gaa ggc cca acc aac gca agg ttc cgc atc gtg ttg gaa cat gaa	739	
Pro Glu Gly Pro Thr Asn Ala Arg Phe Arg Ile Val Leu Glu His Glu		
200 205 210		
tcg ggc gcc gta tcg cac att tct gcc agc aag att gac cgc ttg gag	787	
Ser Gly Ala Val Ser His Ile Ser Ala Ser Lys Ile Asp Arg Leu Glu		
215 220 225		
tcc tgg gaa atc cgc ttg gtg ggc gag cgc ggc tcc tac gta tcc aac	835	

Ser Trp Glu Ile Arg Leu Val Gly Glu Arg Gly Ser Tyr Val Ser Asn
 230 235 240 245
 tac acc gac gtg cag acc gtg gcg atc aaa cag gga ctt cga cca acc 883
 Tyr Thr Asp Val Gln Thr Val Ala Ile Lys Gln Gly Leu Arg Pro Thr
 250 255 260
 aat gac cgc gaa cac tgg ggc tac gaa tcg gag gag cgg tgg ggc acc 931
 Asn Asp Arg Glu His Trp Gly Tyr Glu Ser Glu Glu Arg Trp Gly Thr
 265 270 275
 ttg gtt acc gat gaa ggc tca aag gtg att cct tca gca caa ggc gat 979
 Leu Val Thr Asp Glu Gly Ser Lys Val Ile Pro Ser Ala Gln Gly Asp
 280 285 290
 tac acc cgc ttc tac gat gcc ttt gcc ttg gct gtg gaa aac ggt ggc 1027
 Tyr Thr Arg Phe Tyr Asp Ala Phe Ala Leu Ala Val Glu Asn Gly Gly
 295 300 305
 gca ggg ccg gtg cct gca cgt gaa ggt gtt gca gtg ctc aag gtg ttg 1075
 Ala Gly Pro Val Pro Ala Arg Glu Gly Val Ala Val Leu Lys Val Leu
 310 315 320 325
 gat gct gta gcc cag agc gct gcg gaa aaa cgc acc att gag ttg agc 1123
 Asp Ala Val Ala Gln Ser Ala Ala Glu Lys Arg Thr Ile Glu Leu Ser
 330 335 340
 taaggagaag tgctgctggc tgc 1146

<210> 304

<211> 341

<212> PRT

<213> Corynebacterium glutamicum

<400> 304

Met Thr Ile Arg Ile Gly Leu Val Gly Tyr Gly Val Gly Gly Arg Leu
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 Phe His Thr Pro Tyr Ile Gln Ala Ser Thr His Cys Glu Leu Val Gly
 20 25 30
 Val Val Ala Arg Ser Glu Gly Thr Lys Ala Ala Val Ala Glu Asp Leu
 35 40 45
 Pro Asp Val Ala Ile Val Gly Ser Leu Thr Glu Leu Leu Glu Leu Gly
 50 55 60
 Val Asp Ala Val Val Ile Ser Thr Pro Pro Ala Thr Arg Arg Glu Leu
 65 70 75 80
 Ala Leu Glu Ala Ile Asn Ala Gly Val Ala Val Val Ala Asp Lys Pro
 85 90 95
 Phe Ala Pro Ser Ala Ala Asp Ala Met Glu Leu Val Glu Ala Ala Glu
 100 105 110
 Lys Ala Gly Val Leu Leu Asn Val Phe His Asn Arg Arg Asn Asp Thr
 115 120 125
 His Ile Val Thr Ala Leu Gly Ile Gln Glu Glu Leu Gly Ala Met Arg

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<400> 305
gtaggtgagt cttcgtgaga taccctccggc cagtcataca gttcaaccaa gctccaccac 60
ccagataaaa acctgcgggt tgcgttttag gagaattccc atg agt gat caa aaa 115
                                         Met Ser Asp Gln Lys
                                         1                               5
att gtt gtt ggc ctg cta ggc atc acc cac ccg cat gcg tcg gcg cgg 163
Ile Val Val Gly Leu Leu Gly Ile Thr His Pro His Ala Ser Ala Arg

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10					15					20						
gtg	cgt	gcc	ctc	cgt	gaa	att	gat	ggg	gta	gag	gtc	gtc	gcc	gcc	gcg	211
Val	Arg	Ala	Leu	Arg	Glu	Ile	Asp	Gly	Val	Glu	Val	Val	Ala	Ala	Ala	
			25					30					35			
gat	act	gat	tcc	cgc	ctc	cag	tac	ttc	acc	gac	aaa	tat	gat	gtt	gaa	259
Asp	Thr	Asp	Ser	Arg	Leu	Gln	Tyr	Phe	Thr	Asp	Lys	Tyr	Asp	Val	Glu	
			40				45					50				
ccc	cgc	gag	atc	gat	gac	gtc	ttg	aac	gac	gat	cgc	atc	aac	gcc	atc	307
Pro	Arg	Glu	Ile	Asp	Asp	Val	Leu	Asn	Asp	Asp	Arg	Ile	Asn	Ala	Ile	
		55				60					65					
atg	gtt	cac	tcc	aag	agc	aag	gac	atg	gtc	cct	cac	gcc	aag	cgc	gcg	355
Met	Val	His	Ser	Lys	Ser	Lys	Asp	Met	Val	Pro	His	Ala	Lys	Arg	Ala	
					75					80					85	
ctc	gcg	gcc	gga	aaa	tcc	gtc	gtc	gtg	gag	aag	ccc	ggc	ggg	gga	aca	403
Leu	Ala	Ala	Gly	Lys	Ser	Val	Val	Val	Glu	Lys	Pro	Gly	Gly	Gly	Thr	
				90					95					100		
gtg	gcg	gat	ctt	gag	gag	ctc	ctg	gcc	ctc	aaa	gaa	gct	gcc	gat	cct	451
Val	Ala	Asp	Leu	Glu	Glu	Leu	Leu	Ala	Leu	Lys	Glu	Ala	Ala	Asp	Pro	
			105					110					115			
cag	cga	atc	gtg	cag	gtc	ggg	tac	aac	gtc	cgc	ctg	tct	gaa	tcg	gtt	499
Gln	Arg	Ile	Val	Gln	Val	Gly	Tyr	Asn	Val	Arg	Leu	Ser	Glu	Ser	Val	
		120					125					130				
cag	aga	tta	aaa	gag	ctt	ctc	gac	gcc	ggc	ctc	atc	ggc	gaa	gtc	gtc	547
Gln	Arg	Leu	Lys	Glu	Leu	Leu	Asp	Ala	Gly	Leu	Ile	Gly	Glu	Val	Val	
		135				140					145					
agc	gtg	caa	gca	cgc	ggc	gcc	gca	aaa	gta	ggt	gag	cat	atc	acc	gag	595
Ser	Val	Gln	Ala	Arg	Gly	Ala	Ala	Lys	Val	Gly	Glu	His	Ile	Thr	Glu	
					155					160					165	
cac	ctc	aac	caa	ccc	gca	gac	atg	ggc	ggt	gtg	ttg	tgg	att	ctt	ggc	643
His	Leu	Asn	Gln	Pro	Ala	Asp	Met	Gly	Gly	Val	Leu	Trp	Ile	Leu	Gly	
				170					175					180		
tgc	cac	atg	ctc	gat	gca	ttg	gtg	gaa	gtc	ttc	gga	gct	cca	gaa	tcc	691
Cys	His	Met	Leu	Asp	Ala	Leu	Val	Glu	Val	Phe	Gly	Ala	Pro	Glu	Ser	
			185					190					195			
gtg	aac	gcc	cga	gtg	cat	aag	acc	gca	aaa	ctc	tct	gac	gac	acc	agc	739
Val	Asn	Ala	Arg	Val	His	Lys	Thr	Ala	Lys	Leu	Ser	Asp	Asp	Thr	Ser	
		200					205					210				
cgc	gaa	gac	tca	gcc	tcc	gca	ctg	ctg	tac	tac	cca	gat	ttc	tcc	gtc	787
Arg	Glu	Asp	Ser	Ala	Ser	Ala	Leu	Leu	Tyr	Tyr	Pro	Asp	Phe	Ser	Val	
		215				220					225					
agc	ttc	agc	ttc	gac	ggc	cac	gat	gat	ctg	gaa	tgg	ttc	gaa	agc	tcc	835
Ser	Phe	Ser	Phe	Asp	Gly	His	Asp	Asp	Leu	Glu	Trp	Phe	Glu	Ser	Ser	
					235					240					245	
cga	ctc	acg	gtc	tat	gga	acc	aag	ggc	atg	atc	gaa	gcc	gga	atc	ctc	883
Arg	Leu	Thr	Val	Tyr	Gly	Thr	Lys	Gly	Met	Ile	Glu	Ala	Gly	Ile	Leu	
				250					255					260		

cct cag aca ctg cgc gta tac ctc aat gag tca cgc cag ggc tgg cca 931
 Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser Arg Gln Gly Trp Pro
 265 270 275

cag ggt tgg acc gag tgg acc cag agc tac ttc acc cca ccg ttt gct 979
 Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe Thr Pro Phe Ala
 280 285 290

cgc aca gaa tcc aac aaa ttc tca gag ctt cca gag cta gaa aac atc 1027
 Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro Glu Leu Glu Asn Ile
 295 300 305

agc aac ttc cgc aca gaa atg cag ggg tgg gtg aat tcc att cgc act 1075
 Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val Asn Ser Ile Arg Thr
 310 315 320 325

gga tcc cgc aat gtg gcg cca gtt gag gat gct ctc aca gtc gct cgc 1123
 Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala Leu Thr Val Ala Arg
 330 335 340

att gtc agt gca tgc tac gaa tcc gac aac aac cag ggc att tcc gta 1171
 Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn Gln Gly Ile Ser Val
 345 350 355

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 Asn Ile

<210> 306

<211> 359

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 306

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His Ala Ser Ala Arg Val Arg Ala Leu Arg Glu Ile Asp Gly Val Glu
 20 25 30

Val Val Ala Ala Ala Asp Thr Asp Ser Arg Leu Gln Tyr Phe Thr Asp
 35 40 45

Lys Tyr Asp Val Glu Pro Arg Glu Ile Asp Asp Val Leu Asn Asp Asp
 50 55 60

Arg Ile Asn Ala Ile Met Val His Ser Lys Ser Lys Asp Met Val Pro
 65 70 75 80

His Ala Lys Arg Ala Leu Ala Ala Gly Lys Ser Val Val Val Glu Lys
 85 90 95

Pro Gly Gly Gly Thr Val Ala Asp Leu Glu Glu Leu Leu Ala Leu Lys
 100 105 110

Glu Ala Ala Asp Pro Gln Arg Ile Val Gln Val Gly Tyr Asn Val Arg
 115 120 125

Leu Ser Glu Ser Val Gln Arg Leu Lys Glu Leu Leu Asp Ala Gly Leu

130	135	140
Ile Gly Glu Val Val Ser Val Gln Ala Arg Gly Ala Ala Lys Val Gly		
145	150	155 160
Glu His Ile Thr Glu His Leu Asn Gln Pro Ala Asp Met Gly Gly Val		
	165	170 175
Leu Trp Ile Leu Gly Cys His Met Leu Asp Ala Leu Val Glu Val Phe		
	180	185 190
Gly Ala Pro Glu Ser Val Asn Ala Arg Val His Lys Thr Ala Lys Leu		
	195	200 205
Ser Asp Asp Thr Ser Arg Glu Asp Ser Ala Ser Ala Leu Leu Tyr Tyr		
	210	215 220
Pro Asp Phe Ser Val Ser Phe Ser Phe Asp Gly His Asp Asp Leu Glu		
	225	230 235 240
Trp Phe Glu Ser Ser Arg Leu Thr Val Tyr Gly Thr Lys Gly Met Ile		
	245	250 255
Glu Ala Gly Ile Leu Pro Gln Thr Leu Arg Val Tyr Leu Asn Glu Ser		
	260	265 270
Arg Gln Gly Trp Pro Gln Gly Trp Thr Glu Trp Thr Gln Ser Tyr Phe		
	275	280 285
Thr Pro Pro Phe Ala Arg Thr Glu Ser Asn Lys Phe Ser Glu Leu Pro		
	290	295 300
Glu Leu Glu Asn Ile Ser Asn Phe Arg Thr Glu Met Gln Gly Trp Val		
	305	310 315 320
Asn Ser Ile Arg Thr Gly Ser Arg Asn Val Ala Pro Val Glu Asp Ala		
	325	330 335
Leu Thr Val Ala Arg Ile Val Ser Ala Cys Tyr Glu Ser Asp Asn Asn		
	340	345 350
Gln Gly Ile Ser Val Asn Ile		
	355	

<210> 307

<211> 1212

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1189)

<223> RXN00528

<400> 307

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tcggtcgcgg ccgttatctt ttttaagagga gaaattttag atg agc acg tcc acc 115

Met Ser Thr Ser Thr

1

5

atc	agg	gtt	gcc	att	gcc	gga	gtc	gga	aac	tgc	gcg	acc	tcc	ctc	att	163
Ile	Arg	Val	Ala	Ile	Ala	Gly	Val	Gly	Asn	Cys	Ala	Thr	Ser	Leu	Ile	
			10						15					20		
cag	ggt	gtg	gaa	tat	tac	cga	aat	gcg	gat	cct	tcc	gaa	act	gtc	ccg	211
Gln	Gly	Val	Glu	Tyr	Tyr	Arg	Asn	Ala	Asp	Pro	Ser	Glu	Thr	Val	Pro	
			25					30					35			
ggt	ttg	atg	cac	gtc	aaa	ttc	ggt	gat	tac	cac	gtt	ggc	gac	att	gaa	259
Gly	Leu	Met	His	Val	Lys	Phe	Gly	Asp	Tyr	His	Val	Gly	Asp	Ile	Glu	
		40					45					50				
ttc	gtg	gcc	gcg	ttc	gac	gtc	gac	gcc	gaa	aaa	gta	ggc	atc	gat	ctt	307
Phe	Val	Ala	Ala	Phe	Asp	Val	Asp	Ala	Glu	Lys	Val	Gly	Ile	Asp	Leu	
	55					60					65					
gcc	gac	gcc	acc	gag	gct	tca	caa	aac	tgc	act	atc	aaa	atc	gcc	gat	355
Ala	Asp	Ala	Thr	Glu	Ala	Ser	Gln	Asn	Cys	Thr	Ile	Lys	Ile	Ala	Asp	
	70				75					80					85	
gtc	cca	cag	acc	ggc	atc	aac	gtg	ctg	cgt	ggc	ccg	act	ctc	gac	ggc	403
Val	Pro	Gln	Thr	Gly	Ile	Asn	Val	Leu	Arg	Gly	Pro	Thr	Leu	Asp	Gly	
				90					95					100		
ctg	ggc	gat	cat	tac	cgc	gcg	acc	atc	gac	gag	tcc	acc	gcc	gag	cca	451
Leu	Gly	Asp	His	Tyr	Arg	Ala	Thr	Ile	Asp	Glu	Ser	Thr	Ala	Glu	Pro	
			105					110					115			
gtc	gac	gtt	gtc	cag	gcg	ctt	atc	gac	gca	aaa	gcc	gat	gtt	ttg	gtg	499
Val	Asp	Val	Val	Gln	Ala	Leu	Ile	Asp	Ala	Lys	Ala	Asp	Val	Leu	Val	
		120				125						130				
tcc	tac	ctc	cca	gtg	ggc	tcc	gaa	gaa	gcc	gac	aaa	ttc	tac	gca	caa	547
Ser	Tyr	Leu	Pro	Val	Gly	Ser	Glu	Glu	Ala	Asp	Lys	Phe	Tyr	Ala	Gln	
	135					140					145					
gcc	gcc	atc	gat	gca	ggc	tgc	gcc	ttt	gtc	aac	gct	ctc	cca	gta	ttc	595
Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Phe	Val	Asn	Ala	Leu	Pro	Val	Phe	
	150				155					160					165	
atc	gcc	tcc	gac	cct	gag	tgg	gct	aag	aag	ttc	act	gac	gct	ggc	atc	643
Ile	Ala	Ser	Asp	Pro	Glu	Trp	Ala	Lys	Lys	Phe	Thr	Asp	Ala	Gly	Ile	
				170					175					180		
cca	att	gtt	ggc	gat	gac	atc	aaa	tcc	cag	atc	ggt	gca	acc	atc	acc	691
Pro	Ile	Val	Gly	Asp	Asp	Ile	Lys	Ser	Gln	Ile	Gly	Ala	Thr	Ile	Thr	
			185					190					195			
cac	cgt	gtc	ctc	gca	cgc	ctt	ttt	gaa	gaa	cgt	ggc	gtt	cgc	gta	gat	739
His	Arg	Val	Leu	Ala	Arg	Leu	Phe	Glu	Glu	Arg	Gly	Val	Arg	Val	Asp	
		200				205						210				
cgc	acc	atg	cag	ctc	aac	gtc	ggc	ggc	aac	atg	gac	ttc	aaa	aac	atg	787
Arg	Thr	Met	Gln	Leu	Asn	Val	Gly	Gly	Asn	Met	Asp	Phe	Lys	Asn	Met	
	215					220					225					
ctt	gac	cgc	aat	cgc	ttg	gaa	tcc	aag	aag	gtc	tcc	aaa	acc	caa	gca	835
Leu	Asp	Arg	Asn	Arg	Leu	Glu	Ser	Lys	Lys	Val	Ser	Lys	Thr	Gln	Ala	
	230				235					240					245	

gtg acc tcc aac att cca gat ggt cca ctg tct gga aag gtg gaa gac 883
Val Thr Ser Asn Ile Pro Asp Gly Pro Leu Ser Gly Lys Val Glu Asp
250 255 260

cgc aac gtc cac atc gga cca tcc gac cac gtc caa tgg ctc gat gac 931
Arg Asn Val His Ile Gly Pro Ser Asp His Val Gln Trp Leu Asp Asp
265 270 275

cgc aag tgg gct tat gtc cgc ctc gaa ggc acc gca ttc ggt gga gtt 979
Arg Lys Trp Ala Tyr Val Arg Leu Glu Gly Thr Ala Phe Gly Gly Val
280 285 290

ccc ctc aac ctt gag tac aaa ctc gag gtg tgg gat tca ccc aac tct 1027
Pro Leu Asn Leu Glu Tyr Lys Leu Glu Val Trp Asp Ser Pro Asn Ser
295 300 305

gcc ggc atc atc atc gac gct gtt cgc gcc gcc aag atc gcc ctc gat 1075
Ala Gly Ile Ile Ile Asp Ala Val Arg Ala Ala Lys Ile Ala Leu Asp
310 315 320 325

cgc ggt atc ggc gga ccg atc atg cca gca agc tcc tac ctg atg aag 1123
Arg Gly Ile Gly Gly Pro Ile Met Pro Ala Ser Ser Tyr Leu Met Lys
330 335 340

tcc cca cct gag cag ctt cca gac gat gtt gct tgt gaa cgc cta gag 1171
Ser Pro Pro Glu Gln Leu Pro Asp Asp Val Ala Cys Glu Arg Leu Glu
345 350 355

gca ttc atc atc gag gcg taaaattagg ctaaaaattt ggg 1212
Ala Phe Ile Ile Glu Ala
360

<210> 308

<211> 363

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 308

Met Ser Thr Ser Thr Ile Arg Val Ala Ile Ala Gly Val Gly Asn Cys
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Ala Thr Ser Leu Ile Gln Gly Val Glu Tyr Tyr Arg Asn Ala Asp Pro
20 25 30

Ser Glu Thr Val Pro Gly Leu Met His Val Lys Phe Gly Asp Tyr His
35 40 45

Val Gly Asp Ile Glu Phe Val Ala Ala Phe Asp Val Asp Ala Glu Lys
50 55 60

Val Gly Ile Asp Leu Ala Asp Ala Thr Glu Ala Ser Gln Asn Cys Thr
65 70 75 80

Ile Lys Ile Ala Asp Val Pro Gln Thr Gly Ile Asn Val Leu Arg Gly
85 90 95

Pro Thr Leu Asp Gly Leu Gly Asp His Tyr Arg Ala Thr Ile Asp Glu
100 105 110

Ser Thr Ala Glu Pro Val Asp Val Val Gln Ala Leu Ile Asp Ala Lys

115					120					125						
Ala	Asp	Val	Leu	Val	Ser	Tyr	Leu	Pro	Val	Gly	Ser	Glu	Glu	Ala	Asp	
130					135					140						
Lys	Phe	Tyr	Ala	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Phe	Val	Asn	
145					150					155					160	
Ala	Leu	Pro	Val	Phe	Ile	Ala	Ser	Asp	Pro	Glu	Trp	Ala	Lys	Lys	Phe	
165					170					175						
Thr	Asp	Ala	Gly	Ile	Pro	Ile	Val	Gly	Asp	Asp	Ile	Lys	Ser	Gln	Ile	
180					185					190						
Gly	Ala	Thr	Ile	Thr	His	Arg	Val	Leu	Ala	Arg	Leu	Phe	Glu	Glu	Arg	
195					200					205						
Gly	Val	Arg	Val	Asp	Arg	Thr	Met	Gln	Leu	Asn	Val	Gly	Gly	Asn	Met	
210					215					220						
Asp	Phe	Lys	Asn	Met	Leu	Asp	Arg	Asn	Arg	Leu	Glu	Ser	Lys	Lys	Val	
225					230					235					240	
Ser	Lys	Thr	Gln	Ala	Val	Thr	Ser	Asn	Ile	Pro	Asp	Gly	Pro	Leu	Ser	
245					250					255						
Gly	Lys	Val	Glu	Asp	Arg	Asn	Val	His	Ile	Gly	Pro	Ser	Asp	His	Val	
260					265					270						
Gln	Trp	Leu	Asp	Asp	Arg	Lys	Trp	Ala	Tyr	Val	Arg	Leu	Glu	Gly	Thr	
275					280					285						
Ala	Phe	Gly	Gly	Val	Pro	Leu	Asn	Leu	Glu	Tyr	Lys	Leu	Glu	Val	Trp	
290					295					300						
Asp	Ser	Pro	Asn	Ser	Ala	Gly	Ile	Ile	Ile	Asp	Ala	Val	Arg	Ala	Ala	
305					310					315					320	
Lys	Ile	Ala	Leu	Asp	Arg	Gly	Ile	Gly	Gly	Pro	Ile	Met	Pro	Ala	Ser	
325					330					335						
Ser	Tyr	Leu	Met	Lys	Ser	Pro	Pro	Glu	Gln	Leu	Pro	Asp	Asp	Val	Ala	
340					345					350						
Cys	Glu	Arg	Leu	Glu	Ala	Phe	Ile	Ile	Glu	Ala						
355					360											

<210> 309

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXN03057

<400> 309

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											Leu	Ala	Ser	Asp	Leu	5
											1					
ggt	att	aag	ttc	gtc	gca	gtg	gtg	gat	aaa	gat	cta	gag	act	gct	gag	163
Gly	Ile	Lys	Phe	Val	Ala	Val	Val	Asp	Lys	Asp	Leu	Glu	Thr	Ala	Glu	20
				10					15							
aaa	ttt	gcg	acg	gga	ctt	gga	gct	gct	ggc	gat	tct	tca	gaa	agc	agc	211
Lys	Phe	Ala	Thr	Gly	Leu	Gly	Ala	Ala	Gly	Asp	Ser	Ser	Glu	Ser	Ser	25
			25					30					35			
gtc	aag	gcc	cac	ggc	agc	ctg	ccg	gct	ttg	ttc	tcc	aaa	aag	aag	atc	259
Val	Lys	Ala	His	Gly	Ser	Leu	Pro	Ala	Leu	Phe	Ser	Lys	Lys	Lys	Ile	40
		40					45					50				
gat	gtt	cta	cac	atc	acc	acc	ccc	cac	gac	caa	cac	att	ggg	ttg	gct	307
Asp	Val	Leu	His	Ile	Thr	Thr	Pro	His	Asp	Gln	His	Ile	Gly	Leu	Ala	55
	55					60					65					
ctc	gaa	gcg	cta	cac	cac	ggg	gta	aat	gtc	atc	ctg	gaa	aag	ccg	ttg	355
Leu	Glu	Ala	Leu	His	His	Gly	Val	Asn	Val	Ile	Leu	Glu	Lys	Pro	Leu	70
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Ala	Asn	Glu	Leu	Asp	Gln	Ala	Gln	Arg	Leu	Ile	Asp	Tyr	Leu	Asp	Glu	90
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Asn	Pro	Asp	Gly	Pro	Lys	Ile	Ala	Val	Cys	Tyr	Gln	Asn	Arg	Tyr	Asn	105
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Val	Ser	Ser	Gln	Glu	Leu	Arg	Arg	Leu	Leu	Asp	Ser	Gly	Asp	Leu	Gly	120
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Ala	Ile	Asn	Gly	Ala	Tyr	Ser	Ser	Val	Val	Trp	Thr	Arg	Thr	Pro	Gly	135
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tac	tac	acc	cag	aaa	cct	tgg	cgt	ggc	cag	caa	gca	cac	tcc	ggg	ggg	595
Tyr	Tyr	Thr	Gln	Lys	Pro	Trp	Arg	Gly	Gln	Gln	Ala	His	Ser	Gly	Gly	150
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ggc	ctg	ctg	atg	aac	caa	gca	att	cac	acc	ctg	gat	ctg	ctg	cag	tgg	643
Gly	Leu	Leu	Met	Asn	Gln	Ala	Ile	His	Thr	Leu	Asp	Leu	Leu	Gln	Trp	170
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Phe	Leu	Gly	Lys	Ala	Thr	Glu	Val	Lys	Gly	Thr	Val	Ser	Thr	Asp	Lys	185
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 35 40 45
 Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60
 His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80
 Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95
 Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
 100 105 110
 Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125
 Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp
 130 135 140
 Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln
 145 150 155 160
 Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu
 165 170 175
 Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr
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 His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser
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<223> FRXA02902

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                                         Leu Ala Ser Asp Leu
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Gly Ile Lys Phe Val Ala Val Val Asp Lys Asp Leu Glu Thr Ala Glu
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Lys Phe Ala Thr Gly Leu Gly Ala Ala Gly Asp Ser Ser Glu Ser Ser
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Val Lys Ala His Gly Ser Leu Pro Ala Leu Phe Ser Lys Lys Lys Ile
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Asp Val Leu His Ile Thr Thr Pro His Asp Gln His Ile Gly Leu Ala
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Leu Glu Ala Leu His His Gly Val Asn Val Ile Leu Glu Lys Pro Leu
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Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile Asp Tyr Leu Asp Glu
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Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr Gln Asn Arg Tyr Asn
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Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp Ser Gly Asp Leu Gly
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Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp Thr Arg Thr Pro Gly
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Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln Ala His Ser Gly Gly
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Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu Asp Leu Leu Gln Trp
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ttc ctt gga aag gca aca gaa gtc aag ggc act gtc tcc acc gat aag 691
Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr Val Ser Thr Asp Lys
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tat gcc gat gtc atc gat gtt gaa gac acc gca cac gca tac atc ggt 739
Tyr Ala Asp Val Ile Asp Val Glu Asp Thr Ala His Ala Tyr Ile Gly
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795

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<213> *Corynebacterium glutamicum*

<400> 312

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 20 25 30

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 35 40 45

Ser Lys Lys Lys Ile Asp Val Leu His Ile Thr Thr Pro His Asp Gln
 50 55 60

His Ile Gly Leu Ala Leu Glu Ala Leu His His Gly Val Asn Val Ile
 65 70 75 80

Leu Glu Lys Pro Leu Ala Asn Glu Leu Asp Gln Ala Gln Arg Leu Ile
 85 90 95

Asp Tyr Leu Asp Glu Asn Pro Asp Gly Pro Lys Ile Ala Val Cys Tyr
 100 105 110

Gln Asn Arg Tyr Asn Val Ser Ser Gln Glu Leu Arg Arg Leu Leu Asp
 115 120 125

Ser Gly Asp Leu Gly Ala Ile Asn Gly Ala Tyr Ser Ser Val Val Trp
 130 135 140

Thr Arg Thr Pro Gly Tyr Tyr Thr Gln Lys Pro Trp Arg Gly Gln Gln
 145 150 155 160

Ala His Ser Gly Gly Gly Leu Leu Met Asn Gln Ala Ile His Thr Leu
 165 170 175

Asp Leu Leu Gln Trp Phe Leu Gly Lys Ala Thr Glu Val Lys Gly Thr
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His Ala Tyr Ile Gly His Glu Ser Gly Val His Thr Ser Glu Val Ser
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                                         Met Lys Lys Lys Ile
                                         1 5

gcg gtc gtt acc gga gcg acc gga ggc atg gga att gag atc gtc aaa 163
Ala Val Val Thr Gly Ala Thr Gly Gly Met Gly Ile Glu Ile Val Lys
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Asp Leu Ser Arg Asp His Ile Val Tyr Ala Leu Gly Arg Asn Pro Glu
                        25                        30                        35

cat ctg gca gct ctc gca gag atc gag gga gta gag cct atc gag tcc 259
His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val Glu Pro Ile Glu Ser
                        40                        45                        50

gat atc gtg aag gaa gtg ttg gaa gag gga ggc gtc gac aag cta aaa 307
Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly Val Asp Lys Leu Lys
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aac ctc gac cac gtg gat acg ctg gtg cac gcc gcg gcg gtg gcg cgt 355
Asn Leu Asp His Val Asp Thr Leu Val His Ala Ala Ala Val Ala Arg
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gac acg acc atc gaa gcc ggc agt gtg gcc gaa tgg cac gca cac ctt 403
Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu Trp His Ala His Leu
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Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser Arg Gln Leu Leu Pro
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gcc ctc cgc gcg gca tcc ggc tgc gtc atc tac atc aac tcc ggc gcc 499
Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr Ile Asn Ser Gly Ala
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Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr Ala Ala Ser Lys His
                        135                        140                        145

gcc ctc cgc gga ctc gcc gac gcc ttc cgc aaa gaa gaa gcc aac aac 595
Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys Glu Glu Ala Asn Asn
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ggc atc cgc gtc agc act gtc agc ccc ggc ccc acc aac acc ccc atg 643
Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro Thr Asn Thr Pro Met
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ctg caa ggc ctc atg gac tca caa ggc acc aac ttc cgc cca gag atc 691

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 Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile Arg Phe Val Ile Asp
 200 205 210
 gct ggc gaa acc acc cag atc acc aac gtg gac gta cga cca cgt atc 787
 Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp Val Arg Pro Arg Ile
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 Glu Leu Ala Asp Arg Lys Asp
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 <213> Corynebacterium glutamicum

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 Gly Arg Asn Pro Glu His Leu Ala Ala Leu Ala Glu Ile Glu Gly Val
 35 40 45
 Glu Pro Ile Glu Ser Asp Ile Val Lys Glu Val Leu Glu Glu Gly Gly
 50 55 60
 Val Asp Lys Leu Lys Asn Leu Asp His Val Asp Thr Leu Val His Ala
 65 70 75 80
 Ala Ala Val Ala Arg Asp Thr Thr Ile Glu Ala Gly Ser Val Ala Glu
 85 90 95
 Trp His Ala His Leu Asp Leu Asn Val Ile Val Pro Ala Glu Leu Ser
 100 105 110
 Arg Gln Leu Leu Pro Ala Leu Arg Ala Ala Ser Gly Cys Val Ile Tyr
 115 120 125
 Ile Asn Ser Gly Ala Gly Asn Gly Pro His Pro Gly Asn Thr Ile Tyr
 130 135 140
 Ala Ala Ser Lys His Ala Leu Arg Gly Leu Ala Asp Ala Phe Arg Lys
 145 150 155 160
 Glu Glu Ala Asn Asn Gly Ile Arg Val Ser Thr Val Ser Pro Gly Pro
 165 170 175
 Thr Asn Thr Pro Met Leu Gln Gly Leu Met Asp Ser Gln Gly Thr Asn
 180 185 190
 Phe Arg Pro Glu Ile Tyr Ile Glu Pro Lys Glu Ile Ala Asn Ala Ile
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Arg Phe Val Ile Asp Ala Gly Glu Thr Thr Gln Ile Thr Asn Val Asp
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Val Arg Pro Arg Ile Glu Leu Ala Asp Arg Lys Asp
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<222> (101)..(985)

<223> RXN02654

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 Met Ile Ser Leu Leu
 1 5

aat gat cca cgt acg cta ttc ccg aaa gtc gat ccc cca aag caa agc 163
 Asn Asp Pro Arg Thr Leu Phe Pro Lys Val Asp Pro Pro Lys Gln Ser
 10 15 20

cag ccg gaa cca ggc cta gat ata aaa ctt tcc ccc caa gcc gat att 211
 Gln Pro Glu Pro Gly Leu Asp Ile Lys Leu Ser Pro Gln Ala Asp Ile
 25 30 35

ggt ctc tcc agc tat caa gga agt gga agg ctt aag ggc cgc aag gct 259
 Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu Lys Gly Arg Lys Ala
 40 45 50

ctt att act ggt ggc gat tct ggg att gga gct gcc gta gca atc gct 307
 Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala Ala Val Ala Ile Ala
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 Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala Tyr Leu Pro Glu Glu
 70 75 80 85

caa gcc gat gct gac aga gtg ctc caa gca atc gag gaa aca ggt caa 403
 Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile Glu Glu Thr Gly Gln
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 Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp Pro Glu Tyr Cys Arg
 105 110 115

tcg ctg gtc caa gag acg gtg aac gct tta ggt ggc cta gac atc ttg 499
 Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly Gly Leu Asp Ile Leu
 120 125 130

gtc aac aac gcg tca cgt cag gtg tgg gca cct ggt ttg acc gaa att 547
 Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro Gly Leu Thr Glu Ile
 135 140 145

acc gac gaa aac ttc gac cag act ttg cag gtt aac ctc tat ggt agt 595

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Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser	
				170					175					180		
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Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu	
			185					190					195			
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Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly	
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Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala	
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cca	ggt	cct	ttc	tggt	acg	ccg	ttg	caa	ccc	agc	cat	ggt	cag	cca	caa	835
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln	
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Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly	
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cac	cct	gtt	gag	ttg	gca	ggt	gcg	tac	gtt	ttt	ctc	gct	tct	gac	gaa	931
His	Pro	Val	Glu	Leu	Ala	Gly	Ala	Tyr	Val	Phe	Leu	Ala	Ser	Asp	Glu	
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Ala	Ser	Tyr	Val	Val	Gly	Glu	Thr	Leu	Gly	Val	Thr	Gly	Gly	Thr	Pro	
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Thr	Pro															
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<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 316

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Pro	Gln	Ala	Asp	Ile	Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	
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Lys	Gly	Arg	Lys	Ala	Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	
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Gln	Pro	Glu	Pro	Gly	Leu	Asp	Ile	Lys	Leu	Ser	Pro	Gln	Ala	Asp	Ile	
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Gly	Leu	Ser	Ser	Tyr	Gln	Gly	Ser	Gly	Arg	Leu	Lys	Gly	Arg	Lys	Ala	
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Leu	Ile	Thr	Gly	Gly	Asp	Ser	Gly	Ile	Gly	Ala	Ala	Val	Ala	Ile	Ala	
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Tyr	Ala	Arg	Glu	Gly	Ala	Asp	Val	Ala	Ile	Ala	Tyr	Leu	Pro	Glu	Glu	
70					75				80						85	
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Gln	Ala	Asp	Ala	Asp	Arg	Val	Leu	Gln	Ala	Ile	Glu	Glu	Thr	Gly	Gln	
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Lys	Ala	Phe	Ser	Phe	Pro	Gly	Asp	Leu	Arg	Asp	Pro	Glu	Tyr	Cys	Arg	
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Val	Asn	Asn	Ala	Ser	Arg	Gln	Val	Trp	Ala	Pro	Gly	Leu	Thr	Glu	Ile	
	135					140				145						
acc	gac	gaa	aac	ttc	gac	cag	act	ttg	cag	gtt	aac	ctc	tat	ggc	agt	595
Thr	Asp	Glu	Asn	Phe	Asp	Gln	Thr	Leu	Gln	Val	Asn	Leu	Tyr	Gly	Ser	
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Phe	Arg	Val	Thr	Lys	Ala	Ala	Ile	Pro	His	Leu	Lys	Pro	Gly	Ser	Ser	
				170					175					180		
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Ile	Ile	Phe	Thr	Ser	Ser	Ile	Gln	Ala	Tyr	Gln	Pro	Ser	Glu	Thr	Leu	
			185					190					195			
ttg	gat	tac	gcc	atg	act	aag	gcg	gca	ttg	aac	aat	ttg	tca	aag	ggc	739
Leu	Asp	Tyr	Ala	Met	Thr	Lys	Ala	Ala	Leu	Asn	Asn	Leu	Ser	Lys	Gly	
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Leu	Ala	Ser	Ser	Leu	Ile	Gly	Asp	Gly	Ile	Arg	Val	Asn	Ser	Val	Ala	
	215					220					225					
cca	ggc	cct	ttc	tgg	acg	ccg	ttg	caa	ccc	agc	cat	ggc	cag	cca	caa	835
Pro	Gly	Pro	Phe	Trp	Thr	Pro	Leu	Gln	Pro	Ser	His	Gly	Gln	Pro	Gln	
230					235					240					245	
gag	aaa	ata	gaa	gga	ttt	ggc	cag	cac	gct	ccg	att	gga	aga	gcg	ggc	883
Glu	Lys	Ile	Glu	Gly	Phe	Gly	Gln	His	Ala	Pro	Ile	Gly	Arg	Ala	Gly	

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His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe Leu Ala Ser Asp Glu			
265	270	275	
gcc agc tat gtg gta gga gaa acc ctg gga gtc aca ggt ggg acg ccc			979
Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val Thr Gly Gly Thr Pro			
280	285	290	
acc cca tagtcggtac aagcgggaatc act			1008
Thr Pro			
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<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 318

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20 25 30

Pro Gln Ala Asp Ile Gly Leu Ser Ser Tyr Gln Gly Ser Gly Arg Leu
35 40 45

Lys Gly Arg Lys Ala Leu Ile Thr Gly Gly Asp Ser Gly Ile Gly Ala
50 55 60

Ala Val Ala Ile Ala Tyr Ala Arg Glu Gly Ala Asp Val Ala Ile Ala
65 70 75 80

Tyr Leu Pro Glu Glu Gln Ala Asp Ala Asp Arg Val Leu Gln Ala Ile
85 90 95

Glu Glu Thr Gly Gln Lys Ala Phe Ser Phe Pro Gly Asp Leu Arg Asp
100 105 110

Pro Glu Tyr Cys Arg Ser Leu Val Gln Glu Thr Val Asn Ala Leu Gly
115 120 125

Gly Leu Asp Ile Leu Val Asn Asn Ala Ser Arg Gln Val Trp Ala Pro
130 135 140

Gly Leu Thr Glu Ile Thr Asp Glu Asn Phe Asp Gln Thr Leu Gln Val
145 150 155 160

Asn Leu Tyr Gly Ser Phe Arg Val Thr Lys Ala Ala Ile Pro His Leu
165 170 175

Lys Pro Gly Ser Ser Ile Ile Phe Thr Ser Ser Ile Gln Ala Tyr Gln
180 185 190

Pro Ser Glu Thr Leu Leu Asp Tyr Ala Met Thr Lys Ala Ala Leu Asn
195 200 205

Asn Leu Ser Lys Gly Leu Ala Ser Ser Leu Ile Gly Asp Gly Ile Arg

210	215	220
Val Asn Ser Val Ala Pro Gly Pro Phe Trp Thr Pro Leu Gln Pro Ser		
225	230	235 240
His Gly Gln Pro Gln Glu Lys Ile Glu Gly Phe Gly Gln His Ala Pro		
	245	250 255
Ile Gly Arg Ala Gly His Pro Val Glu Leu Ala Gly Ala Tyr Val Phe		
	260	265 270
Leu Ala Ser Asp Glu Ala Ser Tyr Val Val Gly Glu Thr Leu Gly Val		
	275	280 285
Thr Gly Gly Thr Pro Thr Pro		
290	295	

<210> 319
 <211> 1605
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1582)
 <223> RXN01049

<400> 319
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aagaatattc tttattagtc agaccttttaa aggaaacctt atg gga tca att cca 115
 Met Gly Ser Ile Pro
 1 5

aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163
 Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala
 10 15 20

atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211
 Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser
 25 30 35

ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259
 Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr
 40 45 50

acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307
 Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu
 55 60 65

atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355
 Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn
 70 75 80 85

atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403
 Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser
 90 95 100

tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451
 Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr

105	110	115	
tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu 120 125 130			499
atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr 135 140 145			547
tcc tac cac cca tcg cgc ttg ctg tgg ctg aaa act gag ttc gag aaa Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys Thr Glu Phe Glu Lys 150 155 160 165			595
gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag tac gtc tac Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu Tyr Val Tyr 170 175 180			643
ttc aaa ctt gca ggc atc acc gga atg gct act tcg att gcc gcg tgg Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile Ala Ala Trp 185 190 195			691
agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg act atc ttg Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu Thr Ile Leu 200 205 210			739
gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc aga aac cct Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile Arg Asn Pro 215 220 225			787
gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag tgg aag cac Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys Trp Lys His 230 235 240 245			835
ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc tgg cct tcc Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly Trp Pro Ser 250 255 260			883
aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca gtc gcc gcc Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala Val Ala Ala 265 270 275			931
gct aca tcc ggc gcc atg cgc gtg atc ctt ccg agc gtt ccc gaa cag Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro Ser Val Pro Glu Gln 280 285 290			979
atc ccc tct ggc ctg tgg tgt tac cgc gtt tcc cgc gac cag tgc atc Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser Arg Asp Gln Cys Ile 295 300 305			1027
gtt ggt ggc gca ctc aac gac gtc gga cgc gcc gtc acc tgg ctg gaa Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala Val Thr Trp Leu Glu 310 315 320 325			1075
cgc acc att atc aag cct gaa aac ctc gac gaa gtg ctg atc cgc gaa Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu Val Leu Ile Arg Glu 330 335 340			1123
ccc ctc gaa ggc acc cca gct gtc ctg ccg ttc ttc tcc ggg gaa cgc Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe Phe Ser Gly Glu Arg 345 350 355			1171

tcc atc ggc tgg gca gcc tca gcg cag gcc acg atc acc aac att cag 1219
 Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr Ile Thr Asn Ile Gln
 360 365 370

gaa caa acc ggc cct gaa cac ttg tgg cgc ggc gtt ttc gaa gcc ctc 1267
 Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly Val Phe Glu Ala Leu
 375 380 385

gca ctc tcc tac cag cgc gtt tgg gaa cac atg ggg aaa gcc ggc gca 1315
 Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met Gly Lys Ala Gly Ala
 390 395 400 405

gcc cct gaa cgg gtc atc gca tca gga cga gtc tcc acc gac cac cca 1363
 Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val Ser Thr Asp His Pro
 410 415 420

gaa ttc ctc gcg atg ctt tcc gac gcc ctc gac acc cca gtc atc cct 1411
 Glu Phe Leu Ala Met Leu Ser Asp Ala Leu Asp Thr Pro Val Ile Pro
 425 430 435

ctg gaa atg aag cgc gcc acc ctc cgc ggc acc gca ctt atc gtc ctt 1459
 Leu Glu Met Lys Arg Ala Thr Leu Arg Gly Thr Ala Leu Ile Val Leu
 440 445 450

gag cag ctc gaa cca ggc ggc acg cgc gcg acg cca cca ttc ggc acg 1507
 Glu Gln Leu Glu Pro Gly Gly Thr Arg Ala Thr Pro Pro Phe Gly Thr
 455 460 465

acg cat cag ccg cgc ttt gcg cac cat tac tcc aag gca aga gag ctt 1555
 Thr His Gln Pro Arg Phe Ala His His Tyr Ser Lys Ala Arg Glu Leu
 470 475 480 485

ttc gac gcc ctc tac ctc aag ttg gtc tagcttttcg cagtggaacg 1602
 Phe Asp Ala Leu Tyr Leu Lys Leu Val
 490

cgc 1605

<210> 320

<211> 494

<212> PRT

<213> Corynebacterium glutamicum

<400> 320

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
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Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
 85 90 95
 Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
 100 105 110
 Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
 115 120 125
 Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
 130 135 140
 Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp Leu Lys
 145 150 155 160
 Thr Glu Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile
 165 170 175
 Gly Glu Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr
 180 185 190
 Ser Ile Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu
 195 200 205
 Asp Leu Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly
 210 215 220
 Glu Ile Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp
 225 230 235 240
 Lys Lys Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro
 245 250 255
 Asp Gly Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr
 260 265 270
 Val Ala Val Ala Ala Ala Thr Ser Gly Ala Met Arg Val Ile Leu Pro
 275 280 285
 Ser Val Pro Glu Gln Ile Pro Ser Gly Leu Trp Cys Tyr Arg Val Ser
 290 295 300
 Arg Asp Gln Cys Ile Val Gly Gly Ala Leu Asn Asp Val Gly Arg Ala
 305 310 315 320
 Val Thr Trp Leu Glu Arg Thr Ile Ile Lys Pro Glu Asn Leu Asp Glu
 325 330 335
 Val Leu Ile Arg Glu Pro Leu Glu Gly Thr Pro Ala Val Leu Pro Phe
 340 345 350
 Phe Ser Gly Glu Arg Ser Ile Gly Trp Ala Ala Ser Ala Gln Ala Thr
 355 360 365
 Ile Thr Asn Ile Gln Glu Gln Thr Gly Pro Glu His Leu Trp Arg Gly
 370 375 380
 Val Phe Glu Ala Leu Ala Leu Ser Tyr Gln Arg Val Trp Glu His Met
 385 390 395 400
 Gly Lys Ala Gly Ala Ala Pro Glu Arg Val Ile Ala Ser Gly Arg Val

	405		410		415
Ser Thr Asp	His Pro Glu Phe Leu Ala	Met Leu Ser Asp	Ala Leu Asp		
	420	425	430		
Thr Pro Val	Ile Pro Leu Glu Met Lys Arg	Ala Thr Leu Arg	Gly Thr		
	435	440	445		
Ala Leu Ile	Val Leu Glu Gln Leu Glu Pro Gly	Gly Thr Arg	Ala Thr		
	450	455	460		
Pro Pro Phe	Gly Thr Thr His Gln Pro Arg	Phe Ala His His Tyr	Ser		
465	470	475	480		
Lys Ala Arg	Glu Leu Phe Asp Ala Leu Tyr	Leu Lys Leu Val			
	485	490			

<210> 321
 <211> 1134
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1111)
 <223> FRXA01049

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 gcgtctgctt gcacacctcc taccacccat cgcgcttgct gtg gtg aaa act gag 115
 Val Val Lys Thr Glu
 1 5
 ttc gag aaa gag ttc aac aaa gcc aag tat gtg atg acc atc ggt gag 163
 Phe Glu Lys Glu Phe Asn Lys Ala Lys Tyr Val Met Thr Ile Gly Glu
 10 15 20
 tac gtc tac ttc aaa ctt gca ggc atc acc gga atg gct act tcg att 211
 Tyr Val Tyr Phe Lys Leu Ala Gly Ile Thr Gly Met Ala Thr Ser Ile
 25 30 35
 gcc gcg tgg agt ggc att ttg gac gcc cat acc ggc gaa ctt gat ctg 259
 Ala Ala Trp Ser Gly Ile Leu Asp Ala His Thr Gly Glu Leu Asp Leu
 40 45 50
 act atc ttg gag cac atc ggt gtt gat ccg gct ctg ttc ggt gag atc 307
 Thr Ile Leu Glu His Ile Gly Val Asp Pro Ala Leu Phe Gly Glu Ile
 55 60 65
 aga aac cct gat gaa cca gcc acc gat gcc aaa gtt gtc gac aaa aag 355
 Arg Asn Pro Asp Glu Pro Ala Thr Asp Ala Lys Val Val Asp Lys Lys
 70 75 80 85
 tgg aag cac ctg gaa gaa atc cct tgg ttc cat gcc att cca gac ggc 403
 Trp Lys His Leu Glu Glu Ile Pro Trp Phe His Ala Ile Pro Asp Gly
 90 95 100
 tgg cct tcc aac att ggc cca ggc gcc gtg gat tct aaa acc gtc gca 451
 Trp Pro Ser Asn Ile Gly Pro Gly Ala Val Asp Ser Lys Thr Val Ala

				105				110				115							
gtc	gcc	gcc	gct	aca	tcc	ggc	gcc	atg	cgc	gtg	atc	ctt	ccg	agc	gtt	499			
Val	Ala	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	Ile	Leu	Pro	Ser	Val				
120								125				130							
ccc	gaa	cag	atc	ccc	tct	ggc	ctg	tgg	tgt	tac	cgc	gtt	tcc	cgc	gac	547			
Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	Arg	Val	Ser	Arg	Asp				
135								140				145							
cag	tgc	atc	gtt	ggc	ggc	gca	ctc	aac	gac	gtc	gga	cgc	gcc	gtc	acc	595			
Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	Gly	Arg	Ala	Val	Thr				
150				155				160				165							
tgg	ctg	gaa	cgc	acc	att	atc	aag	cct	gaa	aac	ctc	gac	gaa	gtg	ctg	643			
Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	Leu	Asp	Glu	Val	Leu				
				170				175				180							
atc	cgc	gaa	ccc	ctc	gaa	ggc	acc	cca	gct	gtc	ctg	ccg	ttc	ttc	tcc	691			
Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	Leu	Pro	Phe	Phe	Ser				
185								190				195							
ggg	gaa	cgc	tcc	atc	ggc	tgg	gca	gcc	tca	gcg	cag	gcc	acg	atc	acc	739			
Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	Gln	Ala	Thr	Ile	Thr				
200								205				210							
aac	att	cag	gaa	caa	acc	ggc	cct	gaa	cac	ttg	tgg	cgc	ggc	gtt	ttc	787			
Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	Trp	Arg	Gly	Val	Phe				
215				220				225											
gaa	gcc	ctc	gca	ctc	tcc	tac	cag	cgc	gtt	tgg	gaa	cac	atg	ggg	aaa	835			
Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	Glu	His	Met	Gly	Lys				
230				235				240				245							
gcc	ggc	gca	gcc	cct	gaa	cgg	gtc	atc	gca	tca	gga	cga	gtc	tcc	acc	883			
Ala	Gly	Ala	Ala	Pro	Glu	Arg	Val	Ile	Ala	Ser	Gly	Arg	Val	Ser	Thr				
				250				255				260							
gac	cac	cca	gaa	ttc	ctc	gcg	atg	ctt	tcc	gac	gcc	ctc	gac	acc	cca	931			
Asp	His	Pro	Glu	Phe	Leu	Ala	Met	Leu	Ser	Asp	Ala	Leu	Asp	Thr	Pro				
265								270				275							
gtc	atc	cct	ctg	gaa	atg	aag	cgc	gcc	acc	ctc	cgc	ggc	acc	gca	ctt	979			
Val	Ile	Pro	Leu	Glu	Met	Lys	Arg	Ala	Thr	Leu	Arg	Gly	Thr	Ala	Leu				
280								285				290							
atc	gtc	ctt	gag	cag	ctc	gaa	cca	ggc	ggc	acg	cgc	gcg	acg	cca	cca	1027			
Ile	Val	Leu	Glu	Gln	Leu	Glu	Pro	Gly	Gly	Thr	Arg	Ala	Thr	Pro	Pro				
295				300				305											
ttc	ggc	acg	acg	cat	cag	ccg	cgc	ttt	gcg	cac	cat	tac	tcc	aag	gca	1075			
Phe	Gly	Thr	Thr	His	Gln	Pro	Arg	Phe	Ala	His	His	Tyr	Ser	Lys	Ala				
310				315				320				325							
aga	gag	ctt	ttc	gac	gcc	ctc	tac	ctc	aag	ttg	gtc	tagcttttcg					1121		
Arg	Glu	Leu	Phe																

<210> 322
 <211> 337
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 322

Val	Val	Lys	Thr	Glu	Phe	Glu	Lys	Glu	Phe	Asn	Lys	Ala	Lys	Tyr	Val	1	5	10	15
Met	Thr	Ile	Gly	Glu	Tyr	Val	Tyr	Phe	Lys	Leu	Ala	Gly	Ile	Thr	Gly	20	25	30	
Met	Ala	Thr	Ser	Ile	Ala	Ala	Trp	Ser	Gly	Ile	Leu	Asp	Ala	His	Thr	35	40	45	
Gly	Glu	Leu	Asp	Leu	Thr	Ile	Leu	Glu	His	Ile	Gly	Val	Asp	Pro	Ala	50	55	60	
Leu	Phe	Gly	Glu	Ile	Arg	Asn	Pro	Asp	Glu	Pro	Ala	Thr	Asp	Ala	Lys	65	70	75	80
Val	Val	Asp	Lys	Lys	Trp	Lys	His	Leu	Glu	Glu	Ile	Pro	Trp	Phe	His	85	90	95	
Ala	Ile	Pro	Asp	Gly	Trp	Pro	Ser	Asn	Ile	Gly	Pro	Gly	Ala	Val	Asp	100	105	110	
Ser	Lys	Thr	Val	Ala	Val	Ala	Ala	Thr	Ser	Gly	Ala	Met	Arg	Val	115	120	125		
Ile	Leu	Pro	Ser	Val	Pro	Glu	Gln	Ile	Pro	Ser	Gly	Leu	Trp	Cys	Tyr	130	135	140	
Arg	Val	Ser	Arg	Asp	Gln	Cys	Ile	Val	Gly	Gly	Ala	Leu	Asn	Asp	Val	145	150	155	160
Gly	Arg	Ala	Val	Thr	Trp	Leu	Glu	Arg	Thr	Ile	Ile	Lys	Pro	Glu	Asn	165	170	175	
Leu	Asp	Glu	Val	Leu	Ile	Arg	Glu	Pro	Leu	Glu	Gly	Thr	Pro	Ala	Val	180	185	190	
Leu	Pro	Phe	Phe	Ser	Gly	Glu	Arg	Ser	Ile	Gly	Trp	Ala	Ala	Ser	Ala	195	200	205	
Gln	Ala	Thr	Ile	Thr	Asn	Ile	Gln	Glu	Gln	Thr	Gly	Pro	Glu	His	Leu	210	215	220	
Trp	Arg	Gly	Val	Phe	Glu	Ala	Leu	Ala	Leu	Ser	Tyr	Gln	Arg	Val	Trp	225	230	235	240
Glu	His	Met	Gly	Lys	Ala	Gly	Ala	Ala	Pro	Glu	Arg	Val	Ile	Ala	Ser	245	250	255	
Gly	Arg	Val	Ser	Thr	Asp	His	Pro	Glu	Phe	Leu	Ala	Met	Leu	Ser	Asp	260	265	270	
Ala	Leu	Asp	Thr	Pro	Val	Ile	Pro	Leu	Glu	Met	Lys	Arg	Ala	Thr	Leu	275	280	285	
Arg	Gly	Thr	Ala	Leu	Ile	Val	Leu	Glu	Gln	Leu	Glu	Pro	Gly	Gly	Thr				

<400> 323															
aagcacagca attgagcaat actcccatgc atgttttcgc gtgatcacgc tatatcctta 60															
aagaatatcc tttattagtc agacctttaa aggaaacctt atg gga tca att cca 115															
Met Gly Ser Ile Pro 5															
1															
aca atg tcc atc cct ttt gat gac tca cgt gga cct tat gtc ctt gct 163															
Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly Pro Tyr Val Leu Ala 20															
10 15															
atg gat att ggt tcc act gca tca cga ggt gga ctt tat gat gct tcc 211															
Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly Leu Tyr Asp Ala Ser 35															
25 30															
ggc tgc cca atc aaa ggc acc aag cag cgc gaa tcc cat gaa ttc acc 259															
Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu Ser His Glu Phe Thr 50															
40 45															
acc ggt gag ggc gtt tcc acc att gat gct gac cag gtg gtt tcg gag 307															
Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp Gln Val Val Ser Glu 65															
55 60															
atc acc tca gtt att aat ggc att ttg aac gcg gct gat cat cac aac 355															
Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala Ala Asp His His Asn 85															
70 75 80															
atc aaa gat cag atc gcc gct gtc gcg cta gat tct ttt gca tcc tca 403															
Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp Ser Phe Ala Ser Ser 100															
90 95															
tta atc ttg gtc gat ggt gaa ggc aat gcg ctc acc ccg tgc att acc 451															
Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu Thr Pro Cys Ile Thr 115															
105 110															
tac gcg gat tct cgt tct gca cag tat gtg gag cag ctg cgc gcg gaa 499															
Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu Gln Leu Arg Ala Glu 120 125 130															

atc gat gag aag gcc tac cac ggc cgc acc ggc gtc tgc ttg cac acc 547
 Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly Val Cys Leu His Thr
 135 140 145

tcc tac cac cca tcg cgc ttg ctg tgg tgaaaactga gttcgagaaa 594
 Ser Tyr His Pro Ser Arg Leu Leu Trp
 150 155

gag 597

<210> 324

<211> 158

<212> PRT

<213> Corynebacterium glutamicum

<400> 324

Met Gly Ser Ile Pro Thr Met Ser Ile Pro Phe Asp Asp Ser Arg Gly
 1 5 10 15

Pro Tyr Val Leu Ala Met Asp Ile Gly Ser Thr Ala Ser Arg Gly Gly
 20 25 30

Leu Tyr Asp Ala Ser Gly Cys Pro Ile Lys Gly Thr Lys Gln Arg Glu
 35 40 45

Ser His Glu Phe Thr Thr Gly Glu Gly Val Ser Thr Ile Asp Ala Asp
 50 55 60

Gln Val Val Ser Glu Ile Thr Ser Val Ile Asn Gly Ile Leu Asn Ala
 65 70 75 80

Ala Asp His His Asn Ile Lys Asp Gln Ile Ala Ala Val Ala Leu Asp
 85 90 95

Ser Phe Ala Ser Ser Leu Ile Leu Val Asp Gly Glu Gly Asn Ala Leu
 100 105 110

Thr Pro Cys Ile Thr Tyr Ala Asp Ser Arg Ser Ala Gln Tyr Val Glu
 115 120 125

Gln Leu Arg Ala Glu Ile Asp Glu Lys Ala Tyr His Gly Arg Thr Gly
 130 135 140

Val Cys Leu His Thr Ser Tyr His Pro Ser Arg Leu Leu Trp
 145 150 155

<210> 325

<211> 1065

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1042)

<223> RXA00202

<400> 325

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aaacaaaacc	tctaagtaat	tcctgaaagg	aaattttcac	atg	tac	gct	cgt	aaa	115
				Met	Tyr	Ala	Arg	Lys	
				1				5	
ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct	163								
Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala									
	10	15	20						
tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat	211								
Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp									
	25	30	35						
ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg	259								
Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val									
	40	45	50						
cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc	307								
Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr									
	55	60	65						
ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag	355								
Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln									
	70	75	80					85	
ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca	403								
Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro									
	90	95	100						
act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct	451								
Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala									
	105	110	115						
gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg	499								
Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val									
	120	125	130						
gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct	547								
Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala									
	135	140	145						
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg	595								
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu									
	150	155	160					165	
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt	643								
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe									
	170	175	180						
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag	691								
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln									
	185	190	195						
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg	739								
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu									
	200	205	210						
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag	787								
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu									
	215	220	225						
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat	835								

Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp
 230 235 240 245

gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt 883
 Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val
 250 255 260

gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg 931
 Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu
 265 270 275

gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac 979
 Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp
 280 285 290

gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac 1027
 Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn
 295 300 305

gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt 1065
 Val Ala Asp Phe Lys
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<210> 326

<211> 314

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 326

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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
 20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
 35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60

Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80

Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95

Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110

Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125

Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140

Gly Ala Gln Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160

Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp

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ccacattcca tcaaaaatga gtgaagggtt gcatcgccac atg act aac ttg acg 115																
Met Thr Asn Leu Thr 5																
agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac 163																
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr 20																
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag 211																
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys 35																
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat 259																
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His 40 45 50																
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc 307																
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly																

55					60					65									
gag	tac	ctg	ctt	gct	gag	ctg	gag	cgt	ttg	ggc	gtg	gac	aac	cag	tac	355			
Glu	Tyr	Leu	Leu	Ala	Glu	Leu	Glu	Arg	Leu	Gly	Val	Asp	Asn	Gln	Tyr				
70					75					80					85				
gtt	gcc	acc	gat	cag	act	ttt	aag	acc	cca	gtg	acc	ttc	tgt	gaa	att	403			
Val	Ala	Thr	Asp	Gln	Thr	Phe	Lys	Thr	Pro	Val	Thr	Phe	Cys	Glu	Ile				
				90					95					100					
ttc	cca	ccg	gat	gat	ttc	cca	ctg	tac	ttc	tac	cgc	gaa	cca	aag	gct	451			
Phe	Pro	Pro	Asp	Asp	Phe	Pro	Leu	Tyr	Phe	Tyr	Arg	Glu	Pro	Lys	Ala				
			105					110					115						
ccg	gat	ctc	aat	att	gaa	tcc	gca	gac	gtc	agc	ctg	gac	gat	gtg	cgc	499			
Pro	Asp	Leu	Asn	Ile	Glu	Ser	Ala	Asp	Val	Ser	Leu	Asp	Asp	Val	Arg				
		120					125					130							
gaa	gcc	gat	att	ttg	tgg	ttc	aca	ctc	act	ggt	ttc	agt	gaa	gag	cca	547			
Glu	Ala	Asp	Ile	Leu	Trp	Phe	Thr	Leu	Thr	Gly	Phe	Ser	Glu	Glu	Pro				
	135					140					145								
agc	cgc	ggc	aca	cac	cgc	gag	atc	ttg	act	act	cgt	gcg	aac	cgt	cgc	595			
Ser	Arg	Gly	Thr	His	Arg	Glu	Ile	Leu	Thr	Thr	Arg	Ala	Asn	Arg	Arg				
150					155					160					165				
cac	acc	atc	ttt	gat	ctg	gac	tac	cga	cca	atg	ttc	tgg	gaa	tcc	cca	643			
His	Thr	Ile	Phe	Asp	Leu	Asp	Tyr	Arg	Pro	Met	Phe	Trp	Glu	Ser	Pro				
				170					175					180					
gaa	gag	gcc	acc	aag	cag	gcg	gaa	tgg	gcg	ttg	cag	cat	tcc	acg	gtg	691			
Glu	Glu	Ala	Thr	Lys	Gln	Ala	Glu	Trp	Ala	Leu	Gln	His	Ser	Thr	Val				
			185					190					195						
gcg	gtt	ggc	aac	aag	gaa	gaa	tgc	gaa	atc	gca	gtg	ggc	gag	acc	gag	739			
Ala	Val	Gly	Asn	Lys	Glu	Glu	Cys	Glu	Ile	Ala	Val	Gly	Glu	Thr	Glu				
		200					205					210							
cca	gag	cgc	gcg	ggc	cga	gca	ctg	ttg	gaa	cgc	ggt	gtg	gag	ttg	gcc	787			
Pro	Glu	Arg	Ala	Gly	Arg	Ala	Leu	Leu	Glu	Arg	Gly	Val	Glu	Leu	Ala				
		215				220					225								
atc	gtc	aag	cag	gga	cct	aag	ggt	gtc	atg	gcg	atg	acc	aag	gac	gaa	835			
Ile	Val	Lys	Gln	Gly	Pro	Lys	Gly	Val	Met	Ala	Met	Thr	Lys	Asp	Glu				
230					235					240					245				
acc	gta	gaa	gtt	cct	ccg	ttc	ttc	gtc	gat	gtc	atc	aac	ggt	ctt	ggt	883			
Thr	Val	Glu	Val	Pro	Pro	Phe	Phe	Val	Asp	Val	Ile	Asn	Gly	Leu	Gly				
				250					255					260					
gcc	ggc	gat	gca	ttc	ggc	ggc	gcg	ctg	tgc	cac	ggt	ctg	ctc	tct	gaa	931			
Ala	Gly	Asp	Ala	Phe	Gly	Gly	Ala	Leu	Cys	His	Gly	Leu	Leu	Ser	Glu				
			265					270					275						
tgg	ccg	ttg	gaa	aag	gtt	ctc	cgt	ttt	gcc	aac	acc	gcg	ggt	gcg	ctt	979			
Trp	Pro	Leu	Glu	Lys	Val	Leu	Arg	Phe	Ala	Asn	Thr	Ala	Gly	Ala	Leu				
		280					285					290							
gtg	gcg	tcc	cgt	ctt	gaa	tgc	tcc	acc	gca	atg	cct	act	acc	gat	gag	1027			
Val	Ala	Ser	Arg	Leu	Glu	Cys	Ser	Thr	Ala	Met	Pro	Thr	Thr	Asp	Glu				
	295					300					305								

gtg gaa gcc tcc ctc aac cag aaa gtc tgatatgact cctccgatta 1074
 Val Glu Ala Ser Leu Asn Gln Lys Val
 310 315

tct 1077

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<211> 318

<212> PRT

<213> Corynebacterium glutamicum

<400> 328

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Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val
 20 25 30

Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val
 35 40 45

Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly
 50 55 60

Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly
 65 70 75 80

Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val
 85 90 95

Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr
 100 105 110

Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser
 115 120 125

Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly
 130 135 140

Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr
 145 150 155 160

Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg Pro Met
 165 170 175

Phe Trp Glu Ser Pro Glu Glu Ala Thr Lys Gln Ala Glu Trp Ala Leu
 180 185 190

Gln His Ser Thr Val Ala Val Gly Asn Lys Glu Glu Cys Glu Ile Ala
 195 200 205

Val Gly Glu Thr Glu Pro Glu Arg Ala Gly Arg Ala Leu Leu Glu Arg
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Gly Val Glu Leu Ala Ile Val Lys Gln Gly Pro Lys Gly Val Met Ala
 225 230 235 240

Met Thr Lys Asp Glu Thr Val Glu Val Pro Pro Phe Phe Val Asp Val
 245 250 255

<400> 329																
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Met Thr Asn Leu Thr																115
1 5																
agc act cac gaa gtc cta gct atc ggc cgc ttg ggc gta gat att tac																163
Ser Thr His Glu Val Leu Ala Ile Gly Arg Leu Gly Val Asp Ile Tyr																
10 15 20																
cca ctt caa agt gga gta gga ctg gcc gat gtt caa tct ttc ggc aag																211
Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val Gln Ser Phe Gly Lys																
25 30 35																
tac ctc ggc gga agc gca gca aac gtt tct gtt gca gcc gcc cgc cat																259
Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val Ala Ala Ala Arg His																
40 45 50																
gga cac aat tcc gca ctg ctg tcc cgt gtg gga aat gat cct ttc ggc																307
Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly Asn Asp Pro Phe Gly																
55 60 65																
gag tac ctg ctt gct gag ctg gag cgt ttg ggc gtg gac aac cag tac																355
Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly Val Asp Asn Gln Tyr																
70 75 80 85																
gtt gcc acc gat cag act ttt aag acc cca gtg acc ttc tgt gaa att																403
Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val Thr Phe Cys Glu Ile																
90 95 100																
ttc cca ccg gat gat ttc cca ctg tac ttc tac cgc gaa cca aag gct																451
Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr Arg Glu Pro Lys Ala																
105 110 115																
ccg gat ctc aat att gaa tcc gca gac gtc agc ctg gac gat gtg cgc																499
Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser Leu Asp Asp Val Arg																

120	125	130	
gaa gcc gat att ttg tgg ttc aca ctc act ggt ttc agt gaa gag cca			547
Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly Phe Ser Glu Glu Pro			
135	140	145	
agc cgc ggc aca cac cgc gag atc ttg act act cgt gcg aac cgt cgc			595
Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr Arg Ala Asn Arg Arg			
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cac acc atc ttt gat ctg gac tac cga			622
His Thr Ile Phe Asp Leu Asp Tyr Arg			
170			

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<211> 174

<212> PRT

<213> Corynebacterium glutamicum

<400> 330

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Gly Val Asp Ile Tyr Pro Leu Gln Ser Gly Val Gly Leu Ala Asp Val			
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Gln Ser Phe Gly Lys Tyr Leu Gly Gly Ser Ala Ala Asn Val Ser Val			
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Ala Ala Ala Arg His Gly His Asn Ser Ala Leu Leu Ser Arg Val Gly			
50	55	60	
Asn Asp Pro Phe Gly Glu Tyr Leu Leu Ala Glu Leu Glu Arg Leu Gly			
65	70	75	80
Val Asp Asn Gln Tyr Val Ala Thr Asp Gln Thr Phe Lys Thr Pro Val			
85	90	95	
Thr Phe Cys Glu Ile Phe Pro Pro Asp Asp Phe Pro Leu Tyr Phe Tyr			
100	105	110	
Arg Glu Pro Lys Ala Pro Asp Leu Asn Ile Glu Ser Ala Asp Val Ser			
115	120	125	
Leu Asp Asp Val Arg Glu Ala Asp Ile Leu Trp Phe Thr Leu Thr Gly			
130	135	140	
Phe Ser Glu Glu Pro Ser Arg Gly Thr His Arg Glu Ile Leu Thr Thr			
145	150	155	160
Arg Ala Asn Arg Arg His Thr Ile Phe Asp Leu Asp Tyr Arg			
165	170		

<210> 331

<211> 1767

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(1744)

<223> RXN00799

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ctgactacga tggttaagaaa taaggaaaga gattaccatt atg tct caa gag cgg 115
Met Ser Gln Glu Arg
1 5

cct caa atc ggc tcc cgc ctc tct cgt gtc att gaa caa gac ggc cta 163
Pro Gln Ile Gly Ser Arg Leu Ser Arg Val Ile Glu Gln Asp Gly Leu
10 15 20

caa ttc cgc gat ctc gac ggc gac ggc gta ctt gca cct tat gaa gat 211
Gln Phe Arg Asp Leu Asp Gly Asp Val Leu Ala Pro Tyr Glu Asp
25 30 35

tgg cgt cta acc cca gca gag cgt gcc gct gac ctg gtg aaa cgt atg 259
Trp Arg Leu Thr Pro Ala Glu Arg Ala Ala Asp Leu Val Lys Arg Met
40 45 50

aat gtg gaa gaa aaa gcg ggc ctg atg atc atc ggt tcg cac tac ccc 307
Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile Gly Ser His Tyr Pro
55 60 65

gga tac tcg cct ttg gcg ccg gag agt gaa ggc aaa gac gcg gaa aag 355
Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly Lys Asp Ala Glu Lys
70 75 80 85

tgc gag cct ttg ctg aac cct gtc gat atg tgg cgt gag gat aac ccg 403
Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp Arg Glu Asp Asn Pro
90 95 100

atc acg ggt gtt cct ttc acc gag cct gtg ctg gca act tct tcc act 451
Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu Ala Thr Ser Ser Thr
105 110 115

gaa aat gcc att aac ctg cgc aat cag cgt tac tta att gtt cgt gac 499
Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr Leu Ile Val Arg Asp
120 125 130

aac ctg cca gct cgt ggg ctt gct act tgg acc aat gct gtt cag gaa 547
Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr Asn Ala Val Gln Glu
135 140 145

gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg aat 595
Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser Asn
150 155 160 165

cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag tcc 643
Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu Ser
170 175 180

gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg ctt 691
Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala Leu
185 190 195

cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa gaa 739
Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys Glu

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200						205						210						
tgg	cgt	gcc	ggt	ggt	gtg	cac	aag	ctg	tac	ggt	tac	atg	gct	gac	ctc	787		
Trp	Arg	Ala	Gly	Gly	Val	His	Lys	Leu	Tyr	Gly	Tyr	Met	Ala	Asp	Leu			
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gct	tct	gag	cct	cgt	tgg	tcc	cgc	ttc	aac	ggt	act	ttt	ggt	gag	gat	835		
Ala	Ser	Glu	Pro	Arg	Trp	Ser	Arg	Phe	Asn	Gly	Thr	Phe	Gly	Glu	Asp			
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ccg	gag	ttg	atc	tct	gat	tac	atc	gct	gct	ggt	gtg	cgt	ggt	ttg	cag	883		
Pro	Glu	Leu	Ile	Ser	Asp	Tyr	Ile	Ala	Ala	Val	Val	Arg	Gly	Leu	Gln			
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Gly	Pro	Glu	Leu	Ser	Lys	Asn	Ser	Val	Ser	Thr	Thr	Ile	Lys	His	Phe			
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cca	ggt	ggc	ggc	gtg	cgc	ctc	gac	ggc	cac	gat	cct	cac	ttc	cac	tgg	979		
Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His	Trp			
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ggt	cag	acc	aat	gag	tac	cca	acc	gaa	gat	gcg	ctg	ggc	aag	tac	cat	1027		
Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr	His			
	295					300					305							
ctg	cct	cct	ttc	cag	gca	gct	atc	gac	gct	ggc	tgc	gcc	tcg	atc	atg	1075		
Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile	Met			
310					315					320					325			
cct	tac	tac	gca	cgg	cca	atg	aac	aac	tcc	gcc	aac	cag	ctc	gat	cag	1123		
Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp	Gln			
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cag	ctg	tgg	caa	aac	ccg	acc	acg	cag	ttc	gaa	gag	ggt	gcg	ttt	gcc	1171		
Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe	Ala			
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tac	aac	cgc	acc	ttc	att	cag	gat	ttg	ctt	cgc	gac	gcc	atg	ggc	cac	1219		
Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly	His			
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cgt	ggg	tac	gtc	aac	tcc	gac	tcc	ggc	gtc	atc	gac	gcc	atg	atg	tgg	1267		
Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met	Trp			
	375					380					385							
ggc	gtg	gag	gaa	ctc	agc	gag	cca	gaa	cgc	ttc	gcc	gca	gca	gtg	cgt	1315		
Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val	Arg			
390					395					400					405			
gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	ctc	1363		
Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu	Leu			
				410					415					420				
gaa	gca	ggt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	cca	1411		
Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln	Pro			
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gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggt	ctg	ttt	gag	aac	1459		
Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu	Asn			
		440					445					450						

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 Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile Ile Gly Ala Pro Glu
 455 460 465

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 Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp Ser Val Thr Leu Leu
 470 475 480 485

cgt aac aac ccc atc cgt gct gcc act gga tcc tgc agc aag cct gaa 1603
 Arg Asn Asn Pro Ile Arg Ala Ala Thr Gly Ser Cys Ser Lys Pro Glu
 490 495 500

gat cta ccc att ggt tac tgg ccg tac caa gat cga cga ggt tca act 1651
 Asp Leu Pro Ile Gly Tyr Trp Pro Tyr Gln Asp Arg Arg Gly Ser Thr
 505 510 515

aca gct gga agc agc cat tcg cgc aga act ccc agg ggt aac ctt ggt 1699
 Thr Ala Gly Ser Ser His Ser Arg Arg Thr Pro Arg Gly Asn Leu Gly
 520 525 530

gtc ttc cga gtc aga agc aga tct tgc aat cgt gtg ggc tcg ccc 1744
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<211> 548

<212> PRT

<213> Corynebacterium glutamicum

<400> 332

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 35 40 45

Leu Val Lys Arg Met Asn Val Glu Glu Lys Ala Gly Leu Met Ile Ile
 50 55 60

Gly Ser His Tyr Pro Gly Tyr Ser Pro Leu Ala Pro Glu Ser Glu Gly
 65 70 75 80

Lys Asp Ala Glu Lys Cys Glu Pro Leu Leu Asn Pro Val Asp Met Trp
 85 90 95

Arg Glu Asp Asn Pro Ile Thr Gly Val Pro Phe Thr Glu Pro Val Leu
 100 105 110

Ala Thr Ser Ser Thr Glu Asn Ala Ile Asn Leu Arg Asn Gln Arg Tyr
 115 120 125

Leu Ile Val Arg Asp Asn Leu Pro Ala Arg Gly Leu Ala Thr Trp Thr
 130 135 140

Asn Ala Val Gln Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val
 145 150 155 160
 Ala Phe Ala Ser Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe
 165 170 175
 Gly Val Asn Glu Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu
 180 185 190
 Gly Leu Ala Ala Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr
 195 200 205
 Glu Ala Ala Lys Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly
 210 215 220
 Tyr Met Ala Asp Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly
 225 230 235 240
 Thr Phe Gly Glu Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val
 245 250 255
 Val Arg Gly Leu Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr
 260 265 270
 Thr Ile Lys His Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp
 275 280 285
 Pro His Phe His Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala
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 Leu Gly Lys Tyr His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly
 305 310 315 320
 Cys Ala Ser Ile Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala
 325 330 335
 Asn Gln Leu Asp Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu
 340 345 350
 Glu Val Ala Phe Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg
 355 360 365
 Asp Ala Met Gly His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile
 370 375 380
 Asp Ala Met Met Trp Gly Val Glu Glu Leu Ser Glu Pro Glu Arg Phe
 385 390 395 400
 Ala Ala Ala Val Arg Ala Gly Thr Asp Ile Phe Ser Asp Met Ala Asn
 405 410 415
 Pro Arg Arg Leu Leu Glu Ala Val Ala Glu Gly His Leu Asp Glu Ser
 420 425 430
 Glu Leu Asn Gln Pro Val Gln Arg Leu Leu Glu Glu Ile Phe Gln Leu
 435 440 445
 Gly Leu Phe Glu Asn Pro Tyr Val Ser Glu Asp Glu Ala Glu Lys Ile
 450 455 460
 Ile Gly Ala Pro Glu Val Ser Ala Leu Gly Asn Lys Ala Gln Leu Asp

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<210> 333
<211> 1607
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (1)..(1584)
<223> FRXA00799
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<400> 333																
cta	caa	ttc	cgc	gat	ctc	gac	ggc	gac	ggc	gta	ctt	gca	cct	tat	gaa	48
Leu	Gln	Phe	Arg	Asp	Leu	Asp	Gly	Asp	Gly	Val	Leu	Ala	Pro	Tyr	Glu	
1				5		10				15						
gat	tgg	cgt	cta	acc	cca	gca	gag	cgt	gcc	gct	gac	ctg	gtg	aaa	cgt	96
Asp	Trp	Arg	Leu	Thr	Pro	Ala	Glu	Arg	Ala	Ala	Asp	Leu	Val	Lys	Arg	
			20		25				30							
atg	aat	gtg	gaa	gaa	aaa	gcg	ggc	ctg	atg	atc	atc	ggt	tcg	cac	tac	144
Met	Asn	Val	Glu	Glu	Lys	Ala	Gly	Leu	Met	Ile	Ile	Gly	Ser	His	Tyr	
			35		40				45							
ccc	gga	tac	tcg	cct	ttg	gcg	ccg	gag	agt	gaa	ggc	aaa	gac	gcg	gaa	192
Pro	Gly	Tyr	Ser	Pro	Leu	Ala	Pro	Glu	Ser	Glu	Gly	Lys	Asp	Ala	Glu	
50		55				60										
aag	tgc	gag	cct	ttg	ctg	aac	cct	gtc	gat	atg	tgg	cgt	gag	gat	aac	240
Lys	Cys	Glu	Pro	Leu	Leu	Asn	Pro	Val	Asp	Met	Trp	Arg	Glu	Asp	Asn	
65		70				75				80						
ccg	atc	acg	ggt	gtt	cct	ttc	acc	gag	cct	gtg	ctg	gca	act	tct	tcc	288
Pro	Ile	Thr	Gly	Val	Pro	Phe	Thr	Glu	Pro	Val	Leu	Ala	Thr	Ser	Ser	
				85		90				95						
act	gaa	aat	gcc	att	aac	ctg	cgc	aat	cag	cgt	tac	tta	att	gtt	cgt	336
Thr	Glu	Asn	Ala	Ile	Asn	Leu	Arg	Asn	Gln	Arg	Tyr	Leu	Ile	Val	Arg	
			100		105				110							
gac	aac	ctg	cca	gct	cgt	ggg	ctt	gct	act	tgg	acc	aat	gct	gtt	cag	384
Asp	Asn	Leu	Pro	Ala	Arg	Gly	Leu	Ala	Thr	Trp	Thr	Asn	Ala	Val	Gln	
115		120				125										

gaa gtc gcg gag cga tcc cgt ttg ggt att cct gtt gcg ttt gcg tcg Glu Val Ala Glu Arg Ser Arg Leu Gly Ile Pro Val Ala Phe Ala Ser 130 135 140	432
aat cct cgt aac cac gtc gcg ctc gtt gcg cag ttc ggt gtg aac gag Asn Pro Arg Asn His Val Ala Leu Val Ala Gln Phe Gly Val Asn Glu 145 150 155 160	480
tcc gcg ggt gtg ttc tct gag tgg cct ggc gag ctg ggt ctt gct gcg Ser Ala Gly Val Phe Ser Glu Trp Pro Gly Glu Leu Gly Leu Ala Ala 165 170 175	528
ctt cgc gat gct gaa ctg atg gag act ttc ggt acc gag gct gct aaa Leu Arg Asp Ala Glu Leu Met Glu Thr Phe Gly Thr Glu Ala Ala Lys 180 185 190	576
gaa tgg cgt gcc ggt ggt gtg cac aag ctg tac ggt tac atg gct gac Glu Trp Arg Ala Gly Gly Val His Lys Leu Tyr Gly Tyr Met Ala Asp 195 200 205	624
ctc gct tct gag cct cgt tgg tcc cgc ttc aac ggt act ttt ggt gag Leu Ala Ser Glu Pro Arg Trp Ser Arg Phe Asn Gly Thr Phe Gly Glu 210 215 220	672
gat ccg gag ttg atc tct gat tac atc gct gct gtt gtg cgt ggt ttg Asp Pro Glu Leu Ile Ser Asp Tyr Ile Ala Ala Val Val Arg Gly Leu 225 230 235 240	720
cag ggc cct gag ctg tcc aag aat tcc gtg tcg acc acc att aag cac Gln Gly Pro Glu Leu Ser Lys Asn Ser Val Ser Thr Thr Ile Lys His 245 250 255	768
ttc cca ggt ggc ggc gtg cgc ctc gac ggc cac gat cct cac ttc cac Phe Pro Gly Gly Gly Val Arg Leu Asp Gly His Asp Pro His Phe His 260 265 270	816
tgg ggt cag acc aat gag tac cca acc gaa gat gcg ctg ggc aag tac Trp Gly Gln Thr Asn Glu Tyr Pro Thr Glu Asp Ala Leu Gly Lys Tyr 275 280 285	864
cat ctg cct cct ttc cag gca gct atc gac gct ggc tgc gcc tcg atc His Leu Pro Pro Phe Gln Ala Ala Ile Asp Ala Gly Cys Ala Ser Ile 290 295 300	912
atg cct tac tac gca cgg cca atg aac aac tcc gcc aac cag ctc gat Met Pro Tyr Tyr Ala Arg Pro Met Asn Asn Ser Ala Asn Gln Leu Asp 305 310 315 320	960
cag cag ctg tgg caa aac ccg acc acg cag ttc gaa gag gtt gcg ttt Gln Gln Leu Trp Gln Asn Pro Thr Thr Gln Phe Glu Glu Val Ala Phe 325 330 335	1008
gcc tac aac cgc acc ttc att cag gat ttg ctt cgc gac gcc atg ggc Ala Tyr Asn Arg Thr Phe Ile Gln Asp Leu Leu Arg Asp Ala Met Gly 340 345 350	1056
cac cgt ggg tac gtc aac tcc gac tcc ggc gtc atc gac gcc atg atg His Arg Gly Tyr Val Asn Ser Asp Ser Gly Val Ile Asp Ala Met Met 355 360 365	1104
tgg ggc gtg gag gaa ctc agc gag cca gaa cgc ttc gcc gca gca gtg	1152

Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val		
370						375					380						
cgt	gca	ggc	acc	gac	att	ttc	tcc	gac	atg	gct	aac	cca	cgt	cga	ctg	1200	
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu		
385					390					395					400		
ctc	gaa	gca	ggt	gct	gag	gga	cac	ctt	gat	gag	tca	gag	ctg	aat	cag	1248	
Leu	Glu	Ala	Val	Ala	Glu	Gly	His	Leu	Asp	Glu	Ser	Glu	Leu	Asn	Gln		
				405					410					415			
cca	gtc	cag	cga	ctc	ctg	gag	gaa	atc	ttc	cag	ctt	ggt	ctg	ttt	gag	1296	
Pro	Val	Gln	Arg	Leu	Leu	Glu	Glu	Ile	Phe	Gln	Leu	Gly	Leu	Phe	Glu		
			420					425					430				
aac	cca	tat	gtc	tct	gaa	gat	gaa	gca	gaa	aag	atc	att	ggt	gcg	cca	1344	
Asn	Pro	Tyr	Val	Ser	Glu	Asp	Glu	Ala	Glu	Lys	Ile	Ile	Gly	Ala	Pro		
		435					440					445					
gag	gtt	tct	gca	ttg	ggc	aac	aaa	gca	cag	ctt	gat	tcc	gtc	acc	ttg	1392	
Glu	Val	Ser	Ala	Leu	Gly	Asn	Lys	Ala	Gln	Leu	Asp	Ser	Val	Thr	Leu		
	450					455					460						
ctg	cgt	aac	aac	ccc	atc	cgt	gct	gcc	act	gga	tcc	tgc	agc	aag	cct	1440	
Leu	Arg	Asn	Asn	Pro	Ile	Arg	Ala	Ala	Thr	Gly	Ser	Cys	Ser	Lys	Pro		
465					470					475					480		
gaa	gat	cta	ccc	att	ggt	tac	tgg	ccg	tac	caa	gat	cga	cga	ggt	tca	1488	
Glu	Asp	Leu	Pro	Ile	Gly	Tyr	Trp	Pro	Tyr	Gln	Asp	Arg	Arg	Gly	Ser		
				485					490					495			
act	aca	gct	gga	agc	agc	cat	tcg	cgc	aga	act	ccc	agg	ggt	aac	ctt	1536	
Thr	Thr	Ala	Gly	Ser	Ser	His	Ser	Arg	Arg	Thr	Pro	Arg	Gly	Asn	Leu		
			500					505					510				
ggt	gtc	ttc	cga	gtc	aga	agc	aga	tct	tgc	aat	cgt	gtg	ggc	tgc	ccc	1584	
Gly	Val	Phe	Arg	Val	Arg	Ser	Arg	Ser	Cys	Asn	Arg	Val	Gly	Ser	Pro		
		515					520					525					
tgaaaattgca	ctgtttgaag	atg														1607	

<210> 334

<211> 528

<212> PRT

<213> Corynebacterium glutamicum

<400> 334

Leu	Gln	Phe	Arg	Asp	Leu	Asp	Gly	Asp	Gly	Val	Leu	Ala	Pro	Tyr	Glu		
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Asp	Trp	Arg	Leu	Thr	Pro	Ala	Glu	Arg	Ala	Ala	Asp	Leu	Val	Lys	Arg		
			20					25					30				
Met	Asn	Val	Glu	Glu	Lys	Ala	Gly	Leu	Met	Ile	Ile	Gly	Ser	His	Tyr		
		35					40					45					
Pro	Gly	Tyr	Ser	Pro	Leu	Ala	Pro	Glu	Ser	Glu	Gly	Lys	Asp	Ala	Glu		
	50					55					60						
Lys	Cys	Glu	Pro	Leu	Leu	Asn	Pro	Val	Asp	Met	Trp	Arg	Glu	Asp	Asn		

65		70		75		80									
Pro	Ile	Thr	Gly	Val	Pro	Phe	Thr	Glu	Pro	Val	Leu	Ala	Thr	Ser	Ser
			85						90					95	
Thr	Glu	Asn	Ala	Ile	Asn	Leu	Arg	Asn	Gln	Arg	Tyr	Leu	Ile	Val	Arg
			100					105					110		
Asp	Asn	Leu	Pro	Ala	Arg	Gly	Leu	Ala	Thr	Trp	Thr	Asn	Ala	Val	Gln
		115					120					125			
Glu	Val	Ala	Glu	Arg	Ser	Arg	Leu	Gly	Ile	Pro	Val	Ala	Phe	Ala	Ser
	130					135					140				
Asn	Pro	Arg	Asn	His	Val	Ala	Leu	Val	Ala	Gln	Phe	Gly	Val	Asn	Glu
145					150					155					160
Ser	Ala	Gly	Val	Phe	Ser	Glu	Trp	Pro	Gly	Glu	Leu	Gly	Leu	Ala	Ala
				165					170					175	
Leu	Arg	Asp	Ala	Glu	Leu	Met	Glu	Thr	Phe	Gly	Thr	Glu	Ala	Ala	Lys
			180					185					190		
Glu	Trp	Arg	Ala	Gly	Gly	Val	His	Lys	Leu	Tyr	Gly	Tyr	Met	Ala	Asp
		195					200					205			
Leu	Ala	Ser	Glu	Pro	Arg	Trp	Ser	Arg	Phe	Asn	Gly	Thr	Phe	Gly	Glu
	210					215					220				
Asp	Pro	Glu	Leu	Ile	Ser	Asp	Tyr	Ile	Ala	Ala	Val	Val	Arg	Gly	Leu
225					230					235					240
Gln	Gly	Pro	Glu	Leu	Ser	Lys	Asn	Ser	Val	Ser	Thr	Thr	Ile	Lys	His
				245					250					255	
Phe	Pro	Gly	Gly	Gly	Val	Arg	Leu	Asp	Gly	His	Asp	Pro	His	Phe	His
			260					265					270		
Trp	Gly	Gln	Thr	Asn	Glu	Tyr	Pro	Thr	Glu	Asp	Ala	Leu	Gly	Lys	Tyr
		275					280					285			
His	Leu	Pro	Pro	Phe	Gln	Ala	Ala	Ile	Asp	Ala	Gly	Cys	Ala	Ser	Ile
	290				295						300				
Met	Pro	Tyr	Tyr	Ala	Arg	Pro	Met	Asn	Asn	Ser	Ala	Asn	Gln	Leu	Asp
305					310					315					320
Gln	Gln	Leu	Trp	Gln	Asn	Pro	Thr	Thr	Gln	Phe	Glu	Glu	Val	Ala	Phe
				325					330					335	
Ala	Tyr	Asn	Arg	Thr	Phe	Ile	Gln	Asp	Leu	Leu	Arg	Asp	Ala	Met	Gly
			340					345					350		
His	Arg	Gly	Tyr	Val	Asn	Ser	Asp	Ser	Gly	Val	Ile	Asp	Ala	Met	Met
		355					360					365			
Trp	Gly	Val	Glu	Glu	Leu	Ser	Glu	Pro	Glu	Arg	Phe	Ala	Ala	Ala	Val
	370					375					380				
Arg	Ala	Gly	Thr	Asp	Ile	Phe	Ser	Asp	Met	Ala	Asn	Pro	Arg	Arg	Leu
385					390					395					400

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<210> 335
<211> 1632
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1609)
<223> RXA00032
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<400> 335
cacttgctga agacgccac atcgaagacc ttgcagatgt aaacgcaaac gcctaactgt 60

ttttcgagct aaacccatcc ttgaaaggat cttttccacc atg aac acc cca ctc 115
Met Asn Thr Pro Leu
1 5

cag ctc aac act gaa aac ctg cag gaa atc gct tcg act tcc gga gtg 163
Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala Ser Thr Ser Gly Val
10 15 20

cag atc cca gcg ttc aac cgc gct gac gtc gcc ccg ggc att gtc cac 211
Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala Pro Gly Ile Val His
25 30 35

ttc ggt gtt ggc gga ttc cat cgc gct cac caa gcg atg tac ctc aat 259
Phe Gly Val Gly Gly Phe His Arg Ala His Gln Ala Met Tyr Leu Asn
40 45 50

gaa ttg atg aat gag ggc aag gcc ttg gat tgg ggc atc atc ggc atg 307
Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp Gly Ile Ile Gly Met
55 60 65

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ggt gtc atg cct tcc gat gtg cgc atg cgc gat gcc ctg gcc agc caa	355
Gly Val Met Pro Ser Asp Val Arg Met Arg Asp Ala Leu Ala Ser Gln	
70 75 80 85	
gat cac ctt tat acc ctg acc act aaa gct cct gat gga act ctt gat	403
Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro Asp Gly Thr Leu Asp	
90 95 100	
caa aaa atc atc gga tcc atc att gac tac gtg ttc gct ccc gag gac	451
Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val Phe Ala Pro Glu Asp	
105 110 115	
cca gca cgg gcc gtt gca acc ctc gcg cag gac tcc atc cgc att gtt	499
Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp Ser Ile Arg Ile Val	
120 125 130	
tcc ctc acg gtg act gaa ggc gga tac aac atc gat ccg gcg aca gaa	547
Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile Asp Pro Ala Thr Glu	
135 140 145	
gat ttc gac cac acc aac cct cga atc gtt gct gac cgc gaa gcc ctg	595
Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala Asp Arg Glu Ala Leu	
150 155 160 165	
cag gcg ggc gat act tcc act ttg cag acc ttc ttt ggg ttg atc act	643
Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe Phe Gly Leu Ile Thr	
170 175 180	
gcc gca ttg att tcc cga aaa gaa tca gga tct acg cca ttt acc atc	691
Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser Thr Pro Phe Thr Ile	
185 190 195	
atg agc tgc gat aac atc caa ggc aac ggc gat ctg gct aag cgt ttc	739
Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp Leu Ala Lys Arg Phe	
200 205 210	
ttc ctc gcc ttc gca cat tcc gtg tct tct gag ctc ggc gaa tgg gtg	787
Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu Leu Gly Glu Trp Val	
215 220 225	
gaa aac aac gtg gcc ttc ccc aac tcc atg gtg gac cgc atc acc cct	835
Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val Asp Arg Ile Thr Pro	
230 235 240 245	
gaa acc acc gac ggc gac cgc gat gac atc aag gaa atc ggc tac atc	883
Glu Thr Thr Asp Gly Asp Arg Asp Ile Lys Glu Ile Gly Tyr Ile	
250 255 260	
gat gcg tgg cca gtg gtt tct gaa gat ttc acc caa tgg gtc ctc gag	931
Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr Gln Trp Val Leu Glu	
265 270 275	
gat gcc ttc acc cag ggc cgc ccc gcg tac gag gag gtt ggc gtg cag	979
Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu Glu Val Gly Val Gln	
280 285 290	
gtc gtc tcc gac gtg gag cct tat gaa tta atg aag ctg cgc ctg ctc	1027
Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met Lys Leu Arg Leu Leu	
295 300 305	

aac gcc tcc cac cag gga ctt tgc tac ttc ggc cac ttg gct ggc cac 1075
 Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly His Leu Ala Gly His
 310 315 320 325

 cac atg gtc cac gac gtc atg gcg gat acc cgc ttc cag gat ttc ctc 1123
 His Met Val His Asp Val Met Ala Asp Thr Arg Phe Gln Asp Phe Leu
 330 335 340

 ctg gct tac atg gag cgc gaa gcc acc cct acc ctc aag gaa ctt cca 1171
 Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr Leu Lys Glu Leu Pro
 345 350 355

 ggt gtc gat cta gat gct tat cga cgc caa ctc atc gcg cga ttc ggc 1219
 Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu Ile Ala Arg Phe Gly
 360 365 370

 aac gcc gca gtc aaa gac acc gta ccg cgc ctg tgt gcg gaa tcc tcc 1267
 Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu Cys Ala Glu Ser Ser
 375 380 385

 gac cgc att cca aag tgg ctg ttg cca gtc gta cgc gaa aac ctc gca 1315
 Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val Arg Glu Asn Leu Ala
 390 395 400 405

 gca ggc cgc gac gtc aca ctt tct gca gcc atc gtc gca tcc tgg gcg 1363
 Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile Val Ala Ser Trp Ala
 410 415 420

 cgc tac gca gaa ggc acc gac gag cag ggc aac cca ata aag att gtt 1411
 Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn Pro Ile Lys Ile Val
 425 430 435

 gac cgt ttg agt gag cgc gtc caa gaa aac gca tca gga aat cgc acc 1459
 Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala Ser Gly Asn Arg Thr
 440 445 450

 gat att ttg tca ttc atc cgc gac cgt gga atc ttc gga gac ttg gtc 1507
 Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile Phe Gly Asp Leu Val
 455 460 465

 gat gct gaa cca ttc acc aag gca tac tcc gag aca ctg tcc tcc ctt 1555
 Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu Thr Leu Ser Ser Leu
 470 475 480 485

 cat gac cgt ggc gcg gaa gca acc atc gat gca ctt ctt acg cag gta 1603
 His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala Leu Leu Thr Gln Val
 490 495 500

 act gtc taaatccggt gcgcgctagg gtt 1632
 Thr Val

<210> 336

<211> 503

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 336

Met Asn Thr Pro Leu Gln Leu Asn Thr Glu Asn Leu Gln Glu Ile Ala
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Ser Thr Ser Gly Val Gln Ile Pro Ala Phe Asn Arg Ala Asp Val Ala
 20 25 30
 Pro Gly Ile Val His Phe Gly Val Gly Gly Phe His Arg Ala His Gln
 35 40 45
 Ala Met Tyr Leu Asn Glu Leu Met Asn Glu Gly Lys Ala Leu Asp Trp
 50 55 60
 Gly Ile Ile Gly Met Gly Val Met Pro Ser Asp Val Arg Met Arg Asp
 65 70 75 80
 Ala Leu Ala Ser Gln Asp His Leu Tyr Thr Leu Thr Thr Lys Ala Pro
 85 90 95
 Asp Gly Thr Leu Asp Gln Lys Ile Ile Gly Ser Ile Ile Asp Tyr Val
 100 105 110
 Phe Ala Pro Glu Asp Pro Ala Arg Ala Val Ala Thr Leu Ala Gln Asp
 115 120 125
 Ser Ile Arg Ile Val Ser Leu Thr Val Thr Glu Gly Gly Tyr Asn Ile
 130 135 140
 Asp Pro Ala Thr Glu Asp Phe Asp His Thr Asn Pro Arg Ile Val Ala
 145 150 155 160
 Asp Arg Glu Ala Leu Gln Ala Gly Asp Thr Ser Thr Leu Gln Thr Phe
 165 170 175
 Phe Gly Leu Ile Thr Ala Ala Leu Ile Ser Arg Lys Glu Ser Gly Ser
 180 185 190
 Thr Pro Phe Thr Ile Met Ser Cys Asp Asn Ile Gln Gly Asn Gly Asp
 195 200 205
 Leu Ala Lys Arg Phe Phe Leu Ala Phe Ala His Ser Val Ser Ser Glu
 210 215 220
 Leu Gly Glu Trp Val Glu Asn Asn Val Ala Phe Pro Asn Ser Met Val
 225 230 235 240
 Asp Arg Ile Thr Pro Glu Thr Thr Asp Gly Asp Arg Asp Asp Ile Lys
 245 250 255
 Glu Ile Gly Tyr Ile Asp Ala Trp Pro Val Val Ser Glu Asp Phe Thr
 260 265 270
 Gln Trp Val Leu Glu Asp Ala Phe Thr Gln Gly Arg Pro Ala Tyr Glu
 275 280 285
 Glu Val Gly Val Gln Val Val Ser Asp Val Glu Pro Tyr Glu Leu Met
 290 295 300
 Lys Leu Arg Leu Leu Asn Ala Ser His Gln Gly Leu Cys Tyr Phe Gly
 305 310 315 320
 His Leu Ala Gly His His Met Val His Asp Val Met Ala Asp Thr Arg
 325 330 335

Phe Gln Asp Phe Leu Leu Ala Tyr Met Glu Arg Glu Ala Thr Pro Thr
 340 345 350
 Leu Lys Glu Leu Pro Gly Val Asp Leu Asp Ala Tyr Arg Arg Gln Leu
 355 360 365
 Ile Ala Arg Phe Gly Asn Ala Ala Val Lys Asp Thr Val Pro Arg Leu
 370 375 380
 Cys Ala Glu Ser Ser Asp Arg Ile Pro Lys Trp Leu Leu Pro Val Val
 385 390 395 400
 Arg Glu Asn Leu Ala Ala Gly Arg Asp Val Thr Leu Ser Ala Ala Ile
 405 410 415
 Val Ala Ser Trp Ala Arg Tyr Ala Glu Gly Thr Asp Glu Gln Gly Asn
 420 425 430
 Pro Ile Lys Ile Val Asp Arg Leu Ser Glu Arg Val Gln Glu Asn Ala
 435 440 445
 Ser Gly Asn Arg Thr Asp Ile Leu Ser Phe Ile Arg Asp Arg Gly Ile
 450 455 460
 Phe Gly Asp Leu Val Asp Ala Glu Pro Phe Thr Lys Ala Tyr Ser Glu
 465 470 475 480
 Thr Leu Ser Ser Leu His Asp Arg Gly Ala Glu Ala Thr Ile Asp Ala
 485 490 495
 Leu Leu Thr Gln Val Thr Val
 500

<210> 337
 <211> 1098
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1075)
 <223> RXA02528

<400> 337
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 Met Ser Ala Lys Ser
 1 5
 agc ctc aag gaa gtt gct gag tta gct gga gtc ggt tat gcc aca gcc 163
 Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val Gly Tyr Ala Thr Ala
 10 15 20
 tcg agg gca cta tct ggc aag ggg tat gtg tcc ccg cag acg cgg gag 211
 Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser Pro Gln Thr Arg Glu
 25 30 35
 aaa gtt cag gcg gcg gct aaa gag ctg aac tat gta cca aat cag ctg 259
 Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr Val Pro Asn Gln Leu

40	45	50	
gcc aag gcg ttg cgg gaa cat cgc agt gcc ttg gtg ggg gtc att gtt Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu Val Gly Val Ile Val 55 60 65			307
ccg gat ttg tcc aat gag tat tat tcg gaa tcg ctg cag act att cag Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser Leu Gln Thr Ile Gln 70 75 80 85			355
cag gat ctg aaa gct gct ggc tat caa atg ctg gtt gcg gag gcc aac Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu Val Ala Glu Ala Asn 90 95 100			403
agt gtg cag gcg cag gac gtg gtg atg gaa tcg ttg atc tcg att caa Ser Val Gln Ala Gln Asp Val Val Met Glu Ser Leu Ile Ser Ile Gln 105 110 115			451
gct gca gga att atc cac gtt cca gtg gtc ggc tca att gct cct gaa Ala Ala Gly Ile Ile His Val Pro Val Val Gly Ser Ile Ala Pro Glu 120 125 130			499
gga atc ccc atg gtg cag ttg act cgt ggt gaa ttg ggt cct ggt ttc Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu Leu Gly Pro Gly Phe 135 140 145			547
cct cgg gtg ttg tgt gat gat gag gct ggg ttt ttt cag ctg acc gag Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe Phe Gln Leu Thr Glu 150 155 160 165			595
tcg gtg ctg ggc ggc agc gga atg aac att gct gct ttg gtt ggt gaa Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala Ala Leu Val Gly Glu 170 175 180			643
gaa tca ctt tcc acc acg cag gaa cga atg cgc ggt att agt cat gcg Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg Gly Ile Ser His Ala 185 190 195			691
gcg tcg ata tat ggg gct gag gtg acg ttc cat ttt ggc cac tat tct Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His Phe Gly His Tyr Ser 200 205 210			739
gtc gaa tct ggc gaa gag atg gct cag gtg gtg ttt aac aac ggc ctt Val Glu Ser Gly Glu Glu Met Ala Gln Val Val Phe Asn Asn Gly Leu 215 220 225			787
ccc gat gca ttg att gtg gcg tct cct cgg ctg atg gct ggg gtg atg Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu Met Ala Gly Val Met 230 235 240 245			835
cgt gct ttt act cgc ctg aat gtc cgc gtt ccc cac gat gtg gtg att Arg Ala Phe Thr Arg Leu Asn Val Arg Val Pro His Asp Val Val Ile 250 255 260			883
ggg ggt tat gac gat cct gag tgg tac agc ttt gtc ggc gcg ggg att Gly Gly Tyr Asp Asp Pro Glu Trp Tyr Ser Phe Val Gly Ala Gly Ile 265 270 275			931
acc acg ttt gtt cca ccg cat gag gag atg ggg aaa gag gcc gtg cgc Thr Thr Phe Val Pro Pro His Glu Glu Met Gly Lys Glu Ala Val Arg 280 285 290			979

ttg ttg gta gat ctg att gaa aat ccc gaa ctt ccc acc ggc gat gtg 1027
 Leu Leu Val Asp Leu Ile Glu Asn Pro Glu Leu Pro Thr Gly Asp Val
 295 300 305

gtt ttg cag ggg cag gtg atc ctt cgg ggg tcg agc aca cat tcc ggg 1075
 Val Leu Gln Gly Gln Val Ile Leu Arg Gly Ser Ser Thr His Ser Gly
 310 315 320 325

tagaattgcc caaatgtcat caa 1098

<210> 338

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 338

Met Ser Ala Lys Ser Ser Leu Lys Glu Val Ala Glu Leu Ala Gly Val
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Gly Tyr Ala Thr Ala Ser Arg Ala Leu Ser Gly Lys Gly Tyr Val Ser
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Pro Gln Thr Arg Glu Lys Val Gln Ala Ala Ala Lys Glu Leu Asn Tyr
 35 40 45

Val Pro Asn Gln Leu Ala Lys Ala Leu Arg Glu His Arg Ser Ala Leu
 50 55 60

Val Gly Val Ile Val Pro Asp Leu Ser Asn Glu Tyr Tyr Ser Glu Ser
 65 70 75 80

Leu Gln Thr Ile Gln Gln Asp Leu Lys Ala Ala Gly Tyr Gln Met Leu
 85 90 95

Val Ala Glu Ala Asn Ser Val Gln Ala Gln Asp Val Val Met Glu Ser
 100 105 110

Leu Ile Ser Ile Gln Ala Ala Gly Ile Ile His Val Pro Val Val Gly
 115 120 125

Ser Ile Ala Pro Glu Gly Ile Pro Met Val Gln Leu Thr Arg Gly Glu
 130 135 140

Leu Gly Pro Gly Phe Pro Arg Val Leu Cys Asp Asp Glu Ala Gly Phe
 145 150 155 160

Phe Gln Leu Thr Glu Ser Val Leu Gly Gly Ser Gly Met Asn Ile Ala
 165 170 175

Ala Leu Val Gly Glu Glu Ser Leu Ser Thr Thr Gln Glu Arg Met Arg
 180 185 190

Gly Ile Ser His Ala Ala Ser Ile Tyr Gly Ala Glu Val Thr Phe His
 195 200 205

Phe Gly His Tyr Ser Val Glu Ser Gly Glu Glu Met Ala Gln Val Val
 210 215 220

Phe Asn Asn Gly Leu Pro Asp Ala Leu Ile Val Ala Ser Pro Arg Leu

<400> 339																
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gcttctggcc cgcggtctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg																115
Met Gly Gln Cys Thr																5
1																
gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga																163
Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg																20
10 15																
gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc																211
Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile																35
25 30																
cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt																259
His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val																50
40 45																
ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa																307
Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp Asn Ile Glu Val Glu																65
55 60																
gac agc gcc gtt gcc act gtg cgt ttt gaa tgc ggc gcg ttg gcc aca																355
Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser Gly Ala Leu Ala Thr																85
70 75 80																
att tca gcc acc acc gcc gca gag cca gca ctc ggc gca caa gtg cag																403
Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu Gly Ala Gln Val Gln																100
90 95 100																

gtg atg gga aca aag ggt gcc acc atg acg atc ctg gaa ttc cct gaa	451
Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile Leu Glu Phe Pro Glu	
105 110 115	
ggt acc gac ggc agg ctc att gtt cgc agt gaa aac gac acc cgt cga	499
Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu Asn Asp Thr Arg Arg	
120 125 130	
aac cac ccc att cca ccc cgc gga tct tta tcc caa tgc cga tct ttc	547
Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser Gln Cys Arg Ser Phe	
135 140 145	
cat cat caa cgg tgc ttt gat ccc gta tca cac cgc cca gat cgc aga	595
His His Gln Arg Cys Phe Asp Pro Val Ser His Arg Pro Asp Arg Arg	
150 155 160 165	
ctt tat cga tgc gct caa cga agg ccg ccc acc act gat cac cgg ccg	643
Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr Thr Asp His Arg Pro	
170 175 180	
cga tgc cac cag agc tct gaa agt tct cct tgg tgt cta cga atc agc	691
Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp Cys Leu Arg Ile Ser	
185 190 195	
agc cac cca cca gcc ggt ctc ttt gat cta acg gaa gct ttt aaa acg	739
Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr Glu Ala Phe Lys Thr	
200 205 210	
tca cgc caa atc ggt ctt gca cct tta tcc tcc ctg tcc aca cca cct	787
Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser Leu Ser Thr Pro Pro	
215 220 225	
gat caa cta gtg cgc ctc gca gct gcc act ggt ttc tcc ttt gtc ggt	835
Asp Gln Leu Val Arg Leu Ala Ala Thr Gly Phe Ser Phe Val Gly	
230 235 240 245	
ctg cgc gtc atc gca gta acc ccc aac gaa cgt gta tat gac ctt tcc	883
Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg Val Tyr Asp Leu Ser	
250 255 260	
cca gga tcc cca ctg ctg gct gca acc caa caa gcg ttg aaa gaa acc	931
Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln Ala Leu Lys Glu Thr	
265 270 275	
gcc ctg tat gtg ctc gac act gaa ttc cta cag gta aac gca gac acc	979
Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln Val Asn Ala Asp Thr	
280 285 290	
acc cgc gag gcc tgg ctt ccc gca cta gaa gcc gcc gga gca ctg gga	1027
Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala Ala Gly Ala Leu Gly	
295 300 305	
gct aaa acc ttc acc atc gcc gcc ggt gat gac aac att gcg ccc ctg	1075
Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp Asn Ile Ala Pro Leu	
310 315 320 325	
acc gac acg atc ggt gcc atg gtt gac gat gcc cgt gat ttc gga gtc	1123
Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala Arg Asp Phe Gly Val	
330 335 340	

acc cca gcc cta gag cca atc tct tac cgc agc gtg cat tcc att ccg 1171
 Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser Val His Ser Ile Pro
 345 350 355

cag gca gca gca atc gcc aga gac tcc ggc gga aaa gtc gtg gcg gac 1219
 Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly Lys Val Val Ala Asp
 360 365 370

acc ttg cac atg gcc agg ttc gga gcc 1246
 Thr Leu His Met Ala Arg Phe Gly Ala
 375 380

<210> 340

<211> 382

<212> PRT

<213> Corynebacterium glutamicum

<400> 340

Met Gly Gln Cys Thr Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr
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Ala Thr Pro Trp Arg Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu
 20 25 30

Met Thr Gln Ala Ile His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly
 35 40 45

Glu Pro Val Glu Val Phe Gly Tyr Thr Asn Ser Phe Lys His Gly Asp
 50 55 60

Asn Ile Glu Val Glu Asp Ser Ala Val Ala Thr Val Arg Phe Glu Ser
 65 70 75 80

Gly Ala Leu Ala Thr Ile Ser Ala Thr Thr Ala Ala Glu Pro Ala Leu
 85 90 95

Gly Ala Gln Val Gln Val Met Gly Thr Lys Gly Ala Thr Met Thr Ile
 100 105 110

Leu Glu Phe Pro Glu Gly Thr Asp Gly Arg Leu Ile Val Arg Ser Glu
 115 120 125

Asn Asp Thr Arg Arg Asn His Pro Ile Pro Pro Arg Gly Ser Leu Ser
 130 135 140

Gln Cys Arg Ser Phe His His Gln Arg Cys Phe Asp Pro Val Ser His
 145 150 155 160

Arg Pro Asp Arg Arg Leu Tyr Arg Cys Ala Gln Arg Arg Pro Pro Thr
 165 170 175

Thr Asp His Arg Pro Arg Cys His Gln Ser Ser Glu Ser Ser Pro Trp
 180 185 190

Cys Leu Arg Ile Ser Ser His Pro Pro Ala Gly Leu Phe Asp Leu Thr
 195 200 205

Glu Ala Phe Lys Thr Ser Arg Gln Ile Gly Leu Ala Pro Leu Ser Ser
 210 215 220

Leu Ser Thr Pro Pro Asp Gln Leu Val Arg Leu Ala Ala Ala Thr Gly
 225 230 235 240
 Phe Ser Phe Val Gly Leu Arg Val Ile Ala Val Thr Pro Asn Glu Arg
 245 250 255
 Val Tyr Asp Leu Ser Pro Gly Ser Pro Leu Leu Ala Ala Thr Gln Gln
 260 265 270
 Ala Leu Lys Glu Thr Ala Leu Tyr Val Leu Asp Thr Glu Phe Leu Gln
 275 280 285
 Val Asn Ala Asp Thr Thr Arg Glu Ala Trp Leu Pro Ala Leu Glu Ala
 290 295 300
 Ala Gly Ala Leu Gly Ala Lys Thr Phe Thr Ile Ala Ala Gly Asp Asp
 305 310 315 320
 Asn Ile Ala Pro Leu Thr Asp Thr Ile Gly Ala Met Val Asp Asp Ala
 325 330 335
 Arg Asp Phe Gly Val Thr Pro Ala Leu Glu Pro Ile Ser Tyr Arg Ser
 340 345 350
 Val His Ser Ile Pro Gln Ala Ala Ala Ile Ala Arg Asp Ser Gly Gly
 355 360 365
 Lys Val Val Ala Asp Thr Leu His Met Ala Arg Phe Gly Ala
 370 375 380

<210> 341

<211> 412

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(412)

<223> FRXA00309

<400> 341

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gcttctggcc cgcggctcaa aaaatgaaaa aggagccgctc atg ggc caa tgc acg 115
 Met Gly Gln Cys Thr
 1 5

gta gcg ctt tac cga gag cat tcc tat tac aca gca acc cca tgg cga 163
 Val Ala Leu Tyr Arg Glu His Ser Tyr Tyr Thr Ala Thr Pro Trp Arg
 10 15 20

gga acc tgg gca gcc gat ggc ggt gga gtg ctc atg act caa gcc atc 211
 Gly Thr Trp Ala Ala Asp Gly Gly Gly Val Leu Met Thr Gln Ala Ile
 25 30 35

cac tac atc gat ctt ttg tac tgg ctg ttg ggc gaa ccc gtg gaa gtt 259
 His Tyr Ile Asp Leu Leu Tyr Trp Leu Leu Gly Glu Pro Val Glu Val
 40 45 50

ttc ggc tac acc aac tcc ttc aaa cac ggc gac aac atc gaa gtc gaa 307

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<210> 342
<211> 104
<212> PRT
<213> Corvnebacterium glutamicum
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<210> 343  
<211> 558  
<212> DNA  
<213> Corynebacterium glutamicum
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<400> 343
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aaaccgcctt caccaagctt gaagatctag ggaagaaata atg tct gac aag atc 115
                                     Met Ser Asp Lys Ile
                                     1           5

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tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20

gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35

gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50

ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65

gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85

gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100

gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115

gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499
 Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc 558

<210> 344

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 344

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
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Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu

	85		90		95										
Lys	Pro	Ile	Ala	Ile	Glu	Leu	Asp	Ser	Ala	Gln	Arg	Met	Ile	Asp	Ala
			100					105						110	
Cys	Glu	Ser	Ala	Gly	Val	Gln	Leu	Gly	Val	Leu	Phe	Gln	Arg	Arg	Phe
		115					120					125			
Trp	Pro	Ala	Ala	Gln	Lys	Met	Lys	Lys	Glu	Pro	Ser	Trp	Ala	Asn	Ala
	130					135					140				
Arg															
145															

<210> 345
 <211> 558
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(535)
 <223> FRXA00310

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 Met Ser Asp Lys Ile
 1 5
 tgg aaa gtc ggc atc atc ggt tgc ggt gca atc agc cga aac cat atc 163
 Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile Ser Arg Asn His Ile
 10 15 20
 gaa gca gtt cag gca atc ccc ggc gca gaa gtc agc gca gtc tgt gat 211
 Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val Ser Ala Val Cys Asp
 25 30 35
 gtg gat ggt gcg aaa gca tcg gaa acc gca gcg aaa tat gga att tct 259
 Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala Lys Tyr Gly Ile Ser
 40 45 50
 ccc agt ttc acg tct gtc gat gag atc ctc gcc tcc ggg gtg gac att 307
 Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala Ser Gly Val Asp Ile
 55 60 65
 gtc gca gtc tgc acc cca cat cca acc cac gaa aca gtg gtc ctc gcc 355
 Val Ala Val Cys Thr Pro His Pro Thr His Glu Thr Val Val Leu Ala
 70 75 80 85
 gct gct gcc gcc gga gtg cac gtg ctt tgt gag aag cca atc gcc atc 403
 Ala Ala Ala Ala Gly Val His Val Leu Cys Glu Lys Pro Ile Ala Ile
 90 95 100
 gaa ctc gat tcc gca cag cgc atg atc gat gcc tgc gag tcc gca ggg 451
 Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala Cys Glu Ser Ala Gly
 105 110 115
 gtc caa ctt ggc gtg ctc ttc cag cgc cgc ttc tgg ccc gcg gct caa 499

Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe Trp Pro Ala Ala Gln
 120 125 130

aaa atg aaa aag gag ccg tca tgg gcc aat gca cgg tagcgcttta 545
 Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala Arg
 135 140 145

ccgagagcat tcc 558

<210> 346

<211> 145

<212> PRT

<213> Corynebacterium glutamicum

<400> 346

Met Ser Asp Lys Ile Trp Lys Val Gly Ile Ile Gly Cys Gly Ala Ile
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Ser Arg Asn His Ile Glu Ala Val Gln Ala Ile Pro Gly Ala Glu Val
 20 25 30

Ser Ala Val Cys Asp Val Asp Gly Ala Lys Ala Ser Glu Thr Ala Ala
 35 40 45

Lys Tyr Gly Ile Ser Pro Ser Phe Thr Ser Val Asp Glu Ile Leu Ala
 50 55 60

Ser Gly Val Asp Ile Val Ala Val Cys Thr Pro His Pro Thr His Glu
 65 70 75 80

Thr Val Val Leu Ala Ala Ala Ala Gly Val His Val Leu Cys Glu
 85 90 95

Lys Pro Ile Ala Ile Glu Leu Asp Ser Ala Gln Arg Met Ile Asp Ala
 100 105 110

Cys Glu Ser Ala Gly Val Gln Leu Gly Val Leu Phe Gln Arg Arg Phe
 115 120 125

Trp Pro Ala Ala Gln Lys Met Lys Lys Glu Pro Ser Trp Ala Asn Ala
 130 135 140

Arg

145

<210> 347

<211> 1342

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1342)

<223> RXA00041

<400> 347

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												Met	His	Thr	Glu	Leu	
												1				5	
tcc	agt	ttg	cgc	cct	gcg	tac	cat	gtg	act	cct	ccg	cag	ggc	agg	ctc		163
Ser	Ser	Leu	Arg	Pro	Ala	Tyr	His	Val	Thr	Pro	Pro	Gln	Gly	Arg	Leu		
				10					15					20			
aat	gat	ccc	aac	gga	atg	tac	gtc	gat	ggc	gat	acc	ctc	cac	gtc	tac		211
Asn	Asp	Pro	Asn	Gly	Met	Tyr	Val	Asp	Gly	Asp	Thr	Leu	His	Val	Tyr		
			25					30					35				
tac	cag	cac	gat	cca	ggc	ttc	ccc	ttc	gca	cca	aag	cgc	acc	ggc	tgg		259
Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro	Lys	Arg	Thr	Gly	Trp		
		40					45					50					
gct	cac	acc	acc	acg	ccg	ttg	acc	gga	ccg	cag	cga	ttg	cag	tgg	acg		307
Ala	His	Thr	Thr	Thr	Pro	Leu	Thr	Gly	Pro	Gln	Arg	Leu	Gln	Trp	Thr		
	55					60					65						
cac	ctg	ccc	gac	gct	ctt	tac	ccg	gat	gca	tcc	tat	gac	ctg	gat	gga		355
His	Leu	Pro	Asp	Ala	Leu	Tyr	Pro	Asp	Ala	Ser	Tyr	Asp	Leu	Asp	Gly		
	70				75					80					85		
tgc	tat	tcc	ggc	gga	gcc	gta	ttt	act	gac	ggc	aca	ctt	aaa	ctt	ttc		403
Cys	Tyr	Ser	Gly	Gly	Ala	Val	Phe	Thr	Asp	Gly	Thr	Leu	Lys	Leu	Phe		
			90						95					100			
tac	acc	ggc	aac	cta	aaa	att	gac	ggc	aag	cgc	cgc	gcc	acc	caa	aac		451
Tyr	Thr	Gly	Asn	Leu	Lys	Ile	Asp	Gly	Lys	Arg	Arg	Ala	Thr	Gln	Asn		
			105					110					115				
ctc	gtc	gaa	gtc	gag	gac	cca	act	ggg	ctg	atg	ggc	ggc	att	cat	cgc		499
Leu	Val	Glu	Val	Glu	Asp	Pro	Thr	Gly	Leu	Met	Gly	Gly	Ile	His	Arg		
		120					125					130					
cgt	tcg	cct	aaa	aat	ccg	ctt	atc	gac	gga	ccc	gcc	agc	ggc	ttc	aca		547
Arg	Ser	Pro	Lys	Asn	Pro	Leu	Ile	Asp	Gly	Pro	Ala	Ser	Gly	Phe	Thr		
	135					140					145						
ccc	cat	tac	cgc	gat	ccc	atg	atc	agc	cct	gat	ggc	gat	ggc	tgg	aaa		595
Pro	His	Tyr	Arg	Asp	Pro	Met	Ile	Ser	Pro	Asp	Gly	Asp	Gly	Trp	Lys		
					155					160					165		
atg	gtt	ctt	ggg	gcc	caa	cgc	gaa	aac	ctc	acc	ggc	gca	gcg	gtt	cta		643
Met	Val	Leu	Gly	Ala	Gln	Arg	Glu	Asn	Leu	Thr	Gly	Ala	Ala	Val	Leu		
			170						175					180			
tac	cgc	tcg	aca	gat	ctt	gaa	aac	tgg	gaa	ttc	tcc	ggc	gaa	atc	acc		691
Tyr	Arg	Ser	Thr	Asp	Leu	Glu	Asn	Trp	Glu	Phe	Ser	Gly	Glu	Ile	Thr		
			185					190					195				
ttt	gac	ctc	agt	gat	gca	caa	cct	ggc	tct	gct	cct	gat	ctc	gtt	ccc		739
Phe	Asp	Leu	Ser	Asp	Ala	Gln	Pro	Gly	Ser	Ala	Pro	Asp	Leu	Val	Pro		
		200					205					210					
ggc	ggc	tac	atg	tgg	gaa	tgc	ccc	aac	ctt	ttt	acg	ctt	cgc	gat	gaa		787
Gly	Gly	Tyr	Met	Trp	Glu	Cys	Pro	Asn	Leu	Phe	Thr	Leu	Arg	Asp	Glu		
	215					220					225						
gaa	act	ggc	gaa	gat	ctc	gac	gtg	ctg	att	ttc	tgt	cca	caa	gga	ttg		835
Glu	Thr	Gly	Glu	Asp	Leu	Asp	Val	Leu	Ile	Phe	Cys	Pro	Gln	Gly	Leu		

230	235	240	245	
gac cga atc cac gat gag gtt act cac tac gca agc tct gac cag tgc				883
Asp Arg Ile His Asp Glu Val Thr His Tyr Ala Ser Ser Asp Gln Cys	250	255	260	
gga tat gtc gtc ggc aag ctt gaa gga acg acc ttc cgc gtc ttg cga				931
Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr Phe Arg Val Leu Arg	265	270	275	
gga ttc agc gag ctg gat ttc ggc cat gaa ttc tac gca ccg cag gtt				979
Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe Tyr Ala Pro Gln Val	280	285	290	
gca gta aac ggt tct gat gcc tgg ctc gtg ggc tgg atg ggg ctg ccc				1027
Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly Trp Met Gly Leu Pro	295	300	305	
gcg cag gat gat cac cca aca gtt gca cgg gaa gga tgg gtg cac tgc				1075
Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu Gly Trp Val His Cys	310	315	320	325
ctg act gtg ccc cgc aag ctt cat ttg cgc aac cac gcg atc tat caa				1123
Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn His Ala Ile Tyr Gln	330	335	340	
gag ctt ctt ctc cca gag ggg gag tca ggg gta atc aga tct gta tta				1171
Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val Ile Arg Ser Val Leu	345	350	355	
ggt tct gaa cct gtc cga gta gac atc cga ggc aat att tcc ctc gag				1219
Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly Asn Ile Ser Leu Glu	360	365	370	
tgg gat ggt gtc cgt ttg tct gtg gat cgt ggt ggt gat cgt cgc gta				1267
Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly Gly Asp Arg Arg Val	375	380	385	
gct gag gta aaa cct ggc gaa tta gtg atc gcg gac gat aat aca gcc				1315
Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala Asp Asp Asn Thr Ala	390	395	400	405
att gag ata act gca ggt gat gga cag				1342
Ile Glu Ile Thr Ala Gly Asp Gly Gln	410			

<210> 348

<211> 414

<212> PRT

<213> Corynebacterium glutamicum

<400> 348

Met	His	Thr	Glu	Leu	Ser	Ser	Leu	Arg	Pro	Ala	Tyr	His	Val	Thr	Pro
1				5					10					15	

Pro	Gln	Gly	Arg	Leu	Asn	Asp	Pro	Asn	Gly	Met	Tyr	Val	Asp	Gly	Asp
			20					25					30		

Thr	Leu	His	Val	Tyr	Tyr	Gln	His	Asp	Pro	Gly	Phe	Pro	Phe	Ala	Pro
		35					40					45			

Lys Arg Thr Gly Trp Ala His Thr Thr Thr Pro Leu Thr Gly Pro Gln
 50 55 60
 Arg Leu Gln Trp Thr His Leu Pro Asp Ala Leu Tyr Pro Asp Ala Ser
 65 70 75 80
 Tyr Asp Leu Asp Gly Cys Tyr Ser Gly Gly Ala Val Phe Thr Asp Gly
 85 90 95
 Thr Leu Lys Leu Phe Tyr Thr Gly Asn Leu Lys Ile Asp Gly Lys Arg
 100 105 110
 Arg Ala Thr Gln Asn Leu Val Glu Val Glu Asp Pro Thr Gly Leu Met
 115 120 125
 Gly Gly Ile His Arg Arg Ser Pro Lys Asn Pro Leu Ile Asp Gly Pro
 130 135 140
 Ala Ser Gly Phe Thr Pro His Tyr Arg Asp Pro Met Ile Ser Pro Asp
 145 150 155 160
 Gly Asp Gly Trp Lys Met Val Leu Gly Ala Gln Arg Glu Asn Leu Thr
 165 170 175
 Gly Ala Ala Val Leu Tyr Arg Ser Thr Asp Leu Glu Asn Trp Glu Phe
 180 185 190
 Ser Gly Glu Ile Thr Phe Asp Leu Ser Asp Ala Gln Pro Gly Ser Ala
 195 200 205
 Pro Asp Leu Val Pro Gly Gly Tyr Met Trp Glu Cys Pro Asn Leu Phe
 210 215 220
 Thr Leu Arg Asp Glu Glu Thr Gly Glu Asp Leu Asp Val Leu Ile Phe
 225 230 235 240
 Cys Pro Gln Gly Leu Asp Arg Ile His Asp Glu Val Thr His Tyr Ala
 245 250 255
 Ser Ser Asp Gln Cys Gly Tyr Val Val Gly Lys Leu Glu Gly Thr Thr
 260 265 270
 Phe Arg Val Leu Arg Gly Phe Ser Glu Leu Asp Phe Gly His Glu Phe
 275 280 285
 Tyr Ala Pro Gln Val Ala Val Asn Gly Ser Asp Ala Trp Leu Val Gly
 290 295 300
 Trp Met Gly Leu Pro Ala Gln Asp Asp His Pro Thr Val Ala Arg Glu
 305 310 315 320
 Gly Trp Val His Cys Leu Thr Val Pro Arg Lys Leu His Leu Arg Asn
 325 330 335
 His Ala Ile Tyr Gln Glu Leu Leu Leu Pro Glu Gly Glu Ser Gly Val
 340 345 350
 Ile Arg Ser Val Leu Gly Ser Glu Pro Val Arg Val Asp Ile Arg Gly
 355 360 365

Asn Ile Ser Leu Glu Trp Asp Gly Val Arg Leu Ser Val Asp Arg Gly
 370 375 380

Gly Asp Arg Arg Val Ala Glu Val Lys Pro Gly Glu Leu Val Ile Ala
 385 390 395 400

Asp Asp Asn Thr Ala Ile Glu Ile Thr Ala Gly Asp Gly Gln
 405 410

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<211> 720

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(720)

<223> RXA02026

<400> 349

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 Pro Phe His Ile Gln Pro Glu Thr Gly Leu Leu Asn Asp Pro Asn Gly
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ctt att ttt tat aaa ggg aag tat tat gtt tca cat caa tgg ttc cca 96
 Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

tta ggc gca gta cat ggc tta aag tat tgg tat aac tac acg agt gat 144
 Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

gac tta ata aac ttt aaa cct gaa ggg cca ata tta aat cca gat act 192
 Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

aaa tat gac agc cat ggt gtt tat agc ggt agc gct ttt gaa tat aac 240
 Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

ggg cat tta tat tat atg tac aca gga aat cat cga gat aat cat tgg 288
 Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

caa cga cat gcg agt cag atg atc gca cga ttg aaa gaa gac ggt tca 336
 Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

gtt gaa aag ttt cca aag cca gta att agc cag caa cca gaa gga tat 384
 Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

aca agt cat ttt aga gat cct aaa gtt ttt aaa tat ggt gag aaa tat 432
 Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

tat gca atc att ggc gca caa aat aat gat cag caa ggt cga tta tta 480
 Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

ctt tat aat act gaa gat ata att aat tgg cat tat tta ggt gaa ata 528
 Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

aat aca gag tta gat gat ttt gga tat atg tgg gaa tgc cca gat tac 576
 Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr
 180 185 190

ttt aat tta gat aat caa gat gtc ata ctt att tgt cca caa ggt att 624
 Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile
 195 200 205

gaa cca aaa ggc aat cag ttc aaa aat att tat caa agt ggt tat ata 672
 Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile
 210 215 220

ctt gga aag ttt gat att gaa aag tta aca tat gaa cat gaa aat ttt 720
 Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe
 225 230 235 240

<210> 350

<211> 240

<212> PRT

<213> Corynebacterium glutamicum

<400> 350

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Leu Ile Phe Tyr Lys Gly Lys Tyr Tyr Val Ser His Gln Trp Phe Pro
 20 25 30

Leu Gly Ala Val His Gly Leu Lys Tyr Trp Tyr Asn Tyr Thr Ser Asp
 35 40 45

Asp Leu Ile Asn Phe Lys Pro Glu Gly Pro Ile Leu Asn Pro Asp Thr
 50 55 60

Lys Tyr Asp Ser His Gly Val Tyr Ser Gly Ser Ala Phe Glu Tyr Asn
 65 70 75 80

Gly His Leu Tyr Tyr Met Tyr Thr Gly Asn His Arg Asp Asn His Trp
 85 90 95

Gln Arg His Ala Ser Gln Met Ile Ala Arg Leu Lys Glu Asp Gly Ser
 100 105 110

Val Glu Lys Phe Pro Lys Pro Val Ile Ser Gln Gln Pro Glu Gly Tyr
 115 120 125

Thr Ser His Phe Arg Asp Pro Lys Val Phe Lys Tyr Gly Glu Lys Tyr
 130 135 140

Tyr Ala Ile Ile Gly Ala Gln Asn Asn Asp Gln Gln Gly Arg Leu Leu
 145 150 155 160

Leu Tyr Asn Thr Glu Asp Ile Ile Asn Trp His Tyr Leu Gly Glu Ile
 165 170 175

Asn Thr Glu Leu Asp Asp Phe Gly Tyr Met Trp Glu Cys Pro Asp Tyr

180	185	190
Phe Asn Leu Asp Asn Gln Asp Val Ile Leu Ile Cys Pro Gln Gly Ile		
195	200	205
Glu Pro Lys Gly Asn Gln Phe Lys Asn Ile Tyr Gln Ser Gly Tyr Ile		
210	215	220
Leu Gly Lys Phe Asp Ile Glu Lys Leu Thr Tyr Glu His Glu Asn Phe		
225	230	235
		240

<210> 351
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1594)
 <223> RXA02061

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 agacactggc gtaattgagt gaaggcagga caataaagag atg acg aac gtt tcc 115
 Met Thr Asn Val Ser 5
 1
 ggg tat cac cga cca gag ctg cac atc acc gct gaa agt ggt gtt ttg 163
 Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala Glu Ser Gly Val Leu 20
 10 15
 ttt gca cct gca ggc gtt ctg ttg gat gac gac acg tgg cat ttc ttc 211
 Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp Thr Trp His Phe Phe 35
 25 30
 cac cag tac cgt ccc tca cca gat cac ggc ccc agg tgg gcg cac caa 259
 His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro Arg Trp Ala His Gln 50
 40 45
 ttc gca gag cgc act cca ttt gtg tgg gat atc tgc gat gac gtg cta 307
 Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile Cys Asp Asp Val Leu 65
 55 60
 gcc cct gaa ggc gat gaa acc cag gtt cgc gct ggc tca gtg gtg tcc 355
 Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala Gly Ser Val Val Ser 85
 70 75 80
 aac aac ggt ggc gtt gat ctg tac ttc acc tcg gtt gtt ggc ccc act 403
 Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser Val Val Gly Pro Thr 100
 90 95
 tcc act atc cag ttg gca cac atc aac aac atc cgt ggc acc acc gaa 451
 Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile Arg Gly Thr Thr Glu 115
 105 110
 ctg atc aat gag gac gag ctg ggg ctc gat cca gat gtc tcc cga atc 499

Leu	Ile	Asn	Glu	Asp	Glu	Leu	Gly	Leu	Asp	Pro	Asp	Val	Ser	Arg	Ile		
		120					125					130					
ggc	gaa	gtg	gtt	ggc	aac	act	gat	ggt	tat	gta	aag	ttc	cgc	tca	ccg	547	
Gly	Glu	Val	Val	Gly	Asn	Thr	Asp	Gly	Tyr	Val	Lys	Phe	Arg	Ser	Pro		
		135				140					145						
tgc	gtt	atc	cca	ggt	tgg	gaa	gac	caa	gga	aac	cgc	gat	gaa	ggc	cac	595	
Cys	Val	Ile	Pro	Gly	Trp	Glu	Asp	Gln	Gly	Asn	Arg	Asp	Glu	Gly	His		
					155					160					165		
tca	gga	tgg	ttg	atg	ctc	gca	gtt	act	ggc	cca	gtt	gaa	gcc	cca	aca	643	
Ser	Gly	Trp	Leu	Met	Leu	Ala	Val	Thr	Gly	Pro	Val	Glu	Ala	Pro	Thr		
				170					175					180			
gta	gtg	gtc	ctc	gac	tcg	cca	gat	gga	aga	gaa	tgg	tcc	att	aca	ggt	691	
Val	Val	Val	Leu	Asp	Ser	Pro	Asp	Gly	Arg	Glu	Trp	Ser	Ile	Thr	Gly		
			185					190					195				
ccc	ctg	tct	ctc	aac	ggc	ctc	tct	gga	tta	gag	tca	gac	gaa	gtt	cta	739	
Pro	Leu	Ser	Leu	Asn	Gly	Leu	Ser	Gly	Leu	Glu	Ser	Asp	Glu	Val	Leu		
		200					205					210					
gtt	gct	cct	cgc	atg	att	cgt	ctg	cgc	gat	gaa	gtg	gat	cat	gaa	atc	787	
Val	Ala	Pro	Arg	Met	Ile	Arg	Leu	Arg	Asp	Glu	Val	Asp	His	Glu	Ile		
		215				220					225						
tac	gat	gtc	ctc	att	gtc	acc	att	gaa	caa	gac	ggg	att	gac	att	tcg	835	
Tyr	Asp	Val	Leu	Ile	Val	Thr	Ile	Glu	Gln	Asp	Gly	Ile	Asp	Ile	Ser		
		230			235				240						245		
gga	tac	ctg	gta	ggc	cag	ctc	aac	ggc	tca	gaa	ttc	gat	gtg	aag	act	883	
Gly	Tyr	Leu	Val	Gly	Gln	Leu	Asn	Gly	Ser	Glu	Phe	Asp	Val	Lys	Thr		
				250				255						260			
cca	ttt	acc	cgc	atc	gat	ttt	ggc	cat	gat	ttc	tct	cgc	ccc	cgc	aac	931	
Pro	Phe	Thr	Arg	Ile	Asp	Phe	Gly	His	Asp	Phe	Ser	Arg	Pro	Arg	Asn		
			265				270						275				
acc	aac	tac	gcc	gaa	acc	acc	atc	ggc	tac	gac	ttc	gcc	cac	atc	ttt	979	
Thr	Asn	Tyr	Ala	Glu	Thr	Thr	Ile	Gly	Tyr	Asp	Phe	Ala	His	Ile	Phe		
		280					285					290					
ggt	ctc	atg	aat	ggc	gta	ggt	cgt	ttg	gac	tcc	ccc	act	gag	cat	ctc	1027	
Gly	Leu	Met	Asn	Gly	Val	Gly	Arg	Leu	Asp	Ser	Pro	Thr	Glu	His	Leu		
		295				300					305						
agt	tgg	aag	gaa	gaa	ggc	tgg	gca	aac	gct	att	tct	ttc	cca	cgt	att	1075	
Ser	Trp	Lys	Glu	Glu	Gly	Trp	Ala	Asn	Ala	Ile	Ser	Phe	Pro	Arg	Ile		
					315				320						325		
gtc	acg	ctc	cag	gac	ggt	acg	gtc	ttc	cag	acc	cct	cca	gaa	gga	ttg	1123	
Val	Thr	Leu	Gln	Asp	Gly	Thr	Val	Phe	Gln	Thr	Pro	Pro	Glu	Gly	Leu		
				330					335					340			
ctt	gat	gcc	att	cat	gaa	tcc	gag	gca	gcg	gca	ggt	tgg	acc	gga	ctg	1171	
Leu	Asp	Ala	Ile	His	Glu	Ser	Glu	Ala	Ala	Ala	Gly	Trp	Thr	Gly	Leu		
			345					350					355				
tgc	gaa	atc	cca	tca	aac	agc	gca	gtt	gaa	gtg	gcg	ttg	aag	gac	caa	1219	
Cys	Glu	Ile	Pro	Ser	Asn	Ser	Ala	Val	Glu	Val	Ala	Leu	Lys	Asp	Gln		

360	365	370	
gaa ggt gaa atc gct gca aca atc act cac cgc cac aat cag cta gtc			1267
Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg His Asn Gln Leu Val			
375	380	385	
ggt gat cgg tcc atg aac ccc aac cac gcg ggt gat cca cac gcg att			1315
Val Asp Arg Ser Met Asn Pro Asn His Ala Gly Asp Pro His Ala Ile			
390	395	400	405
gca cca ttg act gat gat gaa aca gat tca ctg ttc att gtc gtt gac			1363
Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu Phe Ile Val Val Asp			
410	415		420
ggc tct aca gta gaa gtt ttt gct gat ggc ggt tat gta tca atg gca			1411
Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly Tyr Val Ser Met Ala			
425	430		435
agc cgt gtg tat ttc aac aac gga cca ttc agc gaa ttt gag gtc acc			1459
Ser Arg Val Tyr Phe Asn Asn Gly Pro Phe Ser Glu Phe Glu Val Thr			
440	445		450
acc acc ggt gac gca agc att att cgc cag gaa agt cac ttc cct gtt			1507
Thr Thr Gly Asp Ala Ser Ile Ile Arg Gln Glu Ser His Phe Pro Val			
455	460		465
gat ttc agt tcg gtg tcc cta gat ata gat gat ctc act gcg ctc atg			1555
Asp Phe Ser Ser Val Ser Leu Asp Ile Asp Asp Leu Thr Ala Leu Met			
470	475	480	485
cag ttc gat gaa aac gaa ccg cat gaa ggc cca gtg aga taagagttag			1604
Gln Phe Asp Glu Asn Glu Pro His Glu Gly Pro Val Arg			
490	495		
atgcgttcca gcc			1617

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<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 352

Met Thr Asn Val Ser Gly Tyr His Arg Pro Glu Leu His Ile Thr Ala
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Glu Ser Gly Val Leu Phe Ala Pro Ala Gly Val Leu Leu Asp Asp Asp
20 25 30

Thr Trp His Phe Phe His Gln Tyr Arg Pro Ser Pro Asp His Gly Pro
35 40 45

Arg Trp Ala His Gln Phe Ala Glu Arg Thr Pro Phe Val Trp Asp Ile
50 55 60

Cys Asp Asp Val Leu Ala Pro Glu Gly Asp Glu Thr Gln Val Arg Ala
65 70 75 80

Gly Ser Val Val Ser Asn Asn Gly Gly Val Asp Leu Tyr Phe Thr Ser
85 90 95

Val Val Gly Pro Thr Ser Thr Ile Gln Leu Ala His Ile Asn Asn Ile
 100 105 110
 Arg Gly Thr Thr Glu Leu Ile Asn Glu Asp Glu Leu Gly Leu Asp Pro
 115 120 125
 Asp Val Ser Arg Ile Gly Glu Val Val Gly Asn Thr Asp Gly Tyr Val
 130 135 140
 Lys Phe Arg Ser Pro Cys Val Ile Pro Gly Trp Glu Asp Gln Gly Asn
 145 150 155 160
 Arg Asp Glu Gly His Ser Gly Trp Leu Met Leu Ala Val Thr Gly Pro
 165 170 175
 Val Glu Ala Pro Thr Val Val Val Leu Asp Ser Pro Asp Gly Arg Glu
 180 185 190
 Trp Ser Ile Thr Gly Pro Leu Ser Leu Asn Gly Leu Ser Gly Leu Glu
 195 200 205
 Ser Asp Glu Val Leu Val Ala Pro Arg Met Ile Arg Leu Arg Asp Glu
 210 215 220
 Val Asp His Glu Ile Tyr Asp Val Leu Ile Val Thr Ile Glu Gln Asp
 225 230 235 240
 Gly Ile Asp Ile Ser Gly Tyr Leu Val Gly Gln Leu Asn Gly Ser Glu
 245 250 255
 Phe Asp Val Lys Thr Pro Phe Thr Arg Ile Asp Phe Gly His Asp Phe
 260 265 270
 Ser Arg Pro Arg Asn Thr Asn Tyr Ala Glu Thr Thr Ile Gly Tyr Asp
 275 280 285
 Phe Ala His Ile Phe Gly Leu Met Asn Gly Val Gly Arg Leu Asp Ser
 290 295 300
 Pro Thr Glu His Leu Ser Trp Lys Glu Glu Gly Trp Ala Asn Ala Ile
 305 310 315 320
 Ser Phe Pro Arg Ile Val Thr Leu Gln Asp Gly Thr Val Phe Gln Thr
 325 330 335
 Pro Pro Glu Gly Leu Leu Asp Ala Ile His Glu Ser Glu Ala Ala Ala
 340 345 350
 Gly Trp Thr Gly Leu Cys Glu Ile Pro Ser Asn Ser Ala Val Glu Val
 355 360 365
 Ala Leu Lys Asp Gln Glu Gly Glu Ile Ala Ala Thr Ile Thr His Arg
 370 375 380
 His Asn Gln Leu Val Val Asp Arg Ser Met Asn Pro Asn His Ala Gly
 385 390 395 400
 Asp Pro His Ala Ile Ala Pro Leu Thr Asp Asp Glu Thr Asp Ser Leu
 405 410 415
 Phe Ile Val Val Asp Gly Ser Thr Val Glu Val Phe Ala Asp Gly Gly

Val Arg

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<221> CDS
<222> (101)..(1282)
<223> RXN01369
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gtcagccacg	acctattcca	ttgaagaaaa	ggacttgtaa	atg	gag	cta	ttg	gaa	115							
				Met	Glu	Leu	Leu	Glu								
				1				5								
ggc	tca	ctg	cgc	acc	tac	cca	tgg	ggt	tca	aga	aca	ctg	atc	gct	gat	163
Gly	Ser	Leu	Arg	Thr	Tyr	Pro	Trp	Gly	Ser	Arg	Thr	Leu	Ile	Ala	Asp	
				10				15						20		
ctc	aaa	ggc	gaa	gaa	tca	cca	tcg	tct	cgc	cca	gag	gcc	gaa	gtc	tgg	211
Leu	Lys	Gly	Glu	Glu	Ser	Pro	Ser	Ser	Arg	Pro	Glu	Ala	Glu	Val	Trp	
			25					30					35			
ttc	ggt	gcc	cac	cca	gga	tca	cca	tca	acc	atc	ggt	gga	aac	gca	ctc	259
Phe	Gly	Ala	His	Pro	Gly	Ser	Pro	Ser	Thr	Ile	Gly	Gly	Asn	Ala	Leu	
		40					45					50				
aac	gaa	gtc	atc	gca	gcg	aac	ccc	gaa	gaa	gca	ttg	ggc	acg	cgt	gtt	307
Asn	Glu	Val	Ile	Ala	Ala	Asn	Pro	Glu	Glu	Ala	Leu	Gly	Thr	Arg	Val	
	55					60				65						
gcc	gaa	gcg	ttt	gaa	aat	gag	ctt	cca	ttc	ctc	ctc	aaa	atc	ctc	gca	355
Ala	Glu	Ala	Phe	Glu	Asn	Glu	Leu	Pro	Phe	Leu	Leu	Lys	Ile	Leu	Ala	
70					75					80					85	
gcg	gga	gca	ccc	cta	tca	ctg	cag	gcc	cac	cca	tcg	ctg	gaa	cag	gcc	403
Ala	Gly	Ala	Pro	Leu	Ser	Leu	Gln	Ala	His	Pro	Ser	Leu	Glu	Gln	Ala	
				90				95						100		
cgt	gaa	gga	ttc	gcc	cgc	gaa	aac	tca	gca	gga	att	gac	ctc	ggc	gca	451
Arg	Glu	Gly	Phe	Ala	Arg	Glu	Asn	Ser	Ala	Gly	Ile	Asp	Leu	Gly	Ala	

105	110	115	
ccg aac cgc aac tac cgc gac cca aac cac aag cca gag ctg atc gtt Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val 120 125 130			499
gct ctc acg gaa ttc atc gcg atg gca ggc ttc cgc cca ctg cgg aac Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn 135 140 145			547
acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr 150 155 160 165			595
cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu 170 175 180			643
ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile 185 190 195			691
gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg 200 205 210			739
gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu 215 220 225			787
cag tac ccc ggc gat gtc ggc gtt ctg ggt gct ctg ctg ttg aac ttc Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala Leu Leu Leu Asn Phe 230 235 240 245			835
tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca aac ctt Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala Asn Leu 250 255 260			883
cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac tcc gac His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn Ser Asp 265 270 275			931
aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc ccg gag Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val Pro Glu 280 285 290			979
ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc gtg gac Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg Val Asp 295 300 305			1027
gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc aac gaa Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile Asn Glu 310 315 320 325			1075
ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc aac cac Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala Asn His 330 335 340			1123
gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc ttg gaa Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser Leu Glu 345 350 355			1171

gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca tgg gtt 1219
 Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala Trp Val
 360 365 370

cca gca aac gac cca acc att gcg atg cgt tct gag gac gca gaa gta 1267
 Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala Glu Val
 375 380 385

ttc ctc gct agg gtt tagatctttt tagattaaaa tca 1305
 Phe Leu Ala Arg Val
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<210> 354

<211> 394

<212> PRT

<213> Corynebacterium glutamicum

<400> 354

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Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
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Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu
 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro
 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
 100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
 115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe
 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu
 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu
 165 170 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys
 180 185 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu
 195 200 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile
 210 215 220

Ile Glu Leu Asn Glu Gln Tyr Pro Gly Asp Val Gly Val Leu Gly Ala
 225 230 235 240
 Leu Leu Leu Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu
 245 250 255
 Asp Ala Ala Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile
 260 265 270
 Met Ala Asn Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr
 275 280 285
 Val Asp Val Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu
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 Asn Ala Arg Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro
 305 310 315 320
 Val Pro Ile Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu
 325 330 335
 Ala Glu Ala Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly
 340 345 350
 Thr Val Ser Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly
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 Glu Asp Ala Glu Val Phe Leu Ala Arg Val
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 1 5 10 15
 aac ttc tac aaa ctt gcc cca ggc gaa gcc ctc tac ctc gac gcc gca 96
 Asn Phe Tyr Lys Leu Ala Pro Gly Glu Ala Leu Tyr Leu Asp Ala Ala
 20 25 30
 aac ctt cac gca tac atc agc ggc ctc ggc gta gag atc atg gcg aac 144
 Asn Leu His Ala Tyr Ile Ser Gly Leu Gly Val Glu Ile Met Ala Asn
 35 40 45
 tcc gac aac gtg ctc cgc ggt gga ctg aca tcc aaa tac gtc gac gtc 192
 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
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ccg gag ctt gtg cgc gtg ttg gat ttc aac tct ttg gaa aac gct cgc 240
 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80

 gtg gac gtt gaa gaa gac ggt gca acg acc cac tac cca gtt cca atc 288
 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95

 aac gaa ttc caa ctc gat cgc gtt gca gtt cag ggc gaa gca gaa gcc 336
 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110

 aac cac gat ggt ccc atg att gtt ctg tgc acc tcc gga act gtt tcc 384
 Asn His Asp Gly Pro Met Ile Val Leu Cys Thr Ser Gly Thr Val Ser
 115 120 125

 ttg gaa gca ggg gag aag acc ctc gaa gta gca gca ggt cac gcc gca 432
 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala
 130 135 140

 tgg gtt cca gca aac gac cca acc att gcg atg cgt tct gag gac gca 480
 Trp Val Pro Ala Asn Asp Pro Thr Ile Ala Met Arg Ser Glu Asp Ala
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 <213> Corynebacterium glutamicum

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 35 40 45

 Ser Asp Asn Val Leu Arg Gly Gly Leu Thr Ser Lys Tyr Val Asp Val
 50 55 60

 Pro Glu Leu Val Arg Val Leu Asp Phe Asn Ser Leu Glu Asn Ala Arg
 65 70 75 80

 Val Asp Val Glu Glu Asp Gly Ala Thr Thr His Tyr Pro Val Pro Ile
 85 90 95

 Asn Glu Phe Gln Leu Asp Arg Val Ala Val Gln Gly Glu Ala Glu Ala
 100 105 110

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 115 120 125

 Leu Glu Ala Gly Glu Lys Thr Leu Glu Val Ala Ala Gly His Ala Ala

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g t c a g c c a c g a c c t a t t t c c a t t g a a g a a a a g g a c t t g t a a a t g g a g c t a t t g g a 115															
Met Glu Leu Leu Glu 1 5															
g g c t c a c t g c g c a c c t a c c c a t g g g t t c a a g a a c a c t g a t c g c t g a t 163															
Gly Ser Leu Arg Thr Tyr Pro Trp Gly Ser Arg Thr Leu Ile Ala Asp 10 15 20															
c t c a a a g g c g a a g a a t c a c c a t c g t c t c g c c a g a g c g c g a a g t c t g g 211															
Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro Glu Ala Glu Val Trp 25 30 35															
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Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile Gly Gly Asn Ala Leu 40 45 50															
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Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala Leu Gly Thr Arg Val 55 60 65															
g c c g a a g c g t t t g a a a a t g a g c t t c c a t t c c t c c t c a a a a t c c t c g c a 355															
Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu Leu Lys Ile Leu Ala 70 75 80 85															
g c g g g a g c a c c c t a t c a c t g c a g g c c a c c c a t c g c t g g a c a g g c c 403															
Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro Ser Leu Glu Gln Ala 90 95 100															
c g t g a a g g a t t c g c c c g c g a a a a c t c a g c a g g a a t t g a c c t c g g c g c a 451															
Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly Ile Asp Leu Gly Ala 105 110 115															
c c g a a c c g c a a c t a c c g c g a c c c a a a c c a c a a g c c a g a g c t g a t c g t t 499															
Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys Pro Glu Leu Ile Val 120 125 130															
g c t c t c a c g g a a t t c a t c g c g a t g g c a g g c t t c c g c c c a c t g c g g a a c 547															
Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe Arg Pro Leu Arg Asn 135 140 145															

acc ctc acc att ttc gac gcc ctc gcc tgc gaa ccc ctc gac cgc tac 595
 Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu Pro Leu Asp Arg Tyr
 150 155 160 165

cgc agc atg ctc acc gtc gac aac gag gaa gaa tcc ctc cgc gca ctg 643
 Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu Ser Leu Arg Ala Leu
 170 175 180

ttt acc acc tgg atc acc atc ccc atc ggt aaa cga cac gaa ctc atc 691
 Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys Arg His Glu Leu Ile
 185 190 195

gat gcc ctc atc agc aac gcc cac acc tac ctt gag gca agc gat cgt 739
 Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu Glu Ala Ser Asp Arg
 200 205 210

gac gag gac atc gca ttc gtg ctc tca cac atc atc gag ctc aac gaa 787
 Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile Ile Glu Leu Asn Glu
 215 220 225

cag tac ccc ggc gat gtc ggc 808
 Gln Tyr Pro Gly Asp Val Gly
 230 235

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<211> 236

<212> PRT

<213> Corynebacterium glutamicum

<400> 358

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Thr Leu Ile Ala Asp Leu Lys Gly Glu Glu Ser Pro Ser Ser Arg Pro
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Glu Ala Glu Val Trp Phe Gly Ala His Pro Gly Ser Pro Ser Thr Ile
 35 40 45

Gly Gly Asn Ala Leu Asn Glu Val Ile Ala Ala Asn Pro Glu Glu Ala
 50 55 60

Leu Gly Thr Arg Val Ala Glu Ala Phe Glu Asn Glu Leu Pro Phe Leu
 65 70 75 80

Leu Lys Ile Leu Ala Ala Gly Ala Pro Leu Ser Leu Gln Ala His Pro
 85 90 95

Ser Leu Glu Gln Ala Arg Glu Gly Phe Ala Arg Glu Asn Ser Ala Gly
 100 105 110

Ile Asp Leu Gly Ala Pro Asn Arg Asn Tyr Arg Asp Pro Asn His Lys
 115 120 125

Pro Glu Leu Ile Val Ala Leu Thr Glu Phe Ile Ala Met Ala Gly Phe
 130 135 140

Arg Pro Leu Arg Asn Thr Leu Thr Ile Phe Asp Ala Leu Ala Cys Glu
 145 150 155 160

Pro Leu Asp Arg Tyr Arg Ser Met Leu Thr Val Asp Asn Glu Glu Glu
 165 170 175

Ser Leu Arg Ala Leu Phe Thr Thr Trp Ile Thr Ile Pro Ile Gly Lys
 180 185 190

Arg His Glu Leu Ile Asp Ala Leu Ile Ser Asn Ala His Thr Tyr Leu
 195 200 205

Glu Ala Ser Asp Arg Asp Glu Asp Ile Ala Phe Val Leu Ser His Ile
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<210> 359

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (1)..(1752)

<223> RXA02611

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aag att gag gcc ggc cag ggt tgc gat gag ttg tat aac gac ttt gag	96
Lys Ile Glu Ala Gly Gln Gly Ser Asp Glu Leu Tyr Asn Asp Phe Glu	
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cac ggg gct cag ctg ttt gag cgt gct gcg gag aat ttg tct aaa gag	144
His Gly Ala Gln Leu Phe Glu Arg Ala Ala Glu Asn Leu Ser Lys Glu	
35 40 45	
gat agg act gcg ctt ttc gac gtc gcc tcc tct ctg cgg cgc ggc ggc	192
Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly	
50 55 60	
gat gta cgc gca cgt ctc gcc cca gcg ctc acc gcg agt gtc act cat	240
Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His	
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ctt tta gaa ctt aac ccg ttg cgt gag ttg gtc acg atg ggt gaa aac	288
Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn	
85 90 95	
ctg cag gtt cgt gtc gag cgt cgt gcc gct ttg gtc aac tct tgg tat	336
Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr	
100 105 110	
gag ctt ttc cct cgt tcc aca ggt ggt tgg gat gag tcc ggc acc ccc	384
Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro	
115 120 125	
ggt cat ggc act ttc gct acc act gct cag gcg ttg gag cgt gtc gcg	432

Val	His	Gly	Thr	Phe	Ala	Thr	Thr	Ala	Gln	Ala	Leu	Glu	Arg	Val	Ala		
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aag	atg	ggc	ttc	gat	act	gtt	tac	ttc	ccg	ccg	atc	cat	ccg	att	ggc	480	
Lys	Met	Gly	Phe	Asp	Thr	Val	Tyr	Phe	Pro	Pro	Ile	His	Pro	Ile	Gly		
145					150				155						160		
gag	gtc	aac	cgc	aag	ggc	cgc	aat	aat	acg	ctg	acc	ccg	gaa	cct	cat	528	
Glu	Val	Asn	Arg	Lys	Gly	Arg	Asn	Asn	Thr	Leu	Thr	Pro	Glu	Pro	His		
				165					170					175			
gat	gtg	ggg	tgc	ccg	tgg	gct	att	ggg	tct	aaa	gat	ggg	ggg	cat	gat	576	
Asp	Val	Gly	Ser	Pro	Trp	Ala	Ile	Gly	Ser	Lys	Asp	Gly	Gly	His	Asp		
			180					185					190				
gca	acg	cat	ccg	cgg	ttg	ggc	acc	att	gaa	gat	ttc	cag	gcg	ttg	ttg	624	
Ala	Thr	His	Pro	Arg	Leu	Gly	Thr	Ile	Glu	Asp	Phe	Gln	Ala	Leu	Leu		
		195					200					205					
gct	cgc	gca	cgg	gaa	ctc	aat	ttg	gaa	gtt	gca	ctc	gat	cta	gct	ctg	672	
Ala	Arg	Ala	Arg	Glu	Leu	Asn	Leu	Glu	Val	Ala	Leu	Asp	Leu	Ala	Leu		
	210					215					220						
cag	gct	gcc	cct	gat	cat	cca	tgg	gcg	cag	gaa	cac	cgc	gag	ttt	ttc	720	
Gln	Ala	Ala	Pro	Asp	His	Pro	Trp	Ala	Gln	Glu	His	Arg	Glu	Phe	Phe		
225					230					235					240		
acg	gtg	ttg	gct	gat	ggc	acc	att	gcg	tat	gca	gaa	aac	cca	ccg	aag	768	
Thr	Val	Leu	Ala	Asp	Gly	Thr	Ile	Ala	Tyr	Ala	Glu	Asn	Pro	Pro	Lys		
				245					250					255			
aag	tac	cag	gat	att	tat	ccc	atc	aac	ttt	gat	aat	gat	gct	ccg	aag	816	
Lys	Tyr	Gln	Asp	Ile	Tyr	Pro	Ile	Asn	Phe	Asp	Asn	Asp	Ala	Pro	Lys		
			260					265					270				
atc	tac	gaa	gag	gtc	tat	cgt	gtg	gtg	aag	ttc	tgg	gtg	gat	ttg	ggg	864	
Ile	Tyr	Glu	Glu	Val	Tyr	Arg	Val	Val	Lys	Phe	Trp	Val	Asp	Leu	Gly		
		275					280					285					
gtg	acc	aca	ttc	cgc	gtg	gat	aac	ccg	cac	act	aag	ccc	gct	aat	ttc	912	
Val	Thr	Thr	Phe	Arg	Val	Asp	Asn	Pro	His	Thr	Lys	Pro	Ala	Asn	Phe		
	290					295					300						
tgg	cag	tgg	ctt	att	tct	gcc	atc	cat	aaa	tca	aac	cct	gag	gtc	att	960	
Trp	Gln	Trp	Leu	Ile	Ser	Ala	Ile	His	Lys	Ser	Asn	Pro	Glu	Val	Ile		
305					310					315					320		
ttc	cta	gcg	gag	gcg	tct	act	cgc	ccg	gca	cgt	ctg	tat	ttc	ttg	tcc	1008	
Phe	Leu	Ala	Glu	Ala	Ser	Thr	Arg	Pro	Ala	Arg	Leu	Tyr	Phe	Leu	Ser		
				325					330					335			
aag	att	ggg	ttc	tcc	cag	tct	tac	acc	tac	ttc	acc	tgg	aag	gtc	acc	1056	
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr		
			340					345					350				
aac	gag	gag	ctc	acc	gag	ttc	gct	act	gag	atc	gcc	ccc	atg	gcg	gat	1104	
Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp		
		355					360				365						
att	tct	cgt	ccg	aac	ctg	ttt	gtg	aac	act	ccc	gac	att	ttg	cat	gcg	1152	
Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala		

370	375	380	
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Ser Leu Gln His Gly Gly Arg Ala Met Phe Ala Ile Arg Ala Ala Leu			
385	390	395	400
gcc gcc acg atg tct cct gtg tgg ggc gta tat tcc gga tat gag ctc			1248
Ala Ala Thr Met Ser Pro Val Trp Gly Val Tyr Ser Gly Tyr Glu Leu			
	405	410	415
ttt gag cac gag gcc gtc aag cct ggt tgc gaa gag tac ttg gat tct			1296
Phe Glu His Glu Ala Val Lys Pro Gly Ser Glu Glu Tyr Leu Asp Ser			
	420	425	430
gag aag tac gag ctg cgt ccc cgc gat ttc gag ggt gct ctg gaa cgt			1344
Glu Lys Tyr Glu Leu Arg Pro Arg Asp Phe Glu Gly Ala Leu Glu Arg			
	435	440	445
ggc gat tct ctc gag gat tac atc gct ctg ctc aac cag atc cgt cgc			1392
Gly Asp Ser Leu Glu Asp Tyr Ile Ala Leu Leu Asn Gln Ile Arg Arg			
	450	455	460
gcg aac cct gcc ttg cag caa cta cgc aac atc cac ttc cac gaa gcg			1440
Ala Asn Pro Ala Leu Gln Gln Leu Arg Asn Ile His Phe His Glu Ala			
	465	470	475
gac aat gat cag atc atc gcc tac tcc aag gtt gat gct ttg acc gga			1488
Asp Asn Asp Gln Ile Ile Ala Tyr Ser Lys Val Asp Ala Leu Thr Gly			
	485	490	495
aat acc gtg ttg att gtg gtc aac ttg gat cca cgt agt gct cgt gag			1536
Asn Thr Val Leu Ile Val Val Asn Leu Asp Pro Arg Ser Ala Arg Glu			
	500	505	510
gct act gtt cgc ctt gat ctt gga gcg ctt ggc tta gaa gcg ggt gca			1584
Ala Thr Val Arg Leu Asp Leu Gly Ala Leu Gly Leu Glu Ala Gly Ala			
	515	520	525
cag ttt gag gtg cgc gat gcg atc acc ggc tcc cgt tac ctg tgg tca			1632
Gln Phe Glu Val Arg Asp Ala Ile Thr Gly Ser Arg Tyr Leu Trp Ser			
	530	535	540
gag acg aac ttt gtc cgc ctc gag ccc cta cgc gat gtc gcc cac atc			1680
Glu Thr Asn Phe Val Arg Leu Glu Pro Leu Arg Asp Val Ala His Ile			
	545	550	555
ttt gtt ctt cct gaa ctt cca gcg tct cgc cgt gag cgt ctc gcg tgg			1728
Phe Val Leu Pro Glu Leu Pro Ala Ser Arg Arg Glu Arg Leu Ala Trp			
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cgc gaa atc aag acc tac cgc gcg taatttccca tctctgtacc ttc			1775
Arg Glu Ile Lys Thr Tyr Arg Ala			
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<212> PRT

<213> Corynebacterium glutamicum

<400> 360

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 20 25 30
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 35 40 45
 Asp Arg Thr Ala Leu Phe Asp Val Ala Ser Ser Leu Arg Arg Gly Gly
 50 55 60
 Asp Val Arg Ala Arg Leu Ala Pro Ala Leu Thr Ala Ser Val Thr His
 65 70 75 80
 Leu Leu Glu Leu Asn Pro Leu Arg Glu Leu Val Thr Met Gly Glu Asn
 85 90 95
 Leu Gln Val Arg Val Glu Arg Arg Ala Ala Leu Val Asn Ser Trp Tyr
 100 105 110
 Glu Leu Phe Pro Arg Ser Thr Gly Gly Trp Asp Glu Ser Gly Thr Pro
 115 120 125
 Val His Gly Thr Phe Ala Thr Thr Ala Gln Ala Leu Glu Arg Val Ala
 130 135 140
 Lys Met Gly Phe Asp Thr Val Tyr Phe Pro Pro Ile His Pro Ile Gly
 145 150 155 160
 Glu Val Asn Arg Lys Gly Arg Asn Asn Thr Leu Thr Pro Glu Pro His
 165 170 175
 Asp Val Gly Ser Pro Trp Ala Ile Gly Ser Lys Asp Gly Gly His Asp
 180 185 190
 Ala Thr His Pro Arg Leu Gly Thr Ile Glu Asp Phe Gln Ala Leu Leu
 195 200 205
 Ala Arg Ala Arg Glu Leu Asn Leu Glu Val Ala Leu Asp Leu Ala Leu
 210 215 220
 Gln Ala Ala Pro Asp His Pro Trp Ala Gln Glu His Arg Glu Phe Phe
 225 230 235 240
 Thr Val Leu Ala Asp Gly Thr Ile Ala Tyr Ala Glu Asn Pro Pro Lys
 245 250 255
 Lys Tyr Gln Asp Ile Tyr Pro Ile Asn Phe Asp Asn Asp Ala Pro Lys
 260 265 270
 Ile Tyr Glu Glu Val Tyr Arg Val Val Lys Phe Trp Val Asp Leu Gly
 275 280 285
 Val Thr Thr Phe Arg Val Asp Asn Pro His Thr Lys Pro Ala Asn Phe
 290 295 300
 Trp Gln Trp Leu Ile Ser Ala Ile His Lys Ser Asn Pro Glu Val Ile
 305 310 315 320
 Phe Leu Ala Glu Ala Ser Thr Arg Pro Ala Arg Leu Tyr Phe Leu Ser

				325						330					335
Lys	Ile	Gly	Phe	Ser	Gln	Ser	Tyr	Thr	Tyr	Phe	Thr	Trp	Lys	Val	Thr
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Asn	Glu	Glu	Leu	Thr	Glu	Phe	Ala	Thr	Glu	Ile	Ala	Pro	Met	Ala	Asp
		355					360					365			
Ile	Ser	Arg	Pro	Asn	Leu	Phe	Val	Asn	Thr	Pro	Asp	Ile	Leu	His	Ala
	370					375					380				
Ser	Leu	Gln	His	Gly	Gly	Arg	Ala	Met	Phe	Ala	Ile	Arg	Ala	Ala	Leu
385					390					395					400
Ala	Ala	Thr	Met	Ser	Pro	Val	Trp	Gly	Val	Tyr	Ser	Gly	Tyr	Glu	Leu
				405					410					415	
Phe	Glu	His	Glu	Ala	Val	Lys	Pro	Gly	Ser	Glu	Glu	Tyr	Leu	Asp	Ser
			420					425					430		
Glu	Lys	Tyr	Glu	Leu	Arg	Pro	Arg	Asp	Phe	Glu	Gly	Ala	Leu	Glu	Arg
		435					440					445			
Gly	Asp	Ser	Leu	Glu	Asp	Tyr	Ile	Ala	Leu	Leu	Asn	Gln	Ile	Arg	Arg
	450					455					460				
Ala	Asn	Pro	Ala	Leu	Gln	Gln	Leu	Arg	Asn	Ile	His	Phe	His	Glu	Ala
465					470					475					480
Asp	Asn	Asp	Gln	Ile	Ile	Ala	Tyr	Ser	Lys	Val	Asp	Ala	Leu	Thr	Gly
				485					490					495	
Asn	Thr	Val	Leu	Ile	Val	Val	Asn	Leu	Asp	Pro	Arg	Ser	Ala	Arg	Glu
			500					505					510		
Ala	Thr	Val	Arg	Leu	Asp	Leu	Gly	Ala	Leu	Gly	Leu	Glu	Ala	Gly	Ala
			515				520					525			
Gln	Phe	Glu	Val	Arg	Asp	Ala	Ile	Thr	Gly	Ser	Arg	Tyr	Leu	Trp	Ser
	530					535					540				
Glu	Thr	Asn	Phe	Val	Arg	Leu	Glu	Pro	Leu	Arg	Asp	Val	Ala	His	Ile
545					550					555					560
Phe	Val	Leu	Pro	Glu	Leu	Pro	Ala	Ser	Arg	Arg	Glu	Arg	Leu	Ala	Trp
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Arg	Glu	Ile	Lys	Thr	Tyr	Arg	Ala								
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 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(2293)
 <223> RXA02612

<400> 361

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Ala Ser His Ile Thr Ile Pro Glu Ala Asp Leu Ala Arg Leu Arg His
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Cys Asn His His Asp Pro His Gly Phe Tyr Gly Trp His Glu Thr Glu
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gct ggt tcg gtt atc cgc acg cgc cag gtc ggc gcg acg cag gtt aat 259
Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly Ala Thr Gln Val Asn
                                     40 45 50
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Leu Leu Ile Asp Asp Thr Ser His Val Met Thr Pro Ile Gly Asp Asp
                                     55 60 65
att ttc gca att gac tta ggt cac cgc gag cgc gct gac tat cgc ttg 355
Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg Ala Asp Tyr Arg Leu
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gaa gtc acc tgg cct gat caa gaa ccg cag gtc aag gct gat cca tac 403
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tac ttc ctc ccc acc gta ggc gag atg gat att tac ctc ttc tct gag 451
Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile Tyr Leu Phe Ser Glu
                                     105 110 115
gga cgc cat gag cgt ttg tgg gag att ctc ggt gcc aac atc aag acc 499
Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly Ala Asn Ile Lys Thr
                                     120 125 130
tac caa act gcg ctc gga aca gtt cgt ggc acc gca ttt act gtg tgg 547
Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr Ala Phe Thr Val Trp
                                     135 140 145
gct cca aac gca att ggc tgc gca gtg gtc ggt ggc ttc aac ggt tgg 595
Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly Gly Phe Asn Gly Trp
                                     150 155 160 165
aat gca tcc cag cat ccg atg cgt tct atg ggt ggt tcg ggt ctg tgg 643
Asn Ala Ser Gln His Pro Met Arg Ser Met Gly Gly Ser Gly Leu Trp
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gag ctg ttc atc cca ggc ata gag gaa ggc gaa gtg tac aaa ttc gcc 691
Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu Val Tyr Lys Phe Ala
                                     185 190 195
gtc caa acc agg gaa ggc caa cgt cgt gat aag gcc gat ccg atg gct 739
Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys Ala Asp Pro Met Ala
                                     200 205 210
cgt cgc gca gaa ctg gcg ccg gca acc gga tct att gtc gct tcc tct 787
Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser Ile Val Ala Ser Ser

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215	220	225	
gag tac cag tgg cag gat tcc gag tgg ctg cgc gag cgt tcc caa act 835 Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg Glu Arg Ser Gln Thr 245 230 235 240			
gat ctc gca tcc aag cca atg agt gtc tac gag gtc cac ctc ggt tct 883 Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu Val His Leu Gly Ser 260 250 255			
tgg cgc tgg ggt aag aac tat gag gat ttg gct act gag ctg gtt gat 931 Trp Arg Trp Gly Lys Asn Tyr Glu Asp Leu Ala Thr Glu Leu Val Asp 275 265 270			
tac gtc gca gat ctt ggc tac acc cac gtg gaa ttc ctc cct gtc gca 979 Tyr Val Ala Asp Leu Gly Tyr Thr His Val Glu Phe Leu Pro Val Ala 290 280 285			
gag cac ccc ttc ggt ggt tcc tgg ggt tac cag gtc acc ggc tac tac 1027 Glu His Pro Phe Gly Gly Ser Trp Gly Tyr Gln Val Thr Gly Tyr Tyr 305 295 300			
gca ccg acc tct cgt tgg ggt act cca gat cag ttc cgt gcg cta gtc 1075 Ala Pro Thr Ser Arg Trp Gly Thr Pro Asp Gln Phe Arg Ala Leu Val 325 310 315 320			
gac gct ttc cac gcc cgc ggt att ggc gtg atc atg gac tgg gtt cct 1123 Asp Ala Phe His Ala Arg Gly Ile Gly Val Ile Met Asp Trp Val Pro 340 330 335			
gcc cac ttc cct aag gat gat tgg gct ctt gcc cgc ttt gat ggc gaa 1171 Ala His Phe Pro Lys Asp Asp Trp Ala Leu Ala Arg Phe Asp Gly Glu 355 345 350			
gcc ctc tat gaa cac cct gac tgg agg cgc ggc gaa caa aag gat tgg 1219 Ala Leu Tyr Glu His Pro Asp Trp Arg Arg Gly Glu Gln Lys Asp Trp 370 360 365			
ggc acc ctg gtc ttt gac ttc ggt cgc aac gaa gtc cgc aac ttc ctc 1267 Gly Thr Leu Val Phe Asp Phe Gly Arg Asn Glu Val Arg Asn Phe Leu 385 375 380			
gtc gct aat gcg ttg tac tgg att gaa gaa ttc cac atc gat ggt ctg 1315 Val Ala Asn Ala Leu Tyr Trp Ile Glu Glu Phe His Ile Asp Gly Leu 405 390 395 400			
cgc gtc gac gcc gtg gcc tcc atg ctg tac ctc gat tac tcc cgt gag 1363 Arg Val Asp Ala Val Ala Ser Met Leu Tyr Leu Asp Tyr Ser Arg Glu 420 410 415			
cac ggc gaa tgg gaa cca aac atc tac ggt ggt cgc gag aac ctc gag 1411 His Gly Glu Trp Glu Pro Asn Ile Tyr Gly Gly Arg Glu Asn Leu Glu 435 425 430			
gca gtg cag ttc ctg cag gaa atg aac gcc acg gtg ctg cga ctg cac 1459 Ala Val Gln Phe Leu Gln Glu Met Asn Ala Thr Val Leu Arg Leu His 450 440 445			
cct ggt gcg ctc acc atc gct gag gaa tca act tca tgg cct ggc gtg 1507 Pro Gly Ala Leu Thr Ile Ala Glu Glu Ser Thr Ser Trp Pro Gly Val 465 455 460			

acc gca cca acg tgg gac ggc ggc ttg gga ttc tcc ctc aag tgg aac	1555
Thr Ala Pro Thr Trp Asp Gly Gly Leu Gly Phe Ser Leu Lys Trp Asn	
470 475 480 485	
atg ggc tgg atg cac gac acc tta gag tac ttc tcc aaa aac cct gtg	1603
Met Gly Trp Met His Asp Thr Leu Glu Tyr Phe Ser Lys Asn Pro Val	
490 495 500	
cac cgc gca ttc cac cac agt gag ctc act ttc tcc ttg gtg tac gca	1651
His Arg Ala Phe His His Ser Glu Leu Thr Phe Ser Leu Val Tyr Ala	
505 510 515	
ttc tct gag cgt ttt gta ctt ccg atc tct cac gat gaa gtc gtc cac	1699
Phe Ser Glu Arg Phe Val Leu Pro Ile Ser His Asp Glu Val Val His	
520 525 530	
ggc aag ggt tcc ctg tgg gac cgt atg cct ggc gat acg tgg aac aag	1747
Gly Lys Gly Ser Leu Trp Asp Arg Met Pro Gly Asp Thr Trp Asn Lys	
535 540 545	
gcc gct ggt ctt cgc acc ttc ctt gcg tac atg tgg tca cac cca ggc	1795
Ala Ala Gly Leu Arg Thr Phe Leu Ala Tyr Met Trp Ser His Pro Gly	
550 555 560 565	
aag aag ctg ctt ttc atg ggt cag gag ttt ggt cag cgt gaa gag tgg	1843
Lys Lys Leu Leu Phe Met Gly Gln Glu Phe Gly Gln Arg Glu Glu Trp	
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gct gaa ggc cag gga ctg cca tgg gat att gtc gac ggc tgg caa ggc	1891
Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val Asp Gly Trp Gln Gly	
585 590 595	
gag tac cac gaa gcc atc cgc act ctg acc cgc tcc ctc aac ggt gtc	1939
Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg Ser Leu Asn Gly Val	
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tac tca gac tcc cct gcg ctg cac act cag gat ttc acc gga gaa ggc	1987
Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp Phe Thr Gly Glu Gly	
615 620 625	
ttc aca tgg aat aag ggc gac gac gcc acc aac aac att ttg gcg ttc	2035
Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn Asn Ile Leu Ala Phe	
630 635 640 645	
act cgt ttc ggc agc gac ggc tcc cag atg ctg tgt gta ttc aac ctg	2083
Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu Cys Val Phe Asn Leu	
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tct gga acc tcc cag cct gag tac cag ctc ggt gtt gca gcg ggt ggc	2131
Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly Val Ala Ala Gly Gly	
665 670 675	
gaa tgg aag ctc gtt ctc aac act gat gat gct gaa ttc ctc ggt gca	2179
Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala Glu Phe Leu Gly Ala	
680 685 690	
gaa aac gat atc gct act tcc gtt caa gca gca gcg aca cca cgc gat	2227
Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala Ala Thr Pro Arg Asp	
695 700 705	

aat ttc gcc tac tca ctc tca ctg cat gtc cca gcg atg agt gct cag 2275
 Asn Phe Ala Tyr Ser Leu Ser Leu His Val Pro Ala Met Ser Ala Gln
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ttc tac tca ctg cag aag taggacacag gaaaatgcat cct 2316
 Phe Tyr Ser Leu Gln Lys
 730

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<212> PRT

<213> Corynebacterium glutamicum

<400> 362

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 20 25 30

Trp His Glu Thr Glu Ala Gly Ser Val Ile Arg Thr Arg Gln Val Gly
 35 40 45

Ala Thr Gln Val Asn Leu Leu Ile Asp Asp Thr Ser His Val Met Thr
 50 55 60

Pro Ile Gly Asp Asp Ile Phe Ala Ile Asp Leu Gly His Arg Glu Arg
 65 70 75 80

Ala Asp Tyr Arg Leu Glu Val Thr Trp Pro Asp Gln Glu Pro Gln Val
 85 90 95

Lys Ala Asp Pro Tyr Tyr Phe Leu Pro Thr Val Gly Glu Met Asp Ile
 100 105 110

Tyr Leu Phe Ser Glu Gly Arg His Glu Arg Leu Trp Glu Ile Leu Gly
 115 120 125

Ala Asn Ile Lys Thr Tyr Gln Thr Ala Leu Gly Thr Val Arg Gly Thr
 130 135 140

Ala Phe Thr Val Trp Ala Pro Asn Ala Ile Gly Cys Ala Val Val Gly
 145 150 155 160

Gly Phe Asn Gly Trp Asn Ala Ser Gln His Pro Met Arg Ser Met Gly
 165 170 175

Gly Ser Gly Leu Trp Glu Leu Phe Ile Pro Gly Ile Glu Glu Gly Glu
 180 185 190

Val Tyr Lys Phe Ala Val Gln Thr Arg Glu Gly Gln Arg Arg Asp Lys
 195 200 205

Ala Asp Pro Met Ala Arg Arg Ala Glu Leu Ala Pro Ala Thr Gly Ser
 210 215 220

Ile Val Ala Ser Ser Glu Tyr Gln Trp Gln Asp Ser Glu Trp Leu Arg
 225 230 235 240

Glu Arg Ser Gln Thr Asp Leu Ala Ser Lys Pro Met Ser Val Tyr Glu

245										250					255				
Val	His	Leu	Gly	Ser	Trp	Arg	Trp	Gly	Lys	Asn	Tyr	Glu	Asp	Leu	Ala				
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Thr	Glu	Leu	Val	Asp	Tyr	Val	Ala	Asp	Leu	Gly	Tyr	Thr	His	Val	Glu				
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Phe	Leu	Pro	Val	Ala	Glu	His	Pro	Phe	Gly	Gly	Ser	Trp	Gly	Tyr	Gln				
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Val	Thr	Gly	Tyr	Tyr	Ala	Pro	Thr	Ser	Arg	Trp	Gly	Thr	Pro	Asp	Gln				
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Phe	Arg	Ala	Leu	Val	Asp	Ala	Phe	His	Ala	Arg	Gly	Ile	Gly	Val	Ile				
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Met	Asp	Trp	Val	Pro	Ala	His	Phe	Pro	Lys	Asp	Asp	Trp	Ala	Leu	Ala				
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Arg	Phe	Asp	Gly	Glu	Ala	Leu	Tyr	Glu	His	Pro	Asp	Trp	Arg	Arg	Gly				
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Glu	Gln	Lys	Asp	Trp	Gly	Thr	Leu	Val	Phe	Asp	Phe	Gly	Arg	Asn	Glu				
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Val	Arg	Asn	Phe	Leu	Val	Ala	Asn	Ala	Leu	Tyr	Trp	Ile	Glu	Glu	Phe				
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His	Ile	Asp	Gly	Leu	Arg	Val	Asp	Ala	Val	Ala	Ser	Met	Leu	Tyr	Leu				
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Asp	Tyr	Ser	Arg	Glu	His	Gly	Glu	Trp	Glu	Pro	Asn	Ile	Tyr	Gly	Gly				
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Arg	Glu	Asn	Leu	Glu	Ala	Val	Gln	Phe	Leu	Gln	Glu	Met	Asn	Ala	Thr				
		435					440					445							
Val	Leu	Arg	Leu	His	Pro	Gly	Ala	Leu	Thr	Ile	Ala	Glu	Glu	Ser	Thr				
	450					455					460								
Ser	Trp	Pro	Gly	Val	Thr	Ala	Pro	Thr	Trp	Asp	Gly	Gly	Leu	Gly	Phe				
465					470					475					480				
Ser	Leu	Lys	Trp	Asn	Met	Gly	Trp	Met	His	Asp	Thr	Leu	Glu	Tyr	Phe				
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Ser	Lys	Asn	Pro	Val	His	Arg	Ala	Phe	His	His	Ser	Glu	Leu	Thr	Phe				
			500					505					510						
Ser	Leu	Val	Tyr	Ala	Phe	Ser	Glu	Arg	Phe	Val	Leu	Pro	Ile	Ser	His				
		515					520					525							
Asp	Glu	Val	Val	His	Gly	Lys	Gly	Ser	Leu	Trp	Asp	Arg	Met	Pro	Gly				
	530					535					540								
Asp	Thr	Trp	Asn	Lys	Ala	Ala	Gly	Leu	Arg	Thr	Phe	Leu	Ala	Tyr	Met				
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Trp	Ser	His	Pro	Gly	Lys	Lys	Leu	Leu	Phe	Met	Gly	Gln	Glu	Phe	Gly				
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Gln Arg Glu Glu Trp Ala Glu Gly Gln Gly Leu Pro Trp Asp Ile Val
 580 585
 Asp Gly Trp Gln Gly Glu Tyr His Glu Ala Ile Arg Thr Leu Thr Arg
 595 600 605
 Ser Leu Asn Gly Val Tyr Ser Asp Ser Pro Ala Leu His Thr Gln Asp
 610 615 620
 Phe Thr Gly Glu Gly Phe Thr Trp Asn Lys Gly Asp Asp Ala Thr Asn
 625 630 635 640
 Asn Ile Leu Ala Phe Thr Arg Phe Gly Ser Asp Gly Ser Gln Met Leu
 645 650 655
 Cys Val Phe Asn Leu Ser Gly Thr Ser Gln Pro Glu Tyr Gln Leu Gly
 660 665 670
 Val Ala Ala Gly Gly Glu Trp Lys Leu Val Leu Asn Thr Asp Asp Ala
 675 680 685
 Glu Phe Leu Gly Ala Glu Asn Asp Ile Ala Thr Ser Val Gln Ala Ala
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 Arg Leu Arg Asp Leu Gly Met Arg Asn Tyr Trp Gly Tyr Asn Ser Phe
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 ggc ttc ttt gcg ccc tac aac gat tac gct gcc aac aag aac ccc ggt 144
 Gly Phe Phe Ala Pro Tyr Asn Asp Tyr Ala Ala Asn Lys Asn Pro Gly
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 ggc gcc gtg gcc gag ttc aaa ggc ttg gtg cgc agc tac cac gaa gcg 192
 Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala
 50 55 60
 ggc ctc gaa gta att ttg gat gtg gtc tac aac cac acc gcc gag ggc 240
 Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly

65	70					75					80					
aac cac atg ggc ccc acc atc gcg ttc cga ggc att gac aac gag gcg	288															
Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala																
	85					90					95					
tac tac cga ctg gtt gag ggc gat cgc cgt cat tac atg gac tac acc	336															
Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr																
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ggt act ggt aac tcc ctc aat gtc cgc gac ccg cac tca ctg cag ctg	384															
Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu																
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att atg gat tcg ctg cgc tac tgg gtc acc gag atg cat gtc gac ggc	432															
Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly																
	130					135					140					
ttc cgc ttc gac ctt gcc tct acc ctt gct cgt gaa ttt gat gat gtt	480															
Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val																
	145					150					155					160
gac cgc ctg gca acc ttc ttc gac ctg gtc caa caa gac ccg gtg gtc	528															
Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val																
	165					170					175					
tcc cag gtc aag ctc att gct gag ccg tgg gat gtt ggc gaa ggc gga	576															
Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly																
	180					185					190					
tac caa gtg ggt aac ttc cca cca ctg tgg act gag tgg aac ggt aaa	624															
Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr Glu Trp Asn Gly Lys																
	195					200					205					
tac cgc gac act gtc cgt gat ttc tgg cgt ggt gag cca gca acc ttg	672															
Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly Glu Pro Ala Thr Leu																
	210					215					220					
ggt gaa ttc gct tcc cga cta act ggt tcc tct gat ttg tat gca aac	720															
Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser Asp Leu Tyr Ala Asn																
	225					230					235					240
aac ggc cgt cgc ccc act gca tcg atc aac ttt gtg act gct cac gac	768															
Asn Gly Arg Arg Pro Thr Ala Ser Ile Asn Phe Val Thr Ala His Asp																
	245					250					255					
ggc ttc acc ctc aat gac ttg gtc agt tac aac gag aag cac aac atg	816															
Gly Phe Thr Leu Asn Asp Leu Val Ser Tyr Asn Glu Lys His Asn Met																
	260					265					270					
gcc aac ggt gaa gac ggt cgg gac ggt gaa tca cac aac cgt tcc tgg	864															
Ala Asn Gly Glu Asp Gly Arg Asp Gly Glu Ser His Asn Arg Ser Trp																
	275					280					285					
aac tgt ggc gtc gaa gga cca act gac gat cct gag att atg cag ctg	912															
Asn Cys Gly Val Glu Gly Pro Thr Asp Asp Pro Glu Ile Met Gln Leu																
	290					295					300					
cgt gct cag caa cga cgc aac ttc ctc acc acc ttg ttg ctg tcc cag	960															
Arg Ala Gln Gln Arg Arg Asn Phe Leu Thr Thr Leu Leu Leu Ser Gln																
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ggc acc cct atg ttg tcc cac ggt gat gaa atg gcc cgt acc caa aac	1008
Gly Thr Pro Met Leu Ser His Gly Asp Glu Met Ala Arg Thr Gln Asn	
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ggc aac aac aac gtc tac tgc caa gac aat gaa ctg gcg tgg gtg aat	1056
Gly Asn Asn Asn Val Tyr Cys Gln Asp Asn Glu Leu Ala Trp Val Asn	
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Trp Asp Gln Ala Glu Glu Asn Ala Asp Leu Val Ser Phe Thr Arg Arg	
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Leu Leu Arg Ile Arg Ala Asn His Pro Val Phe Arg Arg Arg Gln Phe	
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Leu Ala Gly Gly Pro Leu Gly Ala Asp Val Arg Asp Arg Asp Ile Ala	
385 390 395 400	
tgg ctg gta cca aat gga acc ttg atg act caa gat gac tgg gac ttc	1248
Trp Leu Val Pro Asn Gly Thr Leu Met Thr Gln Asp Asp Trp Asp Phe	
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gct ttc ggt aaa tca ctg cag gtg ttc ttc aac ggc gat gcc atc gaa	1296
Ala Phe Gly Lys Ser Leu Gln Val Phe Phe Asn Gly Asp Ala Ile Glu	
420 425 430	
gag cct gat tat cga gga cag aaa atc cac gat gac tcc ttc atc ttg	1344
Glu Pro Asp Tyr Arg Gly Gln Lys Ile His Asp Asp Ser Phe Ile Leu	
435 440 445	
atg ttc aac gct cac ttc gaa cct atc gat ttc aat ctc cct cct gag	1392
Met Phe Asn Ala His Phe Glu Pro Ile Asp Phe Asn Leu Pro Pro Glu	
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cat ttc ggt atg aag tgg aag ctt ttg gtc gat acc acc gaa gcg gtg	1440
His Phe Gly Met Lys Trp Lys Leu Leu Val Asp Thr Thr Glu Ala Val	
465 470 475 480	
ggc cac ccg ctg gag gat ctc acc atc gaa gct ggc gga acc atc act	1488
Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala Gly Gly Thr Ile Thr	
485 490 495	
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Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln Val Glu Ala Pro Asp	
500 505 510	
tac acc aag ctt gag gaa aag atc gct gct gaa aag cgt gag caa gaa	1584
Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu	
515 520 525	
ctt gcg gca gag aag gaa gct gct gag aag cgc gaa ttg gaa ctg gcg	1632
Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala	
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Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala	
545 550 555 560	

gaa cgt gct tcg act cag gaa gct gaa ttg gcc cat caa cac ggt gct 1728
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
 565 570 575
 gat gcg att gcc gat gag gta gcg gaa gaa cca caa gag ctg cca caa 1776
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
 580 585 590
 gat gaa gta gcg gca gag gtc gag act gag ccc gac acc gag cct gac 1824
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
 595 600 605
 act gaa tct gac tcc gag cag gct gag gta gct tca gag gag cct gaa 1872
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
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 35 40 45
 Gly Ala Val Ala Glu Phe Lys Gly Leu Val Arg Ser Tyr His Glu Ala
 50 55 60
 Gly Leu Glu Val Ile Leu Asp Val Val Tyr Asn His Thr Ala Glu Gly
 65 70 75 80
 Asn His Met Gly Pro Thr Ile Ala Phe Arg Gly Ile Asp Asn Glu Ala
 85 90 95
 Tyr Tyr Arg Leu Val Glu Gly Asp Arg Arg His Tyr Met Asp Tyr Thr
 100 105 110
 Gly Thr Gly Asn Ser Leu Asn Val Arg Asp Pro His Ser Leu Gln Leu
 115 120 125
 Ile Met Asp Ser Leu Arg Tyr Trp Val Thr Glu Met His Val Asp Gly
 130 135 140
 Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg Glu Phe Asp Asp Val
 145 150 155 160
 Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln Gln Asp Pro Val Val
 165 170 175
 Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp Val Gly Glu Gly Gly

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Tyr	Gln	Val	Gly	Asn	Phe	Pro	Pro	Leu	Trp	Thr	Glu	Trp	Asn	Gly	Lys
		195					200					205			
Tyr	Arg	Asp	Thr	Val	Arg	Asp	Phe	Trp	Arg	Gly	Glu	Pro	Ala	Thr	Leu
	210					215					220				
Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser	Asp	Leu	Tyr	Ala	Asn
225					230					235					240
Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	Val	Thr	Ala	His	Asp
				245					250					255	
Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	Glu	Lys	His	Asn	Met
			260					265					270		
Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	His	Asn	Arg	Ser	Trp
		275					280					285			
Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	Glu	Ile	Met	Gln	Leu
	290					295					300				
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Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	Ala	Arg	Thr	Gln	Asn
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Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	Leu	Ala	Trp	Val	Asn
			340					345					350		
Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	Ser	Phe	Thr	Arg	Arg
		355					360					365			
Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	Arg	Arg	Arg	Gln	Phe
	370					375					380				
Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	Asp	Arg	Asp	Ile	Ala
385					390				395						400
Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	Asp	Asp	Trp	Asp	Phe
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			420					425					430		
Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	Asp	Ser	Phe	Ile	Leu
		435					440					445			
Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe	Asn	Leu	Pro	Pro	Glu
	450					455					460				
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465					470					475					480
Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala	Gly	Gly	Thr	Ile	Thr
				485					490					495	
Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln	Val	Glu	Ala	Pro	Asp
			500					505					510		

Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu Lys Arg Glu Gln Glu
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 Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg Glu Leu Glu Leu Ala
 530 535 540
 Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala Leu His Leu Ala Ala
 545 550 555 560
 Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala His Gln His Gly Ala
 565 570 575
 Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro Gln Glu Leu Pro Gln
 580 585 590
 Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro Asp Thr Glu Pro Asp
 595 600 605
 Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala Ser Glu Glu Pro Glu
 610 615 620
 Ala Asp Glu Glu Glu Lys
 625 630

<210> 365
 <211> 1496
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1473)
 <223> FRXA01884

<400> 365
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 Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
 1 5 10 15
 gaa ttt gat gat gtt gac cgc ctg gca acc ttc ttc gac ctg gtc caa 96
 Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln
 20 25 30
 caa gac ccg gtg gtc tcc cag gtc aag ctc att gct gag ccg tgg gat 144
 Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp
 35 40 45
 gtt ggc gaa ggc gga tac caa gtg ggt aac ttc cca cca ctg tgg act 192
 Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr
 50 55 60
 gag tgg aac ggt aaa tac cgc gac act gtc cgt gat ttc tgg cgt ggt 240
 Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly
 65 70 75 80
 gag cca gca acc ttg ggt gaa ttc gct tcc cga cta act ggt tcc tct 288
 Glu Pro Ala Thr Leu Gly Glu Phe Ala Ser Arg Leu Thr Gly Ser Ser
 85 90 95

gat	ttg	tat	gca	aac	aac	ggc	cgt	cgc	ccc	act	gca	tcg	atc	aac	ttt	336
Asp	Leu	Tyr	Ala	Asn	Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe	
			100					105					110			
gtg	act	gct	cac	gac	ggc	ttc	acc	ctc	aat	gac	ttg	gtc	agt	tac	aac	384
Val	Thr	Ala	His	Asp	Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn	
		115					120					125				
gag	aag	cac	aac	atg	gcc	aac	ggg	gaa	gac	ggg	cgg	gac	ggg	gaa	tca	432
Glu	Lys	His	Asn	Met	Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser	
	130					135					140					
cac	aac	cgt	tcc	tgg	aac	tgt	ggc	gtc	gaa	gga	cca	act	gac	gat	cct	480
His	Asn	Arg	Ser	Trp	Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro	
145					150					155					160	
gag	att	atg	cag	ctg	cgt	gct	cag	caa	cga	cgc	aac	ttc	ctc	acc	acc	528
Glu	Ile	Met	Gln	Leu	Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr	
			165						170					175		
ttg	ttg	ctg	tcc	cag	ggc	acc	cct	atg	ttg	tcc	cac	ggg	gat	gaa	atg	576
Leu	Leu	Leu	Ser	Gln	Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met	
			180				185						190			
gcc	cgt	acc	caa	aac	ggc	aac	aac	aac	gtc	tac	tgc	caa	gac	aat	gaa	624
Ala	Arg	Thr	Gln	Asn	Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu	
		195					200					205				
ctg	gcg	tgg	gtg	aat	tgg	gat	cag	gct	gaa	gaa	aac	gct	gac	ttg	gtg	672
Leu	Ala	Trp	Val	Asn	Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val	
	210					215					220					
agc	ttc	acc	agg	cgt	ttg	ctg	cgt	atc	cga	gca	aac	cac	cca	gta	ttt	720
Ser	Phe	Thr	Arg	Arg	Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe	
225					230					235					240	
agg	cgc	agg	cag	ttc	ctt	gcc	ggg	ggc	cct	ttg	ggc	gcc	gat	gtt	cgt	768
Arg	Arg	Arg	Gln	Phe	Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg	
			245					250						255		
gac	cgc	gat	atc	gca	tgg	ctg	gta	cca	aat	gga	acc	ttg	atg	act	caa	816
Asp	Arg	Asp	Ile	Ala	Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln	
			260				265						270			
gat	gac	tgg	gac	ttc	gct	ttc	ggg	aaa	tca	ctg	cag	gtg	ttc	ttc	aac	864
Asp	Asp	Trp	Asp	Phe	Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn	
		275					280					285				
ggc	gat	gcc	atc	gaa	gag	cct	gat	tat	cga	gga	cag	aaa	atc	cac	gat	912
Gly	Asp	Ala	Ile	Glu	Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp	
	290					295					300					
gac	tcc	ttc	atc	ttg	atg	ttc	aac	gct	cac	ttc	gaa	cct	atc	gat	ttc	960
Asp	Ser	Phe	Ile	Leu	Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe	
305					310					315					320	
aat	ctc	cct	cct	gag	cat	ttc	ggg	atg	aag	tgg	aag	ctt	ttg	gtc	gat	1008
Asn	Leu	Pro	Pro	Glu	His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp	
				325				330						335		
acc	acc	gaa	gcg	gtg	ggc	cac	ccg	ctg	gag	gat	ctc	acc	atc	gaa	gct	1056

Thr Thr Glu Ala Val Gly His Pro Leu Glu Asp Leu Thr Ile Glu Ala
 340 345 350
 ggc gga acc atc act gtt cct gcc cgt tcc acg atg ctg ctg cgc cag 1104
 Gly Gly Thr Ile Thr Val Pro Ala Arg Ser Thr Met Leu Leu Arg Gln
 355 360 365
 gtg gag gct ccg gac tac acc aag ctt gag gaa aag atc gct gct gaa 1152
 Val Glu Ala Pro Asp Tyr Thr Lys Leu Glu Glu Lys Ile Ala Ala Glu
 370 375 380
 aag cgt gag caa gaa ctt gcg gca gag aag gaa gct gct gag aag cgc 1200
 Lys Arg Glu Gln Glu Leu Ala Ala Glu Lys Glu Ala Ala Glu Lys Arg
 385 390 395 400
 gaa ttg gaa ctg gcg gca gca aag gaa gct gaa gat gct gct gag gct 1248
 Glu Leu Glu Leu Ala Ala Ala Lys Glu Ala Glu Asp Ala Ala Glu Ala
 405 410 415
 ctc cac ctt gcg gca gaa cgt gct tcc act cag gaa gct gaa ttg gcc 1296
 Leu His Leu Ala Ala Glu Arg Ala Ser Thr Gln Glu Ala Glu Leu Ala
 420 425 430
 cat caa cac ggt gct gat gcg att gcc gat gag gta gcg gaa gaa cca 1344
 His Gln His Gly Ala Asp Ala Ile Ala Asp Glu Val Ala Glu Glu Pro
 435 440 445
 caa gag ctg cca caa gat gaa gta gcg gca gag gtc gag act gag ccc 1392
 Gln Glu Leu Pro Gln Asp Glu Val Ala Ala Glu Val Glu Thr Glu Pro
 450 455 460
 gac acc gag cct gac act gaa tct gac tcc gag cag gct gag gta gct 1440
 Asp Thr Glu Pro Asp Thr Glu Ser Asp Ser Glu Gln Ala Glu Val Ala
 465 470 475 480
 tca gag gag cct gaa gcg gac gaa gaa gag aag tagtacaccg aaagtggcgt 1493
 Ser Glu Glu Pro Glu Ala Asp Glu Glu Glu Lys
 485 490
 cgc 1496

<210> 366

<211> 491

<212> PRT

<213> Corynebacterium glutamicum

<400> 366

Met His Val Asp Gly Phe Arg Phe Asp Leu Ala Ser Thr Leu Ala Arg
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Glu Phe Asp Asp Val Asp Arg Leu Ala Thr Phe Phe Asp Leu Val Gln
 20 25 30

Gln Asp Pro Val Val Ser Gln Val Lys Leu Ile Ala Glu Pro Trp Asp
 35 40 45

Val Gly Glu Gly Gly Tyr Gln Val Gly Asn Phe Pro Pro Leu Trp Thr
 50 55 60

Glu Trp Asn Gly Lys Tyr Arg Asp Thr Val Arg Asp Phe Trp Arg Gly

65	70					75					80				
Glu	Pro	Ala	Thr	Leu	Gly	Glu	Phe	Ala	Ser	Arg	Leu	Thr	Gly	Ser	Ser
				85					90					95	
Asp	Leu	Tyr	Ala	Asn	Asn	Gly	Arg	Arg	Pro	Thr	Ala	Ser	Ile	Asn	Phe
			100					105					110		
Val	Thr	Ala	His	Asp	Gly	Phe	Thr	Leu	Asn	Asp	Leu	Val	Ser	Tyr	Asn
		115					120					125			
Glu	Lys	His	Asn	Met	Ala	Asn	Gly	Glu	Asp	Gly	Arg	Asp	Gly	Glu	Ser
	130					135					140				
His	Asn	Arg	Ser	Trp	Asn	Cys	Gly	Val	Glu	Gly	Pro	Thr	Asp	Asp	Pro
145					150					155					160
Glu	Ile	Met	Gln	Leu	Arg	Ala	Gln	Gln	Arg	Arg	Asn	Phe	Leu	Thr	Thr
				165					170					175	
Leu	Leu	Leu	Ser	Gln	Gly	Thr	Pro	Met	Leu	Ser	His	Gly	Asp	Glu	Met
			180					185					190		
Ala	Arg	Thr	Gln	Asn	Gly	Asn	Asn	Asn	Val	Tyr	Cys	Gln	Asp	Asn	Glu
		195					200					205			
Leu	Ala	Trp	Val	Asn	Trp	Asp	Gln	Ala	Glu	Glu	Asn	Ala	Asp	Leu	Val
	210					215					220				
Ser	Phe	Thr	Arg	Arg	Leu	Leu	Arg	Ile	Arg	Ala	Asn	His	Pro	Val	Phe
225					230				235						240
Arg	Arg	Arg	Gln	Phe	Leu	Ala	Gly	Gly	Pro	Leu	Gly	Ala	Asp	Val	Arg
				245					250					255	
Asp	Arg	Asp	Ile	Ala	Trp	Leu	Val	Pro	Asn	Gly	Thr	Leu	Met	Thr	Gln
			260					265					270		
Asp	Asp	Trp	Asp	Phe	Ala	Phe	Gly	Lys	Ser	Leu	Gln	Val	Phe	Phe	Asn
		275					280				285				
Gly	Asp	Ala	Ile	Glu	Glu	Pro	Asp	Tyr	Arg	Gly	Gln	Lys	Ile	His	Asp
	290					295					300				
Asp	Ser	Phe	Ile	Leu	Met	Phe	Asn	Ala	His	Phe	Glu	Pro	Ile	Asp	Phe
305					310					315					320
Asn	Leu	Pro	Pro	Glu	His	Phe	Gly	Met	Lys	Trp	Lys	Leu	Leu	Val	Asp
				325					330					335	
Thr	Thr	Glu	Ala	Val	Gly	His	Pro	Leu	Glu	Asp	Leu	Thr	Ile	Glu	Ala
			340					345					350		
Gly	Gly	Thr	Ile	Thr	Val	Pro	Ala	Arg	Ser	Thr	Met	Leu	Leu	Arg	Gln
		355					360					365			
Val	Glu	Ala	Pro	Asp	Tyr	Thr	Lys	Leu	Glu	Glu	Lys	Ile	Ala	Ala	Glu
	370					375					380				
Lys	Arg	Glu	Gln	Glu	Leu	Ala	Ala	Glu	Lys	Glu	Ala	Ala	Glu	Lys	Arg
385					390					395					400

<400> 367															
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Met Thr Ser Thr Ile 5															
gag cac tcg tac caa gtt tgg cct gga cat gct tat cct ctg ggt tca 163															
Glu His Ser Tyr Gln Val Trp Pro Gly His Ala Tyr Pro Leu Gly Ser 20															
acc tat gac ggt gct gga acg aac ttc gca ctc ttc tcc gac gtt gca 211															
Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu Phe Ser Asp Val Ala 35															
gag cgt gtt gag ctg tgt cta tta gat gca gat aac aac gag act cga 259															
Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp Asn Asn Glu Thr Arg 50															
att cca ctc gaa gag cgc gat gcc cac att tgg cat tgc tac ctt cct 307															
Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp His Cys Tyr Leu Pro 65															
ggc gtt caa cct gga cag cgc tac gga ttc cga gtt cat ggc ccg tgg 355															
Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg Val His Gly Pro Trp 85															
aac cca gat gag ggt aag cgg tgc gac gcg aac aaa ctt cta gtt gat 403															
Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn Lys Leu Leu Val Asp 100															

ccc tat gct cgt gct ttc gat gga gat ttt gat gga cat ccg tca cta 451
 Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp Gly His Pro Ser Leu
 105 110 115

ttt tct tac gac atc acc aat cca aat gac ccc aac ggt cgc aat acc 499
 Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro Asn Gly Arg Asn Thr
 120 125 130

gaa gac agc att gat cac aca atg aag tct gtc gtg gtg aac cca ttc 547
 Glu Asp Ser Ile Asp His Thr Met Lys Ser Val Val Val Asn Pro Phe
 135 140 145

<210> 368

<211> 149

<212> PRT

<213> Corynebacterium glutamicum

<400> 368

Met Thr Ser Thr Ile Glu His Ser Tyr Gln Val Trp Pro Gly His Ala
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Tyr Pro Leu Gly Ser Thr Tyr Asp Gly Ala Gly Thr Asn Phe Ala Leu
 20 25 30

Phe Ser Asp Val Ala Glu Arg Val Glu Leu Cys Leu Leu Asp Ala Asp
 35 40 45

Asn Asn Glu Thr Arg Ile Pro Leu Glu Glu Arg Asp Ala His Ile Trp
 50 55 60

His Cys Tyr Leu Pro Gly Val Gln Pro Gly Gln Arg Tyr Gly Phe Arg
 65 70 75 80

Val His Gly Pro Trp Asn Pro Asp Glu Gly Lys Arg Cys Asp Ala Asn
 85 90 95

Lys Leu Leu Val Asp Pro Tyr Ala Arg Ala Phe Asp Gly Asp Phe Asp
 100 105 110

Gly His Pro Ser Leu Phe Ser Tyr Asp Ile Thr Asn Pro Asn Asp Pro
 115 120 125

Asn Gly Arg Asn Thr Glu Asp Ser Ile Asp His Thr Met Lys Ser Val
 130 135 140

Val Val Asn Pro Phe
 145

<210> 369

<211> 1635

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1612)

<223> RXN01550

<400> 369

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cgcaccacaa ggacctcagc aactttgccg agttcactcc gtg cag ctc aat gac 115
                               Val Gln Leu Asn Asp
                               1                               5

act cac cca gtg ttg gct atc cct gag ctt atg cgt ctg ctc atg gac 163
Thr His Pro Val Leu Ala Ile Pro Glu Leu Met Arg Leu Leu Met Asp
                               10                               15                               20

gag cat gac atg ggc tgg gaa gaa tcc tgg gca atc gtg ttc aag acc 211
Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala Ile Val Phe Lys Thr
                               25                               30                               35

ttc gca tac acc aac cac acc gtg ctc acc gaa gct ctt gag cag tgg 259
Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu Ala Leu Glu Gln Trp
                               40                               45                               50

gat cag cag atc ttc caa cag ctg ttc tgg cgc gtg tgg gaa atc atc 307
Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg Val Trp Glu Ile Ile
                               55                               60                               65

aca gag atc gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg 355
Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu
                               70                               75                               80                               85

gat gaa gag acc atc gac cgc atg gct cca atc cag cac ggc act gtt 403
Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile Gln His Gly Thr Val
                               90                               95                               100

cat atg gca tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg 451
His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val
                               105                               110                               115

gca gcg ctg cac acc gag atc atc aag gcc gag acc ttg gct gac tgg 499
Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp
                               120                               125                               130

tac gca ctg tgg cca gag aag ttc aac aac aag act aac ggt gtt acc 547
Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr
                               135                               140                               145

cca cgc cgt tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc 595
Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu
                               150                               155                               160                               165

act cga ctt tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg 643
Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu
                               170                               175                               180

aag aag ctg cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc 691
Lys Lys Leu Arg Ser Tyr Ala Asp Lys Ser Val Leu Glu Glu Leu
                               185                               190                               195

cgc gct atc aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc 739
Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu
                               200                               205                               210

gag cgc cag ggc att gag att gat cca gaa tcc atc ttt gac gtg cag 787
Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln
                               215                               220                               225

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att aag cgc ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr 230 235 240 245	835
gta cta gac ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile 250 255 260	883
cca gca cgc act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val 265 270 275	931
cgc gcc aag gcg att atc aag ctc atc aac tct att gct gac ttg gta Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val 280 285 290	979
aac aac gat cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu 295 300 305	1027
aac tac aac gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val 310 315 320 325	1075
tcc gaa cag att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn 330 335 340	1123
atg aag ttc atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly 345 350 355	1171
gcc aac gta gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile 360 365 370	1219
ttc ggt gct cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu 375 380 385	1267
cca tat gag ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp 390 395 400 405	1315
gcc ctg gat aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr 410 415 420	1363
gac ctc aag cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp 425 430 435	1411
acc tac tac gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp 440 445 450	1459
cgt atg gcc gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met 455 460 465	1507

gcc tgg atc aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc 1555
 Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr
 470 475 480 485

atc cgc gat tat gcc acc gag atc tgg aag ctc gag cca act cct gct 1603
 Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala
 490 495 500

gtt aag aag taggttttaa cctccgcttc taa 1635
 Val Lys Lys

<210> 370

<211> 504

<212> PRT

<213> Corynebacterium glutamicum

<400> 370

Val Gln Leu Asn Asp Thr His Pro Val Leu Ala Ile Pro Glu Leu Met
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Arg Leu Leu Met Asp Glu His Asp Met Gly Trp Glu Glu Ser Trp Ala
 20 25 30

Ile Val Phe Lys Thr Phe Ala Tyr Thr Asn His Thr Val Leu Thr Glu
 35 40 45

Ala Leu Glu Gln Trp Asp Gln Gln Ile Phe Gln Gln Leu Phe Trp Arg
 50 55 60

Val Trp Glu Ile Ile Thr Glu Ile Asp Arg Arg Phe Arg Leu Glu Arg
 65 70 75 80

Ala Ala Asp Gly Leu Asp Glu Glu Thr Ile Asp Arg Met Ala Pro Ile
 85 90 95

Gln His Gly Thr Val His Met Ala Trp Ile Ala Cys Tyr Ala Ala Tyr
 100 105 110

Ser Ile Asn Gly Val Ala Ala Leu His Thr Glu Ile Ile Lys Ala Glu
 115 120 125

Thr Leu Ala Asp Trp Tyr Ala Leu Trp Pro Glu Lys Phe Asn Asn Lys
 130 135 140

Thr Asn Gly Val Thr Pro Arg Arg Trp Leu Arg Met Ile Asn Pro Gly
 145 150 155 160

Leu Ser Asp Leu Leu Thr Arg Leu Ser Gly Ser Asp Asp Trp Val Thr
 165 170 175

Asp Leu Asp Glu Leu Lys Lys Leu Arg Ser Tyr Ala Asp Asp Lys Ser
 180 185 190

Val Leu Glu Glu Leu Arg Ala Ile Lys Ala Ala Asn Lys Gln Asp Phe
 195 200 205

Ala Glu Trp Ile Leu Glu Arg Gln Gly Ile Glu Ile Asp Pro Glu Ser
 210 215 220

Ile Phe Asp Val Gln Ile Lys Arg Leu His Glu Tyr Lys Arg Gln Leu
 225 230 235 240
 Met Asn Ala Leu Tyr Val Leu Asp Leu Tyr Phe Arg Ile Lys Glu Asp
 245 250 255
 Gly Leu Thr Asp Ile Pro Ala Arg Thr Val Ile Phe Gly Ala Lys Ala
 260 265 270
 Ala Pro Gly Tyr Val Arg Ala Lys Ala Ile Ile Lys Leu Ile Asn Ser
 275 280 285
 Ile Ala Asp Leu Val Asn Asn Asp Pro Glu Val Ser Pro Leu Leu Lys
 290 295 300
 Val Val Phe Val Glu Asn Tyr Asn Val Ser Pro Ala Glu His Ile Leu
 305 310 315 320
 Pro Ala Ser Asp Val Ser Glu Gln Ile Ser Thr Ala Gly Lys Glu Ala
 325 330 335
 Ser Gly Thr Ser Asn Met Lys Phe Met Met Asn Gly Ala Leu Thr Leu
 340 345 350
 Gly Thr Met Asp Gly Ala Asn Val Glu Ile Val Asp Ser Val Gly Glu
 355 360 365
 Glu Asn Ala Tyr Ile Phe Gly Ala Arg Val Glu Glu Leu Pro Ala Leu
 370 375 380
 Arg Glu Ser Tyr Glu Pro Tyr Glu Leu Tyr Glu Thr Val Pro Gly Leu
 385 390 395 400
 Lys Arg Ala Leu Asp Ala Leu Asp Asn Gly Thr Leu Asn Asp Asn Asn
 405 410 415
 Ser Gly Leu Phe Tyr Asp Leu Lys His Ser Leu Ile His Gly Tyr Gly
 420 425 430
 Lys Asp Ala Ser Asp Thr Tyr Tyr Val Leu Gly Asp Phe Ala Asp Tyr
 435 440 445
 Arg Glu Thr Arg Asp Arg Met Ala Ala Asp Tyr Ala Ser Asp Pro Leu
 450 455 460
 Gly Trp Ala Arg Met Ala Trp Ile Asn Ile Cys Glu Ser Gly Arg Phe
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 Ser Ser Asp Arg Thr Ile Arg Asp Tyr Ala Thr Glu Ile Trp Lys Leu
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 Glu Pro Thr Pro Ala Val Lys Lys
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<210> 371

<211> 1367

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (1)..(1344)
 <223> FRXA01550

<400> 371

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gat cgc cgc ttc cgt ttg gag cgc gca gcc gat gga ctg gat gaa gag	96
Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu	
20 25 30	
acc atc gac cgc atg gct cca atc cag cgc ggc act gtt cat atg gca	144
Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala	
35 40 45	
tgg att gcc tgt tac gcg gca tat tcc atc aat ggc gtg gca gcg ctg	192
Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu	
50 55 60	
cac acc gag atc atc aag gcc gag acc ttg gct gac tgg tac gca ctg	240
His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu	
65 70 75 80	
tgg cca gag aag ttc aac aac aag act aac ggt gtt acc cca cgc cgt	288
Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg	
85 90 95	
tgg ctg cgc atg atc aac cca ggt ctg tct gac ctg ctc act cga ctt	336
Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu	
100 105 110	
tcc ggt tcc gat gat tgg gta acc gat ctg gat gag ctg aag aag ctg	384
Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu	
115 120 125	
cgc tcc tat gcc gac gat aag tcc gtg ctt gaa gaa ctc cgc gct atc	432
Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile	
130 135 140	
aag gct gct aat aag caa gac ttc gcc gag tgg atc ctc gag cgc cag	480
Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln	
145 150 155 160	
ggc att gag att gat cca gaa tcc atc ttt gac gtg cag att aag cgc	528
Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg	
165 170 175	
ctc cac gag tac aag cgc cag ctc atg aac gcg ctc tac gta cta gac	576
Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp	
180 185 190	
ctt tac ttc cgt att aag gaa gat ggc ctc acc gac atc cca gca cgc	624
Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg	
195 200 205	
act gtc atc ttt ggc gcc aag gcc gcg ccg ggt tat gtc cgc gcc aag	672
Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys	
210 215 220	

gcg att atc aag ctc atc aac tct att gct gac ttg gta aac aac gat 720
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
 225 230 235 240

cct gag gtc tcc ccg ctg ctc aag gtg gtc ttt gta gag aac tac aac 768
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
 245 250 255

gtc tcc cct gct gag cac atc ttg cct gcg tct gat gtc tcc gaa cag 816
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
 260 265 270

att tcc acc gcc ggc aag gaa gcc agc ggt acc tcc aac atg aag ttc 864
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
 275 280 285

atg atg aac ggc gcc ctc acc ctg ggc acc atg gac ggc gcc aac gta 912
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
 290 295 300

gag atc gtg gat tct gtg ggc gag gaa aac gcc tat atc ttc ggt gct 960
 Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
 305 310 315 320

cgc gtg gaa gaa ttg cca gcc ctg cgc gaa agc tac gag cca tat gag 1008
 Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
 325 330 335

ctc tat gag acc gtc cct ggc ctc aag cgc gca ttg gac gcc ctg gat 1056
 Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
 340 345 350

aac ggc acc ctc aac gac aac aac agt ggt ttg ttc tac gac ctc aag 1104
 Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
 355 360 365

cat tcc ttg atc cac ggt tat gga aaa gac gcc agc gac acc tac tac 1152
 His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
 370 375 380

gtg ctt ggc gat ttc gca gat tac cgc gag acc cgc gac cgt atg gcc 1200
 Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
 385 390 395 400

gcc gac tac gcc tcc gat ccc ctg ggt tgg gca cgc atg gcc tgg atc 1248
 Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
 405 410 415

aac att tgc gag tcc ggc cgt ttc tcc tcc gac cgc acc atc cgc gat 1296
 Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
 420 425 430

tat gcc acc gag atc tgg aag ctc gag cca act cct gct gtt aag aag 1344
 Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
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taggttttaa cctccgcttc taa 1367

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<211> 448

<212> PRT

<213> Corynebacterium glutamicum

<400> 372

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 Asp Arg Arg Phe Arg Leu Glu Arg Ala Ala Asp Gly Leu Asp Glu Glu
 20 25 30
 Thr Ile Asp Arg Met Ala Pro Ile Gln Arg Gly Thr Val His Met Ala
 35 40 45
 Trp Ile Ala Cys Tyr Ala Ala Tyr Ser Ile Asn Gly Val Ala Ala Leu
 50 55 60
 His Thr Glu Ile Ile Lys Ala Glu Thr Leu Ala Asp Trp Tyr Ala Leu
 65 70 75 80
 Trp Pro Glu Lys Phe Asn Asn Lys Thr Asn Gly Val Thr Pro Arg Arg
 85 90 95
 Trp Leu Arg Met Ile Asn Pro Gly Leu Ser Asp Leu Leu Thr Arg Leu
 100 105 110
 Ser Gly Ser Asp Asp Trp Val Thr Asp Leu Asp Glu Leu Lys Lys Leu
 115 120 125
 Arg Ser Tyr Ala Asp Asp Lys Ser Val Leu Glu Glu Leu Arg Ala Ile
 130 135 140
 Lys Ala Ala Asn Lys Gln Asp Phe Ala Glu Trp Ile Leu Glu Arg Gln
 145 150 155 160
 Gly Ile Glu Ile Asp Pro Glu Ser Ile Phe Asp Val Gln Ile Lys Arg
 165 170 175
 Leu His Glu Tyr Lys Arg Gln Leu Met Asn Ala Leu Tyr Val Leu Asp
 180 185 190
 Leu Tyr Phe Arg Ile Lys Glu Asp Gly Leu Thr Asp Ile Pro Ala Arg
 195 200 205
 Thr Val Ile Phe Gly Ala Lys Ala Ala Pro Gly Tyr Val Arg Ala Lys
 210 215 220
 Ala Ile Ile Lys Leu Ile Asn Ser Ile Ala Asp Leu Val Asn Asn Asp
 225 230 235 240
 Pro Glu Val Ser Pro Leu Leu Lys Val Val Phe Val Glu Asn Tyr Asn
 245 250 255
 Val Ser Pro Ala Glu His Ile Leu Pro Ala Ser Asp Val Ser Glu Gln
 260 265 270
 Ile Ser Thr Ala Gly Lys Glu Ala Ser Gly Thr Ser Asn Met Lys Phe
 275 280 285
 Met Met Asn Gly Ala Leu Thr Leu Gly Thr Met Asp Gly Ala Asn Val
 290 295 300

Glu Ile Val Asp Ser Val Gly Glu Glu Asn Ala Tyr Ile Phe Gly Ala
305 310 315 320

Arg Val Glu Glu Leu Pro Ala Leu Arg Glu Ser Tyr Glu Pro Tyr Glu
325 330 335

Leu Tyr Glu Thr Val Pro Gly Leu Lys Arg Ala Leu Asp Ala Leu Asp
340 345 350

Asn Gly Thr Leu Asn Asp Asn Asn Ser Gly Leu Phe Tyr Asp Leu Lys
355 360 365

His Ser Leu Ile His Gly Tyr Gly Lys Asp Ala Ser Asp Thr Tyr Tyr
370 375 380

Val Leu Gly Asp Phe Ala Asp Tyr Arg Glu Thr Arg Asp Arg Met Ala
385 390 395 400

Ala Asp Tyr Ala Ser Asp Pro Leu Gly Trp Ala Arg Met Ala Trp Ile
405 410 415

Asn Ile Cys Glu Ser Gly Arg Phe Ser Ser Asp Arg Thr Ile Arg Asp
420 425 430

Tyr Ala Thr Glu Ile Trp Lys Leu Glu Pro Thr Pro Ala Val Lys Lys
435 440 445

<210> 373

<211> 2348

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(2325)

<223> RXN02100

<400> 373

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Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
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gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96
Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
20 25 30

gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144
Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
35 40 45

ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192
Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
50 55 60

aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240
Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
65 70 75 80

tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln 85 90 95	288
cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala 100 105 110	336
gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro 115 120 125	384
ggc gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg 130 135 140	432
atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu 145 150 155 160	480
ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg 165 170 175	528
atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn 180 185 190	576
gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu 195 200 205	624
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220	672
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240	720
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255	768
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu 260 265 270	816
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285	864
ggc caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300	912
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320	960

agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa	1008
Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu	
325 330 335	
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc	1056
Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val	
340 345 350	
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat	1104
Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp	
355 360 365	
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag	1152
Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu	
370 375 380	
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt	1200
Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val	
385 390 395 400	
gct cgc gct gca act gca aag tcc tgg tct cac cgt gga cac acc gaa	1248
Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu	
405 410 415	
gca gaa ctt gcg tgg acc tcc cgc gtt ctg gat cca aac gtg ctg acc	1296
Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr	
420 425 430	
att ggt ttc gca cgt cgc gta tcc acc tac aag cgc ttg acc ttg atg	1344
Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met	
435 440 445	
ctg cgc aac cct gaa cgc ctg cgt tcc atc ttg ctt aat gag gaa cgc	1392
Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg	
450 455 460	
cca gtt cag ttc gtt att gct ggt aag gca cac cca cat gac atg ggt	1440
Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly	
465 470 475 480	
ggc aag aag ctc atg cag gaa atc gtc cac ttc gct gat caa gct ggt	1488
Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly	
485 490 495	
gtc cgt gac cgt ttc ctc ttc ctg cct gat tac gac atc aac ctg gcc	1536
Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala	
500 505 510	
agc tac ctg atc tct ggt gct gac gtg tgg ctg aac aac cca gtg cgc	1584
Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg	
515 520 525	
cct cag gaa gca tcg gga acc tcc ggt atg aag gcc gtc atg aat ggt	1632
Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly	
530 535 540	
ggc ctg acc ctg tcc atc tct gat ggt tgg tgg gat gaa atg cct aag	1680
Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys	
545 550 555 560	
gag acc acc ggc tgg acc atc cca acc gtt gag tcc cag gac ttg gaa	1728

Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu	
565 570 575	
tgc cgc gac cac ctg gaa tcc cag gcg ctg tac gac ctg ctg gaa aac	1776
Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn	
580 585 590	
gaa gtt gca ccg ctg ttt tac aag cgc gac aag aac ggc atc cca cag	1824
Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln	
595 600 605	
gac tgg ctg gac ctg gtt cgc gaa tcc tgg acc acc ctg tca cca atg	1872
Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met	
610 615 620	
gtc acc tcc acc cgc atg gtg cgc gac tac acc acc cag tac tac cgc	1920
Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg	
625 630 635 640	
cca acc aaa cac cag gca gag ctc att gcg cag cct gca gaa gca gcg	1968
Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala	
645 650 655	
gat tac gcg gca tgg ctt gag cac atc aaa gca gag tgg gct ggc gtc	2016
Asp Tyr Ala Ala Trp Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val	
660 665 670	
aag gtc tca gac ctg aag atc agc gag agc gcc atc acg gcg cag gag	2064
Lys Val Ser Asp Leu Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu	
675 680 685	
ctt gaa gtc agc gtt cgc gtt gat tcc ggt tgc ctt aac gac gac gag	2112
Leu Glu Val Ser Val Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu	
690 695 700	
ttc caa gct cag gca ctc ttt ggt gcg ctc gga cac aac ggt gac atc	2160
Phe Gln Ala Gln Ala Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile	
705 710 715 720	
gaa gat cca gaa atc acc gtt ttg acc cca cgc ggc gat ggc gcc tac	2208
Glu Asp Pro Glu Ile Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr	
725 730 735	
gcg gca aag gtc agc act gac ctg cca ggc aac tac ggc atc act gcc	2256
Ala Ala Lys Val Ser Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala	
740 745 750	
cgc gtt gtt cca aac aac agg atg ctg gtc agc cca gcg gaa acc cgc	2304
Arg Val Val Pro Asn Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg	
755 760 765	
ctg atc acc tac ttg gag aac tagggcgaaa ctagctttac caa	2348
Leu Ile Thr Tyr Leu Glu Asn	
770 775	

<210> 374

<211> 775

<212> PRT

<213> Corynebacterium glutamicum

<400> 374

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 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
 85 90 95
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
 100 105 110
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
 115 120 125
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
 130 135 140
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
 145 150 155 160
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
 165 170 175
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val
 305 310 315 320

Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu
 325 330 335
 Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val
 340 345 350
 Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp
 355 360 365
 Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu
 370 375 380
 Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val
 385 390 395 400
 Ala Arg Ala Ala Thr Ala Lys Ser Trp Ser His Arg Gly His Thr Glu
 405 410 415
 Ala Glu Leu Ala Trp Thr Ser Arg Val Leu Asp Pro Asn Val Leu Thr
 420 425 430
 Ile Gly Phe Ala Arg Arg Val Ser Thr Tyr Lys Arg Leu Thr Leu Met
 435 440 445
 Leu Arg Asn Pro Glu Arg Leu Arg Ser Ile Leu Leu Asn Glu Glu Arg
 450 455 460
 Pro Val Gln Phe Val Ile Ala Gly Lys Ala His Pro His Asp Met Gly
 465 470 475 480
 Gly Lys Lys Leu Met Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly
 485 490 495
 Val Arg Asp Arg Phe Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala
 500 505 510
 Ser Tyr Leu Ile Ser Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg
 515 520 525
 Pro Gln Glu Ala Ser Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly
 530 535 540
 Gly Leu Thr Leu Ser Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys
 545 550 555 560
 Glu Thr Thr Gly Trp Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu
 565 570 575
 Cys Arg Asp His Leu Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn
 580 585 590
 Glu Val Ala Pro Leu Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln
 595 600 605
 Asp Trp Leu Asp Leu Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met
 610 615 620
 Val Thr Ser Thr Arg Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg
 625 630 635 640
 Pro Thr Lys His Gln Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala

645										650					655				
Asp	Tyr	Ala	Ala	Trp	Leu	Glu	His	Ile	Lys	Ala	Glu	Trp	Ala	Gly	Val				
			660					665					670						
Lys	Val	Ser	Asp	Leu	Lys	Ile	Ser	Glu	Ser	Ala	Ile	Thr	Ala	Gln	Glu				
		675					680					685							
Leu	Glu	Val	Ser	Val	Arg	Val	Asp	Ser	Gly	Ser	Leu	Asn	Asp	Asp	Glu				
	690					695					700								
Phe	Gln	Ala	Gln	Ala	Leu	Phe	Gly	Ala	Leu	Gly	His	Asn	Gly	Asp	Ile				
705					710				715						720				
Glu	Asp	Pro	Glu	Ile	Thr	Val	Leu	Thr	Pro	Arg	Gly	Asp	Gly	Ala	Tyr				
				725				730						735					
Ala	Ala	Lys	Val	Ser	Thr	Asp	Leu	Pro	Gly	Asn	Tyr	Gly	Ile	Thr	Ala				
			740					745					750						
Arg	Val	Val	Pro	Asn	Asn	Arg	Met	Leu	Val	Ser	Pro	Ala	Glu	Thr	Arg				
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Leu	Ile	Thr	Tyr	Leu	Glu	Asn													
	770					775													

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 <213> Corynebacterium glutamicum

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 <222> (1)..(918)
 <223> FRXA02100

<400> 375																				
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Ile	Ala	Gly	Lys	Ala	His	Pro	His	Asp	Met	Gly	Gly	Lys	Lys	Leu	Met					
1				5				10						15						
cag	gaa	atc	gtc	cac	ttc	gct	gat	caa	gct	ggt	gtc	cgt	gac	cgt	ttc					96
Gln	Glu	Ile	Val	His	Phe	Ala	Asp	Gln	Ala	Gly	Val	Arg	Asp	Arg	Phe					
			20					25					30							
ctc	ttc	ctg	cct	gat	tac	gac	atc	aac	ctg	gcc	agc	tac	ctg	atc	tct					144
Leu	Phe	Leu	Pro	Asp	Tyr	Asp	Ile	Asn	Leu	Ala	Ser	Tyr	Leu	Ile	Ser					
			35				40					45								
ggt	gct	gac	gtg	tgg	ctg	aac	aac	cca	gtg	cgc	cct	cag	gaa	gca	tcg					192
Gly	Ala	Asp	Val	Trp	Leu	Asn	Asn	Pro	Val	Arg	Pro	Gln	Glu	Ala	Ser					
	50					55					60									
gga	acc	tcc	ggt	atg	aag	gcc	gtc	atg	aat	ggt	ggc	ctg	acc	ctg	tcc					240
Gly	Thr	Ser	Gly	Met	Lys	Ala	Val	Met	Asn	Gly	Gly	Leu	Thr	Leu	Ser					
	65				70				75						80					
atc	tct	gat	ggt	tgg	tgg	gat	gaa	atg	cct	aag	gag	acc	acc	ggc	tgg					288
Ile	Ser	Asp	Gly	Trp	Trp	Asp	Glu	Met	Pro	Lys	Glu	Thr	Thr	Gly	Trp					
				85				90						95						

acc atc cca acc gtt gag tcc cag gac ttg gaa tgc cgc gac cac ctg 336
 Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
 100 105 110

gaa tcc cag gcg ctg tac gac ctg ctg gaa aac gaa gtt gca ccg ctg 384
 Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
 115 120 125

ttt tac aag cgc gac aag aac ggc atc cca cag gac tgg ctg gac ctg 432
 Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
 130 135 140

gtt cgc gaa tcc tgg acc acc ctg tca cca atg gtc acc tcc acc cgc 480
 Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
 145 150 155 160

atg gtg cgc gac tac acc acc cag tac tac cgc cca acc aaa cac cag 528
 Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
 165 170 175

gca gag ctc att gcg cag cct gca gaa gca gcg gat tac gcg gca tgg 576
 Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
 180 185 190

ctt gag cac atc aaa gca gag tgg gct ggc gtc aag gtc tca gac ctg 624
 Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
 195 200 205

aag atc agc gag agc gcc atc acg gcg cag gag ctt gaa gtc agc gtt 672
 Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
 210 215 220

cgc gtt gat tcc ggt tcg ctt aac gac gac gag ttc caa gct cag gca 720
 Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

ctc ttt ggt gcg ctc gga cac aac ggt gac atc gaa gat cca gaa atc 768
 Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

acc gtt ttg acc cca cgc ggc gat ggc gcc tac gcg gca aag gtc agc 816
 Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

act gac ctg cca ggc aac tac ggc atc act gcc cgc gtt gtt cca aac 864
 Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

aac agg atg ctg gtc agc cca gcg gaa acc cgc ctg atc acc tac ttg 912
 Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300

gag aac tagggcgaaa ctagctttac caa 941
 Glu Asn
 305

<210> 376

<211> 306

<212> PRT

<213> Corynebacterium glutamicum

<400> 376

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Gln Glu Ile Val His Phe Ala Asp Gln Ala Gly Val Arg Asp Arg Phe
 20 25 30

Leu Phe Leu Pro Asp Tyr Asp Ile Asn Leu Ala Ser Tyr Leu Ile Ser
 35 40 45

Gly Ala Asp Val Trp Leu Asn Asn Pro Val Arg Pro Gln Glu Ala Ser
 50 55 60

Gly Thr Ser Gly Met Lys Ala Val Met Asn Gly Gly Leu Thr Leu Ser
 65 70 75 80

Ile Ser Asp Gly Trp Trp Asp Glu Met Pro Lys Glu Thr Thr Gly Trp
 85 90 95

Thr Ile Pro Thr Val Glu Ser Gln Asp Leu Glu Cys Arg Asp His Leu
 100 105 110

Glu Ser Gln Ala Leu Tyr Asp Leu Leu Glu Asn Glu Val Ala Pro Leu
 115 120 125

Phe Tyr Lys Arg Asp Lys Asn Gly Ile Pro Gln Asp Trp Leu Asp Leu
 130 135 140

Val Arg Glu Ser Trp Thr Thr Leu Ser Pro Met Val Thr Ser Thr Arg
 145 150 155 160

Met Val Arg Asp Tyr Thr Thr Gln Tyr Tyr Arg Pro Thr Lys His Gln
 165 170 175

Ala Glu Leu Ile Ala Gln Pro Ala Glu Ala Ala Asp Tyr Ala Ala Trp
 180 185 190

Leu Glu His Ile Lys Ala Glu Trp Ala Gly Val Lys Val Ser Asp Leu
 195 200 205

Lys Ile Ser Glu Ser Ala Ile Thr Ala Gln Glu Leu Glu Val Ser Val
 210 215 220

Arg Val Asp Ser Gly Ser Leu Asn Asp Asp Glu Phe Gln Ala Gln Ala
 225 230 235 240

Leu Phe Gly Ala Leu Gly His Asn Gly Asp Ile Glu Asp Pro Glu Ile
 245 250 255

Thr Val Leu Thr Pro Arg Gly Asp Gly Ala Tyr Ala Ala Lys Val Ser
 260 265 270

Thr Asp Leu Pro Gly Asn Tyr Gly Ile Thr Ala Arg Val Val Pro Asn
 275 280 285

Asn Arg Met Leu Val Ser Pro Ala Glu Thr Arg Leu Ile Thr Tyr Leu
 290 295 300

Glu Asn

305

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 <222> (1)..(1206)
 <223> FRXA02113

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 Leu Gly Arg Ile Asn Ala Glu Glu Gln Asn Leu Ser Glu Tyr Leu Ser
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 gac aag ctg tgg tac cag gac acc gca gat gca acc gat gct gtc gga 96
 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30
 gat cca ctc gtt gcg tac ttc tcc atg gag ttt ggc att cac cca agc 144
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45
 ctg cca atc tac tct ggc gga ctt ggt gtg ctt gcg ggc gag aac atg 192
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60
 aag tct gca tct gac ttg ggt gtg cca ctg atc ggt gtt ggt ttg ctc 240
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80
 tac acc cac ggc tac ttc acc cag tca ctg tcc ggt gac ggt tgg cag 288
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
 85 90 95
 cag gaa gag tac aag tac cac gat cca gca gaa ctg ccg att gag gca 336
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
 100 105 110
 gtt aaa gat aag aac ggc gag cag gtc act gtt tct gtc acc tac cca 384
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
 115 120 125
 ggt gcg cag gaa gta aag att gca ctg tgg gta gca aac gtt ggc cgc 432
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
 130 135 140
 atc cca ttg ctg ctg ctt gat acc aac atc gag gca aac cca gaa gag 480
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
 145 150 155 160
 ctc cgc aac gtt act gac cgc ctg tac ggt ggc gac aat gag cac cgc 528
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
 165 170 175
 atc aag cag gaa ctc gtt ctc ggt gtt ggt ggc gtc cgc gct gtc aac 576
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190

gca ttc tgc gaa gct cgt ggt ctg aag cgc tca tct gtt gca cac ctc Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu 195 200 205	624
aac gaa ggc cac gca ggt ttc ctg acc ctg gag cgt atc cgc gag cgc Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg 210 215 220	672
atc gca gag ggc atg gag tac cca gca gca ttc gag cag gtt cgt gcg Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala 225 230 235 240	720
tcc aac atc ttc acc acc cac acc cca gtc cca gca ggc atc gac cgc Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg 245 250 255	768
ttc gac atg gag atg gtg cgt cgt tat ctc ggt ggc ggt cag cca gaa Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu 260 265 270	816
gat cag cag ctg tgc gtt ggt gtt cca att gag aag gca ctt gag ctt Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu 275 280 285	864
ggt caa gag tcc gat cca cac cgc ttc aac atg gct cat atg ggc ctt Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu 290 295 300	912
cgc gcg agc caa cat gct aat ggc gtc gca aag ctt cat ggt gaa gta Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val 305 310 315 320	960
agc cgt gac atg ttc gcc ggc ctg tac ccc gga tat gag cct cgt gaa Ser Arg Asp Met Phe Ala Gly Leu Tyr Pro Gly Tyr Glu Pro Arg Glu 325 330 335	1008
gtg ccc atc ggg cac gtc acc aac ggt gtt cac ctg ccg acg tgg gtc Val Pro Ile Gly His Val Thr Asn Gly Val His Leu Pro Thr Trp Val 340 345 350	1056
aag cca gag atg aag gaa ctc atc gat cgc gtc act ggc ggc gct gat Lys Pro Glu Met Lys Glu Leu Ile Asp Arg Val Thr Gly Gly Ala Asp 355 360 365	1104
ctt gcg gtt gct gat tct tgg tca aac cca cag gct gtc gag tct gag Leu Ala Val Ala Asp Ser Trp Ser Asn Pro Gln Ala Val Glu Ser Glu 370 375 380	1152
aag atc tgg aag gtg cgc aac aag ttc cgt gct gac cta gtg gag gtt Lys Ile Trp Lys Val Arg Asn Lys Phe Arg Ala Asp Leu Val Glu Val 385 390 395 400	1200
gct cgc Ala Arg	1206

<210> 378

<211> 402

<212> PRT

<213> Corynebacterium glutamicum

<400> 378

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 Asp Lys Leu Trp Tyr Gln Asp Thr Ala Asp Ala Thr Asp Ala Val Gly
 20 25 30
 Asp Pro Leu Val Ala Tyr Phe Ser Met Glu Phe Gly Ile His Pro Ser
 35 40 45
 Leu Pro Ile Tyr Ser Gly Gly Leu Gly Val Leu Ala Gly Glu Asn Met
 50 55 60
 Lys Ser Ala Ser Asp Leu Gly Val Pro Leu Ile Gly Val Gly Leu Leu
 65 70 75 80
 Tyr Thr His Gly Tyr Phe Thr Gln Ser Leu Ser Gly Asp Gly Trp Gln
 85 90 95
 Gln Glu Glu Tyr Lys Tyr His Asp Pro Ala Glu Leu Pro Ile Glu Ala
 100 105 110
 Val Lys Asp Lys Asn Gly Glu Gln Val Thr Val Ser Val Thr Tyr Pro
 115 120 125
 Gly Ala Gln Glu Val Lys Ile Ala Leu Trp Val Ala Asn Val Gly Arg
 130 135 140
 Ile Pro Leu Leu Leu Leu Asp Thr Asn Ile Glu Ala Asn Pro Glu Glu
 145 150 155 160
 Leu Arg Asn Val Thr Asp Arg Leu Tyr Gly Gly Asp Asn Glu His Arg
 165 170 175
 Ile Lys Gln Glu Leu Val Leu Gly Val Gly Gly Val Arg Ala Val Asn
 180 185 190
 Ala Phe Cys Glu Ala Arg Gly Leu Lys Arg Ser Ser Val Ala His Leu
 195 200 205
 Asn Glu Gly His Ala Gly Phe Leu Thr Leu Glu Arg Ile Arg Glu Arg
 210 215 220
 Ile Ala Glu Gly Met Glu Tyr Pro Ala Ala Phe Glu Gln Val Arg Ala
 225 230 235 240
 Ser Asn Ile Phe Thr Thr His Thr Pro Val Pro Ala Gly Ile Asp Arg
 245 250 255
 Phe Asp Met Glu Met Val Arg Arg Tyr Leu Gly Gly Gly Gln Pro Glu
 260 265 270
 Asp Gln Gln Leu Cys Val Gly Val Pro Ile Glu Lys Ala Leu Glu Leu
 275 280 285
 Gly Gln Glu Ser Asp Pro His Arg Phe Asn Met Ala His Met Gly Leu
 290 295 300
 Arg Ala Ser Gln His Ala Asn Gly Val Ala Lys Leu His Gly Glu Val

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Met Phe Gly Arg Arg																
1 5																
tgg gtg agc gtt gtg gcg tca tgt gtt atc gca agc acg ctg att ctg																163
Trp Val Ser Val Val Ala Ser Cys Val Ile Ala Ser Thr Leu Ile Leu																
10 15 20																
gtg cct tcg cat tcc ggt gcg gag gaa gtc gat caa ctg att gct gat																211
Val Pro Ser His Ser Gly Ala Glu Glu Val Asp Gln Leu Ile Ala Asp																
25 30 35																
atc gag cat gtc tct cag gaa acg tct gcc cag aat gag gaa gtc aaa																259
Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln Asn Glu Glu Val Lys																
40 45 50																
cag ctt gag att gat att gag gct cgt gag gtc acg atc aag gaa gtt																307
Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val Thr Thr Lys Glu Val																
55 60 65																
cag gag cag tcg gta agc tac cgt gag gcg gct gat caa gca tcg gag																355
Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala Asp Gln Ala Ser Glu																
70 75 80 85																
aat gtc gaa gct tat cgt tcg gag atc aat cgg atc gct cag gcg aag																403
Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg Ile Ala Gln Ala Lys																
90 95 100																

tat	cgt	ggc	aca	gtc	acg	gat	cct	ttg	agc	att	gcg	gtg	tct	gca	gaa	451
Tyr	Arg	Gly	Thr	Val	Thr	Asp	Pro	Leu	Ser	Ile	Ala	Val	Ser	Ala	Glu	
			105				110						115			
gat	cca	caa	aac	gtg	att	gat	cgg	atg	agc	tac	ctt	tca	acg	ttg	act	499
Asp	Pro	Gln	Asn	Val	Ile	Asp	Arg	Met	Ser	Tyr	Leu	Ser	Thr	Leu	Thr	
			120				125						130			
aag	tcc	act	agt	gat	gtg	gtt	gaa	tcc	ctc	aac	gcg	gag	act	gag	aag	547
Lys	Ser	Thr	Ser	Asp	Val	Val	Glu	Ser	Leu	Asn	Ala	Glu	Thr	Glu	Lys	
			135				140						145			
tcc	gca	gaa	gct	gtg	tat	caa	gca	aac	cgt	act	aag	gcg	gaa	gcg	gag	595
Ser	Ala	Glu	Ala	Val	Tyr	Gln	Ala	Asn	Arg	Thr	Lys	Ala	Glu	Ala	Glu	
			150				155						165			
ttc	cag	ttg	ggg	cag	ctg	aag	gta	cgc	cag	gcg	gag	ctt	gaa	tct	gaa	643
Phe	Gln	Leu	Gly	Gln	Leu	Lys	Val	Arg	Gln	Ala	Glu	Leu	Glu	Ser	Glu	
			170				175						180			
aag	gaa	gca	ttg	gat	ggg	cga	aaa	tcg	gag	atc	cga	gac	cgg	gtg	gat	691
Lys	Glu	Ala	Leu	Asp	Gly	Arg	Lys	Ser	Glu	Ile	Arg	Asp	Arg	Val	Asp	
			185				190						195			
gcc	ctg	acg	cca	cag	gag	cgg	gaa	atg	tgg	gtt	gct	aag	aat	ggg	cca	739
Ala	Leu	Thr	Pro	Gln	Glu	Arg	Glu	Met	Trp	Val	Ala	Lys	Asn	Gly	Pro	
			200				205						210			
ttg	gac	att	gat	ctg	act	gat	ttg	ctt	ggg	ctt	tcc	gct	gcg	act	tcg	787
Leu	Asp	Ile	Asp	Leu	Thr	Asp	Leu	Leu	Gly	Leu	Ser	Ala	Ala	Thr	Ser	
			215				220						225			
ggg	gcg	gtg	gat	gct	gcc	ttg	tct	aag	ttg	gga	agc	cct	tat	ggg	tgg	835
Gly	Ala	Val	Asp	Ala	Ala	Leu	Ser	Lys	Leu	Gly	Ser	Pro	Tyr	Gly	Trp	
			230				235						245			
ggg	ggc	att	ggc	cca	aat	gag	ttt	gat	tgc	tca	ggg	ttg	atc	tat	tgg	883
Gly	Gly	Ile	Gly	Pro	Asn	Glu	Phe	Asp	Cys	Ser	Gly	Leu	Ile	Tyr	Trp	
			250				255						260			
gcg	tat	cag	cag	atg	ggg	aag	act	ttg	cca	cgt	acg	tct	caa	gct	cag	931
Ala	Tyr	Gln	Gln	Met	Gly	Lys	Thr	Leu	Pro	Arg	Thr	Ser	Gln	Ala	Gln	
			265				270						275			
atg	gct	ggc	gga	acg	ccg	gtg	agc	aga	gat	gag	ctg	cag	cct	ggc	gat	979
Met	Ala	Gly	Gly	Thr	Pro	Val	Ser	Arg	Asp	Glu	Leu	Gln	Pro	Gly	Asp	
			280				285						290			
gtc	att	gga	tat	tac	cca	ggg	gct	act	cac	gtg	gga	ctg	tat	att	ggg	1027
Val	Ile	Gly	Tyr	Tyr	Pro	Gly	Ala	Thr	His	Val	Gly	Leu	Tyr	Ile	Gly	
			295				300						305			
gac	gga	aag	att	gtg	cac	gcc	tca	gac	tac	gga	atc	cct	gtg	cag	gtg	1075
Asp	Gly	Lys	Ile	Val	His	Ala	Ser	Asp	Tyr	Gly	Ile	Pro	Val	Gln	Val	
			310				315						325			
gta	tct	gtt	gat	tca	gca	ccg	ttt	tat	ggg	gcg	cgt	cgc	tac			1117
Val	Ser															

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1140

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<211> 339

<212> PRT

<213> Corynebacterium glutamicum

<400> 380

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Ser Thr Leu Ile Leu Val Pro Ser His Ser Gly Ala Glu Glu Val Asp
 20 25 30

Gln Leu Ile Ala Asp Ile Glu His Val Ser Gln Glu Thr Ser Ala Gln
 35 40 45

Asn Glu Glu Val Lys Gln Leu Glu Ile Asp Ile Glu Ala Arg Glu Val
 50 55 60

Thr Ile Lys Glu Val Gln Glu Gln Ser Val Ser Tyr Arg Glu Ala Ala
 65 70 75 80

Asp Gln Ala Ser Glu Asn Val Glu Ala Tyr Arg Ser Glu Ile Asn Arg
 85 90 95

Ile Ala Gln Ala Lys Tyr Arg Gly Thr Val Thr Asp Pro Leu Ser Ile
 100 105 110

Ala Val Ser Ala Glu Asp Pro Gln Asn Val Ile Asp Arg Met Ser Tyr
 115 120 125

Leu Ser Thr Leu Thr Lys Ser Thr Ser Asp Val Val Glu Ser Leu Asn
 130 135 140

Ala Glu Thr Glu Lys Ser Ala Glu Ala Val Tyr Gln Ala Asn Arg Thr
 145 150 155 160

Lys Ala Glu Ala Glu Phe Gln Leu Gly Gln Leu Lys Val Arg Gln Ala
 165 170 175

Glu Leu Glu Ser Glu Lys Glu Ala Leu Asp Gly Arg Lys Ser Glu Ile
 180 185 190

Arg Asp Arg Val Asp Ala Leu Thr Pro Gln Glu Arg Glu Met Trp Val
 195 200 205

Ala Lys Asn Gly Pro Leu Asp Ile Asp Leu Thr Asp Leu Leu Gly Leu
 210 215 220

Ser Ala Ala Thr Ser Gly Ala Val Asp Ala Ala Leu Ser Lys Leu Gly
 225 230 235 240

Ser Pro Tyr Gly Trp Gly Gly Ile Gly Pro Asn Glu Phe Asp Cys Ser
 245 250 255

Gly Leu Ile Tyr Trp Ala Tyr Gln Gln Met Gly Lys Thr Leu Pro Arg
 260 265 270

Thr Ser Gln Ala Gln Met Ala Gly Gly Thr Pro Val Ser Arg Asp Glu

275	280	285
Leu Gln Pro Gly Asp Val	Ile Gly Tyr Tyr Pro Gly	Ala Thr His Val
290	295	300
Gly Leu Tyr Ile Gly Asp	Gly Lys Ile Val His	Ala Ser Asp Tyr Gly
305	310	315
Ile Pro Val Gln Val Val	Ser Val Asp Ser Ala	Pro Phe Tyr Gly Ala
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Arg Arg Tyr

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 <211> 1959
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1936)
 <223> RXA01478

<400> 381
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 Met Thr Ile Pro Gly
 1 5
 gct tcc aca cag act gat atc cct ctg gac aca ctt ctt gag gat tac 163
 Ala Ser Thr Gln Thr Asp Ile Pro Leu Asp Thr Leu Leu Glu Asp Tyr
 10 15 20
 gcg cta ctg tca gac act cac acc ggc gct ctg ctg tcc aac atg ggc 211
 Ala Leu Leu Ser Asp Thr His Thr Gly Ala Leu Leu Ser Asn Met Gly
 25 30 35
 agt ttg gac tgg ttg tgc ctg cct cgt ttt gat tcc caa gcc atg ttc 259
 Ser Leu Asp Trp Leu Cys Leu Pro Arg Phe Asp Ser Gln Ala Met Phe
 40 45 50
 acc agg ctg ctt ggt gat cgc gag cac gga cac tgg agt ttg cgt gtc 307
 Thr Arg Leu Leu Gly Asp Arg Glu His Gly His Trp Ser Leu Arg Val
 55 60 65
 cca ggt ggt gag gtg atc agc caa aac tac ctc ggc gat tcc ttc gtg 355
 Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu Gly Asp Ser Phe Val
 70 75 80 85
 gtg cag acc gtg tgg cgt tca gag acc ggt act gcc cgg gtt gtt gat 403
 Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr Ala Arg Val Val Asp
 90 95 100
 ttc atg cca att cac ggt caa gaa caa ccc gat atc acc gac ctg gtg 451
 Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp Ile Thr Asp Leu Val
 105 110 115
 cgc tct gtg cac tgc gtg gaa ggc gaa gtg gat gtg gaa tcg atc ctg 499

Arg	Ser	Val	His	Cys	Val	Glu	Gly	Glu	Val	Asp	Val	Glu	Ser	Ile	Leu		
		120					125					130					
cgc	ctg	cgt	ttt	gat	tat	ggc	gag	tcc	act	ccg	tat	ttc	cgc	acc	agc	547	
Arg	Leu	Arg	Phe	Asp	Tyr	Gly	Glu	Ser	Thr	Pro	Tyr	Phe	Arg	Thr	Ser		
		135					140					145					
act	gtc	gac	ggc	atc	agc	atc	gtg	cag	gct	gtc	gcc	ggc	ccc	aat	gcg	595	
Thr	Val	Asp	Gly	Ile	Ser	Ile	Val	Gln	Ala	Val	Ala	Gly	Pro	Asn	Ala		
					155					160					165		
gta	tat	gtt	cgt	gga	cct	gag	atg	cca	cac	cgc	cct	gca	aag	gat	tgt	643	
Val	Tyr	Val	Arg	Gly	Pro	Glu	Met	Pro	His	Arg	Pro	Ala	Lys	Asp	Cys		
				170					175					180			
cac	agt	ggc	acc	ttc	cac	ctg	acg	gcc	ggc	gaa	tcc	gtg	gaa	tgg	gtt	691	
His	Ser	Gly	Thr	Phe	His	Leu	Thr	Ala	Gly	Glu	Ser	Val	Glu	Trp	Val		
			185					190					195				
ctc	acc	tgg	gca	ccg	tcg	ttc	gaa	ccg	cat	ccc	ccc	atg	ccg	gat	tac	739	
Leu	Thr	Trp	Ala	Pro	Ser	Phe	Glu	Pro	His	Pro	Pro	Met	Pro	Asp	Tyr		
		200					205					210					
acc	cgc	tct	ttg	gag	agc	acc	ttg	agc	ttc	tgg	gca	tca	tgg	gtt	gaa	787	
Thr	Arg	Ser	Leu	Glu	Ser	Thr	Leu	Ser	Phe	Trp	Ala	Ser	Trp	Val	Glu		
		215				220					225						
gag	ctc	ccc	cac	cag	cgc	ctc	tac	gac	gct	gaa	gtc	cgc	cgc	tcc	atg	835	
Glu	Leu	Pro	His	Gln	Arg	Leu	Tyr	Asp	Ala	Glu	Val	Arg	Arg	Ser	Met		
		230			235					240					245		
ctc	gta	ctg	cgc	gcc	ttg	acc	gat	cta	caa	acc	ggc	ggc	atc	gtg	gcc	883	
Leu	Val	Leu	Arg	Ala	Leu	Thr	Asp	Leu	Gln	Thr	Gly	Gly	Ile	Val	Ala		
				250					255					260			
gca	ccg	acc	acc	tca	cta	cca	gag	gat	ttc	gga	ggc	atc	cgt	aac	tgg	931	
Ala	Pro	Thr	Thr	Ser	Leu	Pro	Glu	Asp	Phe	Gly	Gly	Ile	Arg	Asn	Trp		
			265					270					275				
gac	tac	cgc	tac	gtg	tgg	ctg	cgc	gac	tcc	gca	ctc	acc	att	gaa	gcc	979	
Asp	Tyr	Arg	Tyr	Val	Trp	Leu	Arg	Asp	Ser	Ala	Leu	Thr	Ile	Glu	Ala		
		280					285					290					
ctc	gtg	gaa	tac	gga	ttc	tcc	caa	gca	gcc	ctc	caa	tgg	cgc	acc	tgg	1027	
Leu	Val	Glu	Tyr	Gly	Phe	Ser	Gln	Ala	Ala	Leu	Gln	Trp	Arg	Thr	Trp		
		295				300					305						
ctg	ctg	cgc	gcc	atc	gca	ggc	gac	ccg	gaa	aac	ctc	cgc	atc	atg	tat	1075	
Leu	Leu	Arg	Ala	Ile	Ala	Gly	Asp	Pro	Glu	Asn	Leu	Arg	Ile	Met	Tyr		
					315					320				325			
ggc	ctc	ggc	ggc	gaa	cga	cac	ctc	cct	gaa	cgc	gaa	ctc	caa	cac	ctg	1123	
Gly	Leu	Gly	Gly	Glu	Arg	His	Leu	Pro	Glu	Arg	Glu	Leu	Gln	His	Leu		
				330					335					340			
cgc	gga	tac	gaa	aac	tcc	gtg	cct	gtt	cgc	gtt	ggc	aat	gga	gcc	gcc	1171	
Arg	Gly	Tyr	Glu	Asn	Ser	Val	Pro	Val	Arg	Val	Gly	Asn	Gly	Ala	Ala		
			345					350				355					
gaa	caa	tac	caa	gca	gat	gtc	gtc	ggc	gaa	gta	atg	gtc	gcg	ctt	gaa	1219	
Glu	Gln	Tyr	Gln	Ala	Asp	Val	Val	Gly	Glu	Val	Met	Val	Ala	Leu	Glu		

360	365	370	
acc atc cgc cgc gcc ggg tgc ctc gag gac gaa ttc tcc tgg ggc atg Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu Phe Ser Trp Gly Met 375 380 385			1267
caa aaa gcc atc ctc gat ttc caa gaa gcc aac ttc gac cgc aag gat Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn Phe Asp Arg Lys Asp 390 395 400 405			1315
caa ggc atc tgg gaa atg cgc tcc gaa ccg caa tat ttc acc cac ggc Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln Tyr Phe Thr His Gly 410 415 420			1363
cgc gcc atg atg tgg gcc ggc ttc gac cgc ggc atc aaa gcc atc gaa Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly Ile Lys Ala Ile Glu 425 430 435			1411
gaa ttc aac ctc gac ggc ccc atc gag cgc tgg cgt gaa ctc cgc gcc Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp Arg Glu Leu Arg Ala 440 445 450			1459
aaa ctc cgc gaa gaa atc atg acc aac ggc ttc aac gaa gag atc caa Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe Asn Glu Glu Ile Gln 455 460 465			1507
tcc ttc acc cag tgc tac gac aac acc caa gtc gac gcc tcg ctg ctt Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val Asp Ala Ser Leu Leu 470 475 480 485			1555
cag ctc gcc caa ata ggc ttc atc ggc ttc gac gat cca aaa atg ctc Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp Asp Pro Lys Met Leu 490 495 500			1603
agc acc gta gcg cgc att gag caa gag ctt ctc gac gcc cac ggc ttt Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu Asp Ala His Gly Phe 505 510 515			1651
ctt cac agg tac cac acc gac ggg tct gac ggc ctt gcc ggc gac gaa Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly Leu Ala Gly Asp Glu 520 525 530			1699
tac ccc ttc ctc atc tgt tca ttc tgg ctg gta gaa caa tac gca agc Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val Glu Gln Tyr Ala Ser 535 540 545			1747
tcc aac cgc ctc gac gag gcc aaa gaa aag atg aac cgc atc ctt gcc Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met Asn Arg Ile Leu Ala 550 555 560 565			1795
gtc caa agc cca ctt ggc cta ctg gct gag gaa tac tcc acc cac cat Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu Tyr Ser Thr His His 570 575 580			1843
ggc agg ctc gct gga aac tac cct cag gcc ttt tcc cac att ggt ctg Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe Ser His Ile Gly Leu 585 590 595			1891
atc agc gct gcc cgt gcc ata aat ttc gaa gaa gcg cga aac agg Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu Ala Arg Asn Arg 600 605 610			1936

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1959

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<211> 612

<212> PRT

<213> Corynebacterium glutamicum

<400> 382

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 20 25 30

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 35 40 45

Ser Gln Ala Met Phe Thr Arg Leu Leu Gly Asp Arg Glu His Gly His
 50 55 60

Trp Ser Leu Arg Val Pro Gly Gly Glu Val Ile Ser Gln Asn Tyr Leu
 65 70 75 80

Gly Asp Ser Phe Val Val Gln Thr Val Trp Arg Ser Glu Thr Gly Thr
 85 90 95

Ala Arg Val Val Asp Phe Met Pro Ile His Gly Gln Glu Gln Pro Asp
 100 105 110

Ile Thr Asp Leu Val Arg Ser Val His Cys Val Glu Gly Glu Val Asp
 115 120 125

Val Glu Ser Ile Leu Arg Leu Arg Phe Asp Tyr Gly Glu Ser Thr Pro
 130 135 140

Tyr Phe Arg Thr Ser Thr Val Asp Gly Ile Ser Ile Val Gln Ala Val
 145 150 155 160

Ala Gly Pro Asn Ala Val Tyr Val Arg Gly Pro Glu Met Pro His Arg
 165 170 175

Pro Ala Lys Asp Cys His Ser Gly Thr Phe His Leu Thr Ala Gly Glu
 180 185 190

Ser Val Glu Trp Val Leu Thr Trp Ala Pro Ser Phe Glu Pro His Pro
 195 200 205

Pro Met Pro Asp Tyr Thr Arg Ser Leu Glu Ser Thr Leu Ser Phe Trp
 210 215 220

Ala Ser Trp Val Glu Glu Leu Pro His Gln Arg Leu Tyr Asp Ala Glu
 225 230 235 240

Val Arg Arg Ser Met Leu Val Leu Arg Ala Leu Thr Asp Leu Gln Thr
 245 250 255

Gly Gly Ile Val Ala Ala Pro Thr Thr Ser Leu Pro Glu Asp Phe Gly
 260 265 270

Gly Ile Arg Asn Trp Asp Tyr Arg Tyr Val Trp Leu Arg Asp Ser Ala
 275 280 285
 Leu Thr Ile Glu Ala Leu Val Glu Tyr Gly Phe Ser Gln Ala Ala Leu
 290 295 300
 Gln Trp Arg Thr Trp Leu Leu Arg Ala Ile Ala Gly Asp Pro Glu Asn
 305 310 315 320
 Leu Arg Ile Met Tyr Gly Leu Gly Gly Glu Arg His Leu Pro Glu Arg
 325 330 335
 Glu Leu Gln His Leu Arg Gly Tyr Glu Asn Ser Val Pro Val Arg Val
 340 345 350
 Gly Asn Gly Ala Ala Glu Gln Tyr Gln Ala Asp Val Val Gly Glu Val
 355 360 365
 Met Val Ala Leu Glu Thr Ile Arg Arg Ala Gly Cys Leu Glu Asp Glu
 370 375 380
 Phe Ser Trp Gly Met Gln Lys Ala Ile Leu Asp Phe Gln Glu Ala Asn
 385 390 395 400
 Phe Asp Arg Lys Asp Gln Gly Ile Trp Glu Met Arg Ser Glu Pro Gln
 405 410 415
 Tyr Phe Thr His Gly Arg Ala Met Met Trp Ala Gly Phe Asp Arg Gly
 420 425 430
 Ile Lys Ala Ile Glu Glu Phe Asn Leu Asp Gly Pro Ile Glu Arg Trp
 435 440 445
 Arg Glu Leu Arg Ala Lys Leu Arg Glu Glu Ile Met Thr Asn Gly Phe
 450 455 460
 Asn Glu Glu Ile Gln Ser Phe Thr Gln Cys Tyr Asp Asn Thr Gln Val
 465 470 475 480
 Asp Ala Ser Leu Leu Gln Leu Ala Gln Ile Gly Phe Ile Gly Phe Asp
 485 490 495
 Asp Pro Lys Met Leu Ser Thr Val Ala Arg Ile Glu Gln Glu Leu Leu
 500 505 510
 Asp Ala His Gly Phe Leu His Arg Tyr His Thr Asp Gly Ser Asp Gly
 515 520 525
 Leu Ala Gly Asp Glu Tyr Pro Phe Leu Ile Cys Ser Phe Trp Leu Val
 530 535 540
 Glu Gln Tyr Ala Ser Ser Asn Arg Leu Asp Glu Ala Lys Glu Lys Met
 545 550 555 560
 Asn Arg Ile Leu Ala Val Gln Ser Pro Leu Gly Leu Leu Ala Glu Glu
 565 570 575
 Tyr Ser Thr His His Gly Arg Leu Ala Gly Asn Tyr Pro Gln Ala Phe
 580 585 590
 Ser His Ile Gly Leu Ile Ser Ala Ala Arg Ala Ile Asn Phe Glu Glu

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595                                     600                                     605

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<223> RXA01888

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                                         Met Ala Asp Val Ala
                                         1      5

aaa gct gct gga gta tcc act gcg ctg gtc tcc atc gtg ttt cgc gat 163
Lys Ala Ala Gly Val Ser Thr Ala Leu Val Ser Ile Val Phe Arg Asp
              10              15              20

gcc ccc gga gca agt gaa tcc acc cgc aac cat gtg aaa gaa aaa gcc 211
Ala Pro Gly Ala Ser Glu Ser Thr Arg Asn His Val Lys Glu Lys Ala
              25              30              35

gcc gaa ctc gga tac att cct gat cga cga gcc caa aaa ctt cgc caa 259
Ala Glu Leu Gly Tyr Ile Pro Asp Arg Arg Ala Gln Lys Leu Arg Gln
              40              45              50

aac cgc tcc gga ctc atc ggt gtg gca ttc gaa atg cac caa gca ttc 307
Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu Met His Gln Ala Phe
              55              60              65

cac ggc gat atc gtc gaa cac ctc tat ccc acc gcc cga aaa cat ggc 355
His Gly Asp Ile Val Glu His Leu Tyr Pro Thr Ala Arg Lys His Gly
              70              75              80              85

ttc gac ctg tac ctt agc gcg atc aca ccg act cgc act gaa aaa gat 403
Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr Arg Thr Glu Lys Asp
              90              95              100

gcc gtc aac gcc ctg atc agg gaa cga tgc gaa gca gta att ctt cta 451
Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu Ala Val Ile Leu Leu
              105              110              115

gga tct cgc atg tca cct agt gat ttg gaa aca atc gca cag caa ctt 499
Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr Ile Ala Gln Gln Leu
              120              125              130

ccc gtc caa gta att gcc cgc ggt tcc gga acc ccc aaa gtc agt tcc 547
Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr Pro Lys Val Ser Ser
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gtc cat gtc gac gac gca gtt ggc gcc caa tta gcc ctc aac cac ctc 595
Val His Val Asp Asp Ala Val Gly Ala Gln Leu Ala Leu Asn His Leu

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Pro Gly Thr Gln Glu		
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35 40 45	
Gln Lys Leu Arg Gln Asn Arg Ser Gly Leu Ile Gly Val Ala Phe Glu	
50 55 60	
Met His Gln Ala Phe His Gly Asp Ile Val Glu His Leu Tyr Pro Thr	
65 70 75 80	
Ala Arg Lys His Gly Phe Asp Leu Tyr Leu Ser Ala Ile Thr Pro Thr	
85 90 95	
Arg Thr Glu Lys Asp Ala Val Asn Ala Leu Ile Arg Glu Arg Cys Glu	
100 105 110	
Ala Val Ile Leu Leu Gly Ser Arg Met Ser Pro Ser Asp Leu Glu Thr	
115 120 125	
Ile Ala Gln Gln Leu Pro Val Gln Val Ile Ala Arg Gly Ser Gly Thr	
130 135 140	
Pro Lys Val Ser Ser Val His Val Asp Asp Ala Val Gly Ala Gln Leu	
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Asp Gly Gly Asp Ala Pro Gly Thr Gln Glu	
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<223> RXN01927

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Gly Ile Asp Ser Ser Thr Gln Ser Cys Lys Ala Leu Leu Val Asp Ala
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gcc acc ggc cag gtt atc gac gaa ggc cgc gcg agt cac ccg agc ggg 211
Ala Thr Gly Gln Val Ile Asp Glu Gly Arg Ala Ser His Pro Ser Gly
25 30 35

tcg	gag	gta	gat	cca	cgt	gcg	tgg	atc	gct	gcg	ctg	gat	caa	gct	acc	259
Ser	Glu	Val	Asp	Pro	Arg	Ala	Trp	Ile	Ala	Ala	Leu	Asp	Gln	Ala	Thr	
		40					45					50				

gag ggg ttg tta gaa cgc gcg gac gct gta tct att gca ggc cag cag 307
Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser Ile Ala Gly Gln Gln
55 60 65

cac ggc atg gtg gcg ttg gat gaa aac gat gaa atc gtt cgc ccg gcg 355
 His Gly Met Val Ala Leu Asp Glu Asn Asp Glu Ile Val Arg Pro Ala
 70 75 80 85

ttg	tta	tgg	aat	gac	act	cgt	tct	gcc	cag	gct	gcg	ttg	gat	ctc	aat	403
Leu	Leu	Trp	Asn	Asp	Thr	Arg	Ser	Ala	Gln	Ala	Ala	Leu	Asp	Leu	Asn	
			90						95					100		

gag gag atc ggc ggc gat cag gct gcg gta gat gcc acg gga agt gtg 451
Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val
105 110 115

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Tyr	Val	Ala	Ser	Leu	Thr	Ala	Thr	Lys	Met	Arg	Trp	Met	Arg	Asp	His	
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gaa cca gaa aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat 547
Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp
135 140 145

ttc ctc acc tgg cat ttg atg gga cgc gga cgc aaa gtc acc gac cat 595
Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His
150 155 160 165

ggt gat gct tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg 643
Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp
170 175 180

cgc acc gat cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct 691
Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro
185 190 195

gaa ctc ctg gcc cca aat gcg att gcg gga aca act cca ggt gga gtg 739
Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val
200 205 210

aaa gtt gct gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt	787
Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu	
215 220 225	
gat ttg cag cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt	835
Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val	
230 235 240 245	
gcc ggc atg acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc	883
Ala Gly Met Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val	
250 255 260	
act ggt ttc gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg	931
Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr	
265 270 275	
ctt aat ggc gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg	979
Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val	
280 285 290	
gaa tgg gaa gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca	1027
Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser	
295 300 305	
ggt ggc gtg acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat	1075
Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn	
310 315 320 325	
cgt ccc gca gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc	1123
Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr	
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cgc gag gac ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg	1171
Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Ala Leu	
345 350 355	
gat gat gct gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag	1219
Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln	
360 365 370	
cgc atc cag ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag	1267
Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu	
375 380 385	
att gcc cct gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct	1315
Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala	
390 395 400 405	
gaa tat gtg gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg	1363
Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser	
410 415 420	
ggt gag gcc acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac	1411
Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His	
425 430 435	
cgc gca cct aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt	1459
Arg Ala Pro Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg	
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1503

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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Leu Asp Gln Ala Thr Glu Gly Leu Leu Glu Arg Ala Asp Ala Val Ser
 50 55 60
 Ile Ala Gly Gln Gln His Gly Met Val Ala Leu Asp Glu Asn Asp Glu
 65 70 75 80
 Ile Val Arg Pro Ala Leu Leu Trp Asn Asp Thr Arg Ser Ala Gln Ala
 85 90 95
 Ala Leu Asp Leu Asn Glu Glu Ile Gly Gly Asp Gln Ala Ala Val Asp
 100 105 110
 Ala Thr Gly Ser Val Tyr Val Ala Ser Leu Thr Ala Thr Lys Met Arg
 115 120 125
 Trp Met Arg Asp His Glu Pro Glu Asn Ala Ala Arg Thr Ala Ser Val
 130 135 140
 Met Leu Pro His Asp Phe Leu Thr Trp His Leu Met Gly Arg Gly Arg
 145 150 155 160
 Lys Val Thr Asp His Gly Asp Ala Ser Gly Thr Gly Tyr Tyr Ser Thr
 165 170 175
 Arg Asp Arg Ala Trp Arg Thr Asp Leu Ala Ala Leu Ala Leu Gly His
 180 185 190
 Glu Val Glu Leu Pro Glu Leu Leu Ala Pro Asn Ala Ile Ala Gly Thr
 195 200 205
 Thr Pro Gly Gly Val Lys Val Ala Ala Gly Thr Gly Asp Asn Ala Ala
 210 215 220
 Ala Ala Leu Gly Leu Asp Leu Gln Pro Gly Asp Val Ser Val Ser Ile
 225 230 235 240
 Gly Thr Ser Gly Val Ala Gly Met Thr Val Gln His Ser Val His Asp
 245 250 255
 Pro Ser Gly Leu Val Thr Gly Phe Ala Asp Ala Thr Gly Ala Tyr Phe
 260 265 270

Pro Leu Ala Cys Thr Leu Asn Gly Ala Pro Val Leu Glu Phe Gly Arg
 275 280 285
 Arg Ile Leu Gly Val Glu Trp Glu Glu Phe Asp Ala Leu Ala Leu Ala
 290 295 300
 Ala Gln Pro Gly Ser Gly Gly Val Thr Leu Gln Pro Tyr Leu Glu Gly
 305 310 315 320
 Glu Arg Thr Pro Asn Arg Pro Ala Ala Arg Gly Val Leu Ala Gly Leu
 325 330 335
 Asn Cys Ala Thr Thr Arg Glu Asp Phe Ala Arg Ala Thr Val Glu Gly
 340 345 350
 Leu Leu Leu Ala Leu Asp Asp Ala Val Thr Ala Leu Val Glu Ala Thr
 355 360 365
 Gly Val Pro Val Gln Arg Ile Gln Leu Ile Gly Gly Gly Ala Arg Ser
 370 375 380
 Gln Ala Val Arg Glu Ile Ala Pro Glu Ile Phe Gly His Glu Ile Val
 385 390 395 400
 Val Pro Glu Pro Ala Glu Tyr Val Ala Leu Gly Ala Ala Arg Gln Ala
 405 410 415
 Ala Trp Ala Leu Ser Gly Glu Ala Thr Pro Pro Gln Trp Pro Thr Pro
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 <222> (1)..(1116)
 <223> FRXA01927

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 Gly Gly Asp Gln Ala Ala Val Asp Ala Thr Gly Ser Val Tyr Val Ala
 20 25 30
 tct tta act gcc acc aaa atg cgg tgg atg cgt gat cat gaa cca gaa 144
 Ser Leu Thr Ala Thr Lys Met Arg Trp Met Arg Asp His Glu Pro Glu
 35 40 45

aat gca gcg cgc acg gcg tcg gtg atg ttg cct cat gat ttc ctc acc	192
Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr	
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tggt cat ttg atg gga cgc gga cgc aaa gtc acc gac cat ggt gat gct	240
Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala	
65 70 75 80	
tct gga acg ggc tac tac agc acg cgt gat cgt gcg tgg cgc acc gat	288
Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp	
85 90 95	
cta gct gcc ttg gcg ctg ggc cat gag gtg gaa ctt cct gaa ctc ctg	336
Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu	
100 105 110	
gcc cca aat gcg att gcg gga aca act cca ggt gga gtg aaa gtt gct	384
Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala	
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gca ggc acg gga gat aat gct gcg gct gcg ctt ggc ctt gat ttg cag	432
Ala Gly Thr Gly Asp Asn Ala Ala Ala Leu Gly Leu Asp Leu Gln	
130 135 140	
cct ggt gat gtc agc gtg tcg atc ggc acc tct ggc gtt gcc ggc atg	480
Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met	
145 150 155 160	
acc gtt caa cat agc gtc cac gat cca tct ggt ttg gtc act ggt ttc	528
Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe	
165 170 175	
gcc gat gcc acg ggt gcg tat ttc ccg ctg gcc tgc acg ctt aat ggc	576
Ala Asp Ala Thr Gly Ala Tyr Phe Pro Leu Ala Cys Thr Leu Asn Gly	
180 185 190	
gca ccg gtg ttg gaa ttc ggc cgc cgc att ctg ggc gtg gaa tgg gaa	624
Ala Pro Val Leu Glu Phe Gly Arg Arg Ile Leu Gly Val Glu Trp Glu	
195 200 205	
gag ttc gat gcg ctt gca ctg gct gct caa ccc ggt tca ggt ggc gtg	672
Glu Phe Asp Ala Leu Ala Leu Ala Ala Gln Pro Gly Ser Gly Gly Val	
210 215 220	
acg ctc cag cct tat ttg gag ggc gag cgt acg ccg aat cgt ccc gca	720
Thr Leu Gln Pro Tyr Leu Glu Gly Glu Arg Thr Pro Asn Arg Pro Ala	
225 230 235 240	
gca cgt ggc gtt ttg gct gga cta aac tgt gca acg acc cgc gag gac	768
Ala Arg Gly Val Leu Ala Gly Leu Asn Cys Ala Thr Thr Arg Glu Asp	
245 250 255	
ttt gcc cga gca act gtt gaa ggc ttg ttg ttg gca ttg gat gat gct	816
Phe Ala Arg Ala Thr Val Glu Gly Leu Leu Leu Ala Leu Asp Asp Ala	
260 265 270	
gta acg gcg ctg gtt gag gcc acg gga gtg ccc gtt cag cgc atc cag	864
Val Thr Ala Leu Val Glu Ala Thr Gly Val Pro Val Gln Arg Ile Gln	
275 280 285	
ctc atc ggt ggc ggc gcg cgt tca cag gcg gtt cgt gag att gcc cct	912

Leu Ile Gly Gly Gly Ala Arg Ser Gln Ala Val Arg Glu Ile Ala Pro
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 gag att ttc ggc cat gag att gtg gtt cca gaa ccc gct gaa tat gtg 960
 Glu Ile Phe Gly His Glu Ile Val Val Pro Glu Pro Ala Glu Tyr Val
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 gcg ttg ggt gca gct cgt cag gcg gca tgg gcg ctg tcg ggt gag gcc 1008
 Ala Leu Gly Ala Ala Arg Gln Ala Ala Trp Ala Leu Ser Gly Glu Ala
 325 330 335
 acg cca ccg cag tgg cca act ccc ggt tcc gat ccg cac cgc gca cct 1056
 Thr Pro Pro Gln Trp Pro Thr Pro Gly Ser Asp Pro His Arg Ala Pro
 340 345 350
 aaa aac act gag ctg agc acg cgt tat gcg aag ctg cgt gct gca acg 1104
 Lys Asn Thr Glu Leu Ser Thr Arg Tyr Ala Lys Leu Arg Ala Ala Thr
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<210> 388

<211> 372

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 388

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 35 40 45
 Asn Ala Ala Arg Thr Ala Ser Val Met Leu Pro His Asp Phe Leu Thr
 50 55 60
 Trp His Leu Met Gly Arg Gly Arg Lys Val Thr Asp His Gly Asp Ala
 65 70 75 80
 Ser Gly Thr Gly Tyr Tyr Ser Thr Arg Asp Arg Ala Trp Arg Thr Asp
 85 90 95
 Leu Ala Ala Leu Ala Leu Gly His Glu Val Glu Leu Pro Glu Leu Leu
 100 105 110
 Ala Pro Asn Ala Ile Ala Gly Thr Thr Pro Gly Gly Val Lys Val Ala
 115 120 125
 Ala Gly Thr Gly Asp Asn Ala Ala Ala Ala Leu Gly Leu Asp Leu Gln
 130 135 140
 Pro Gly Asp Val Ser Val Ser Ile Gly Thr Ser Gly Val Ala Gly Met
 145 150 155 160
 Thr Val Gln His Ser Val His Asp Pro Ser Gly Leu Val Thr Gly Phe

165										170					175				
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Thr	Leu	Gln	Pro	Tyr	Leu	Glu	Gly	Glu	Arg	Thr	Pro	Asn	Arg	Pro	Ala				
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Phe	Ala	Arg	Ala	Thr	Val	Glu	Gly	Leu	Leu	Leu	Ala	Leu	Asp	Asp	Ala				
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Val	Thr	Ala	Leu	Val	Glu	Ala	Thr	Gly	Val	Pro	Val	Gln	Arg	Ile	Gln				
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Leu	Ile	Gly	Gly	Gly	Ala	Arg	Ser	Gln	Ala	Val	Arg	Glu	Ile	Ala	Pro				
		290				295					300								
Glu	Ile	Phe	Gly	His	Glu	Ile	Val	Val	Pro	Glu	Pro	Ala	Glu	Tyr	Val				
305					310					315					320				
Ala	Leu	Gly	Ala	Ala	Arg	Gln	Ala	Ala	Trp	Ala	Leu	Ser	Gly	Glu	Ala				
			325						330					335					
Thr	Pro	Pro	Gln	Trp	Pro	Thr	Pro	Gly	Ser	Asp	Pro	His	Arg	Ala	Pro				
			340					345					350						
Lys	Asn	Thr	Glu	Leu	Ser	Thr	Arg	Tyr	Ala	Lys	Leu	Arg	Ala	Ala	Thr				
		355					360					365							
Gln	Gly	Trp	Tyr																
		370																	

<210> 389
 <211> 844
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(844)
 <223> RXA02729

<400> 389
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 catcgtgaat caatcatcaa ctccacttta aggaagaagg atg gac tcc cca atg 115
 Met Asp Ser Pro Met
 1 5
 agt aac tca acc ggt acc gac att gtc gtt gtc gga tcc atc aat gcc 163
 Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val Gly Ser Ile Asn Ala

10										15										20									
gat	ctc	acc	gca	aaa	gtt	caa	cgc	cac	cct	gaa	cct	gga	gaa	acc	ctc														
Asp	Leu	Thr	Ala	Lys	Val	Gln	Arg	His	Pro	Glu	Pro	Gly	Glu	Thr	Leu														
			25					30						35															
ctg	ggg	agc	ggc	ggc	aca	gtg	agt	gct	ggg	ggc	aaa	ggc	gcc	aac	caa														
Leu	Gly	Ser	Gly	Gly	Thr	Val	Ser	Ala	Gly	Gly	Lys	Gly	Ala	Asn	Gln														
		40					45					50																	
gct	gtg	gcg	gca	gcg	caa	tta	ggg	gcc	aaa	gtc	acc	atg	atc	ggg	gcg														
Ala	Val	Ala	Ala	Ala	Gln	Leu	Gly	Ala	Lys	Val	Thr	Met	Ile	Gly	Ala														
		55				60					65																		
gtc	gga	acc	gat	caa	atg	gct	ggc	gag	gcg	ctg	aca	cat	ttg	cgt	caa														
Val	Gly	Thr	Asp	Gln	Met	Ala	Gly	Glu	Ala	Leu	Thr	His	Leu	Arg	Gln														
	70				75					80					85														
tca	gga	gca	gat	atg	tcc	gcg	att	gcc	act	gtg	gac	ggg	ccc	act	ggg														
Ser	Gly	Ala	Asp	Met	Ser	Ala	Ile	Ala	Thr	Val	Asp	Gly	Pro	Thr	Gly														
				90					95				100																
ctt	gcc	atc	atc	act	gtg	tct	gac	gat	ggg	gaa	aac	acc	atc	atc	gtt														
Leu	Ala	Ile	Ile	Thr	Val	Ser	Asp	Asp	Gly	Glu	Asn	Thr	Ile	Ile	Val														
			105				110						115																
atc	cct	ggc	gct	aac	gct	tct	gtc	acc	gcg	gaa	ttt	gtt	gat	aaa	cac														
Ile	Pro	Gly	Ala	Asn	Ala	Ser	Val	Thr	Ala	Glu	Phe	Val	Asp	Lys	His														
		120					125					130																	
tcc	caa	ctc	att	gag	aac	gcc	ggc	att	gtg	ttg	ctt	cag	ggg	gag	atc														
Ser	Gln	Leu	Ile	Glu	Asn	Ala	Gly	Ile	Val	Leu	Leu	Gln	Gly	Glu	Ile														
		135				140					145																		
cct	gcc	gat	ggg	ttc	gag	cgt	gcc	gtt	gat	ctt	tca	caa	gga	cgt	gtg														
Pro	Ala	Asp	Gly	Phe	Glu	Arg	Ala	Val	Asp	Leu	Ser	Gln	Gly	Arg	Val														
	150				155					160					165														
gtg	atc	aat	ctg	gct	cca	gtt	gtg	ccc	gtg	gga	cat	gat	cag	ctg	cgt														
Val	Ile	Asn	Leu	Ala	Pro	Val	Val	Pro	Val	Gly	His	Asp	Gln	Leu	Arg														
				170				175					180																
cgt	gcc	gat	cca	ttg	ctg	gtc	aac	gaa	cac	gaa	ggc	gct	ctg	gtg	ctg														
Arg	Ala	Asp	Pro	Leu	Leu	Val	Asn	Glu	His	Glu	Gly	Ala	Leu	Val	Leu														
			185				190						195																
gac	atg	ctt	gga	act	cca	gcg	acc	acg	tct	gat	ccc	caa	agt	ttg	gtc														
Asp	Met	Leu	Gly	Thr	Pro	Ala	Thr	Thr	Ser	Asp	Pro	Gln	Ser	Leu	Val														
		200					205					210																	
act	gaa	ttg	ctg	gag	cag	ggg	ttt	act	tcc	gtg	gtg	atg	aca	ctt	ggg														
Thr	Glu	Leu	Leu	Glu	Gln	Gly	Phe	Thr	Ser	Val	Val	Met	Thr	Leu	Gly														
		215				220					225																		
gcc	gaa	ggg	gct	ctg	gtt	ggc	acg	ccg	ggc	caa	ctc	acg	gca	att	cct														
Ala	Glu	Gly	Ala	Leu	Val	Gly	Thr	Pro	Gly	Gln	Leu	Thr	Ala	Ile	Pro														
	230				235					240					245														
acc	cca	aag																											
Thr	Pro	Lys																											

<210> 390
 <211> 248
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 390
 Met Asp Ser Pro Met Ser Asn Ser Thr Gly Thr Asp Ile Val Val Val
 1 5 10 15
 Gly Ser Ile Asn Ala Asp Leu Thr Ala Lys Val Gln Arg His Pro Glu
 20 25 30
 Pro Gly Glu Thr Leu Leu Gly Ser Gly Gly Thr Val Ser Ala Gly Gly
 35 40 45
 Lys Gly Ala Asn Gln Ala Val Ala Ala Ala Gln Leu Gly Ala Lys Val
 50 55 60
 Thr Met Ile Gly Ala Val Gly Thr Asp Gln Met Ala Gly Glu Ala Leu
 65 70 75 80
 Thr His Leu Arg Gln Ser Gly Ala Asp Met Ser Ala Ile Ala Thr Val
 85 90 95
 Asp Gly Pro Thr Gly Leu Ala Ile Ile Thr Val Ser Asp Asp Gly Glu
 100 105 110
 Asn Thr Ile Ile Val Ile Pro Gly Ala Asn Ala Ser Val Thr Ala Glu
 115 120 125
 Phe Val Asp Lys His Ser Gln Leu Ile Glu Asn Ala Gly Ile Val Leu
 130 135 140
 Leu Gln Gly Glu Ile Pro Ala Asp Gly Phe Glu Arg Ala Val Asp Leu
 145 150 155 160
 Ser Gln Gly Arg Val Val Ile Asn Leu Ala Pro Val Val Pro Val Gly
 165 170 175
 His Asp Gln Leu Arg Arg Ala Asp Pro Leu Leu Val Asn Glu His Glu
 180 185 190
 Gly Ala Leu Val Leu Asp Met Leu Gly Thr Pro Ala Thr Thr Ser Asp
 195 200 205
 Pro Gln Ser Leu Val Thr Glu Leu Leu Glu Gln Gly Phe Thr Ser Val
 210 215 220
 Val Met Thr Leu Gly Ala Glu Gly Ala Leu Val Gly Thr Pro Gly Gln
 225 230 235 240
 Leu Thr Ala Ile Pro Thr Pro Lys
 245

<210> 391
 <211> 1026
 <212> DNA
 <213> Corynebacterium glutamicum

<223> RXA02797

acagtctcat gaagccataa taaccacctt ctacaaagat cgacgtagaa tggaataacc 60

gag cac gag gcc ggc ctg att ctg gat caa ttc ggg gca ggc atc gat 691
Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe Gly Ala Gly Ile Asp
185 190 195

tcc atg gat ccc cac gag ctc gcg caa gct ctc ctc gac gcc ggt ttc 739
 Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu Leu Asp Ala Gly Phe
 200 205 210
 gcc tct gtt gtt tta acg ctt gga tcc gca ggc gcg ttg gtc gcc gat 787
 Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly Ala Leu Val Ala Asp
 215 220 225
 gcc acc ggt atc acg gac atc gcc aca cca acg gtg cag gca gtt gac 835
 Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr Val Gln Ala Val Asp
 230 235 240 245
 acc acg gga gcc ggt gac gct ttt gcc gga gcc ttc tgc gca cga cta 883
 Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala Phe Cys Ala Arg Leu
 250 255 260
 att aaa ggc gat tcg ctt atc gac gcc gcc acc cac gca gca cgc gtc 931
 Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr His Ala Ala Arg Val
 265 270 275
 ggc gct tac tcg gtg caa acc gcc gga gcg caa gcg tcc tat ccg gac 979
 Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln Ala Ser Tyr Pro Asp
 280 285 290
 gcg agc gtt tca ctt ccc tct gtt taaaaaaaaact atttaagaag agg 1026
 Ala Ser Val Ser Leu Pro Ser Val
 295 300

<210> 392
 <211> 301
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 392
 Met Asn Asn Arg Ile Val Val Val Gly Ser Ile Asn Ala Asp Leu Asn
 1 5 10 15
 Val Leu Val Asp Arg His Pro Ala Pro Gly Glu Thr Leu Leu Gly Ser
 20 25 30
 Gly Gly His Ile Thr Ala Gly Gly Lys Gly Ala Asn Gln Ala Val Ala
 35 40 45
 Ala Ala Leu Gln Gly Ala Asp Val Ala Phe Val Gly Ala Val Gly Lys
 50 55 60
 Asp Pro Tyr Ala Ala Pro Ala Leu Glu Phe Leu Arg Ser Ser Gly Val
 65 70 75 80
 Asp Leu Thr Ala Val Ser Glu Val Asp Asp Thr Thr Gly Leu Ala Val
 85 90 95
 Ile Thr Val Ala Lys Asp Gly Glu Asn Asn Ile Val Val Ile Pro Gly
 100 105 110
 Ala Asn Ser Leu Val Asn Cys Asp Tyr Val Ser Ser Gln Ser Ala Leu
 115 120 125
 Leu Ala Glu Ala Gly Ile Leu Leu Leu Gln Gly Glu Ile Pro Ala Asp
 130 135 140

Gly Phe Lys Glu Ala Ile His His Thr Met Gly Arg Val Val Val Asn
 145 150 155 160
 Leu Ala Pro Val Ile Glu Val Glu Lys Ser Ala Leu Leu Glu Ala Asp
 165 170 175
 Pro Ile Ile Ala Asn Glu His Glu Ala Gly Leu Ile Leu Asp Gln Phe
 180 185 190
 Gly Ala Gly Ile Asp Ser Met Asp Pro His Glu Leu Ala Gln Ala Leu
 195 200 205
 Leu Asp Ala Gly Phe Ala Ser Val Val Leu Thr Leu Gly Ser Ala Gly
 210 215 220
 Ala Leu Val Ala Asp Ala Thr Gly Ile Thr Asp Ile Ala Thr Pro Thr
 225 230 235 240
 Val Gln Ala Val Asp Thr Thr Gly Ala Gly Asp Ala Phe Ala Gly Ala
 245 250 255
 Phe Cys Ala Arg Leu Ile Lys Gly Asp Ser Leu Ile Asp Ala Ala Thr
 260 265 270
 His Ala Ala Arg Val Gly Ala Tyr Ser Val Gln Thr Ala Gly Ala Gln
 275 280 285
 Ala Ser Tyr Pro Asp Ala Ser Val Ser Leu Pro Ser Val
 290 295 300

<210> 393
 <211> 1161
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1138)
 <223> RXA02730

<400> 393
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 cgattacata aaggtagata atgagataaa gcgaggcgct atg gcg acg gaa aaa 115
 Met Ala Thr Glu Lys
 1 5
 ttc cga ccg act ctt aaa gat gtc gct cgt caa gca ggt gtc tcc atc 163
 Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln Ala Gly Val Ser Ile
 10 15 20
 gcc aca gca tca cga gca cta gcg gat aat ccg gcg gtt gct gca tcg 211
 Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro Ala Val Ala Ala Ser
 25 30 35
 act cgt gaa aga atc caa caa tta gcc tct gat ctg ggt tac cgg gcc 259
 Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp Leu Gly Tyr Arg Ala
 40 45 50

aat gct caa gct cgt gcg ctt cgc agt tct cgc agc aac acc att ggt	307
Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg Ser Asn Thr Ile Gly	
55 60 65	
gtg att gtt ccc agt ttg att aac cat tac ttc gcc gca atg gtt act	355
Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe Ala Ala Met Val Thr	
70 75 80 85	
gaa att caa agc acc gcc agc aaa gct gga ctt gcc acg att atc acc	403
Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu Ala Thr Ile Ile Thr	
90 95 100	
aac agc aat gaa gat gcg acc act atg tct ggg tct ttg gag ttt ctc	451
Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly Ser Leu Glu Phe Leu	
105 110 115	
acc tcg cat ggt gtc gat gga atc atc tgc gta cct aat gag gaa tgc	499
Thr Ser His Gly Val Asp Gly Ile Ile Cys Val Pro Asn Glu Glu Cys	
120 125 130	
gcg aat caa cta gag gac ttg cag aag caa gga atg cca gtg gtg ttg	547
Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly Met Pro Val Val Leu	
135 140 145	
gtt gac cga gag ctt cca gga gac tcc acc atc cca acg gcg acc tct	595
Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile Pro Thr Ala Thr Ser	
150 155 160 165	
aac ccc caa cca gga atc gcc gca gca gta gaa ctc ctg gct cac aac	643
Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu Leu Leu Ala His Asn	
170 175 180	
aac gcg ttg ccg att ggt tac ctc tca ggt ccc atg gac acc tca aca	691
Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro Met Asp Thr Ser Thr	
185 190 195	
ggt aga gag cga tta gag gat ttc aaa gca gcc tgc gcc aac tcc aaa	739
Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala Cys Ala Asn Ser Lys	
200 205 210	
att ggc gaa cag ctc gtt ttt ctg ggt ggg tac gaa caa agc gtt gga	787
Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr Glu Gln Ser Val Gly	
215 220 225	
ttt gaa ggc gct acg aaa ttg ctc gat caa gga gct aaa act ctt ttt	835
Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly Ala Lys Thr Leu Phe	
230 235 240 245	
gcc ggc gat tct atg atg acg atc ggt gtc att gaa gcc tgc cat aag	883
Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile Glu Ala Cys His Lys	
250 255 260	
gct ggt ttg gtt atc ggc aag gat gtc agc gtg att ggt ttt gat aca	931
Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val Ile Gly Phe Asp Thr	
265 270 275	
cat ccg ctt ttt gcc ctg caa cct cat ccg ttg aca gtg att gat caa	979
His Pro Leu Phe Ala Leu Gln Pro His Pro Leu Thr Val Ile Asp Gln	
280 285 290	
aat gta gaa caa cta gcc caa cga gca gtg tct atc ctc acc gaa tta	1027

Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser Ile Leu Thr Glu Leu
 295 300 305
 att gca ggc acg gta cct agc gtg acg aaa act acg atc ccc act gcc 1075
 Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr Thr Ile Pro Thr Ala
 310 315 320 325
 ctt att cat cgt gaa tca atc atc aac tcc act tta agg aag aag gat 1123
 Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr Leu Arg Lys Lys Asp
 330 335 340
 gga ctc ccc aat gag taactcaacc ggtaccgaca ttg 1161
 Gly Leu Pro Asn Glu
 345

<210> 394
 <211> 346
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 394
 Met Ala Thr Glu Lys Phe Arg Pro Thr Leu Lys Asp Val Ala Arg Gln
 1 5 10 15
 Ala Gly Val Ser Ile Ala Thr Ala Ser Arg Ala Leu Ala Asp Asn Pro
 20 25 30
 Ala Val Ala Ala Ser Thr Arg Glu Arg Ile Gln Gln Leu Ala Ser Asp
 35 40 45
 Leu Gly Tyr Arg Ala Asn Ala Gln Ala Arg Ala Leu Arg Ser Ser Arg
 50 55 60
 Ser Asn Thr Ile Gly Val Ile Val Pro Ser Leu Ile Asn His Tyr Phe
 65 70 75 80
 Ala Ala Met Val Thr Glu Ile Gln Ser Thr Ala Ser Lys Ala Gly Leu
 85 90 95
 Ala Thr Ile Ile Thr Asn Ser Asn Glu Asp Ala Thr Thr Met Ser Gly
 100 105 110
 Ser Leu Glu Phe Leu Thr Ser His Gly Val Asp Gly Ile Ile Cys Val
 115 120 125
 Pro Asn Glu Glu Cys Ala Asn Gln Leu Glu Asp Leu Gln Lys Gln Gly
 130 135 140
 Met Pro Val Val Leu Val Asp Arg Glu Leu Pro Gly Asp Ser Thr Ile
 145 150 155 160
 Pro Thr Ala Thr Ser Asn Pro Gln Pro Gly Ile Ala Ala Ala Val Glu
 165 170 175
 Leu Leu Ala His Asn Asn Ala Leu Pro Ile Gly Tyr Leu Ser Gly Pro
 180 185 190
 Met Asp Thr Ser Thr Gly Arg Glu Arg Leu Glu Asp Phe Lys Ala Ala
 195 200 205

Cys Ala Asn Ser Lys Ile Gly Glu Gln Leu Val Phe Leu Gly Gly Tyr
 210 215 220
 Glu Gln Ser Val Gly Phe Glu Gly Ala Thr Lys Leu Leu Asp Gln Gly
 225 230 235 240
 Ala Lys Thr Leu Phe Ala Gly Asp Ser Met Met Thr Ile Gly Val Ile
 245 250 255
 Glu Ala Cys His Lys Ala Gly Leu Val Ile Gly Lys Asp Val Ser Val
 260 265 270
 Ile Gly Phe Asp Thr His Pro Leu Phe Ala Leu Gln Pro His Pro Leu
 275 280 285
 Thr Val Ile Asp Gln Asn Val Glu Gln Leu Ala Gln Arg Ala Val Ser
 290 295 300
 Ile Leu Thr Glu Leu Ile Ala Gly Thr Val Pro Ser Val Thr Lys Thr
 305 310 315 320
 Thr Ile Pro Thr Ala Leu Ile His Arg Glu Ser Ile Ile Asn Ser Thr
 325 330 335
 Leu Arg Lys Lys Asp Gly Leu Pro Asn Glu
 340 345

<210> 395
 <211> 483
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(460)
 <223> RXA02551

<400> 395
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 ttaaaaaaac accgtcgatt tcatttcctt ctctatttac atg tcc gta tgt gaa 115
 Met Ser Val Cys Glu
 1 5
 gcc cac aac ccc gaa aac tac tca acc ggt ggc ggt aac atc atc ggc 163
 Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly Gly Asn Ile Ile Gly
 10 15 20
 gga gtg gtc agc ccc act ctc gcg gct tcc gaa tgg ggt tgg caa gtt 211
 Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu Trp Gly Trp Gln Val
 25 30 35
 gat ccc ctc ggt ttg cgc atc gtc ctg aac aac tac tgg gag cgc tgg 259
 Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn Tyr Trp Glu Arg Trp
 40 45 50
 cag aag cca ctg ttc atc gtc gaa aac gga cta gga gca aag gac gtg 307
 Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu Gly Ala Lys Asp Val
 55 60 65

ctt atc gac gga ccc tcc ggc cca aca gta aac gat gac tac cgc atc 355
 Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn Asp Asp Tyr Arg Ile
 70 75 80 85

aaa tac ctc gac gac ggc ggc tca gga atc ttg aag cgc tac aag aag 403
 Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu Lys Arg Tyr Lys Lys
 90 95 100

aag tcc ttt gat tgg tgc cgc gac atc atc gcc acc aat ggc gaa agc 451
 Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala Thr Asn Gly Glu Ser
 105 110 115

ctg gaa tcc taagaaataa aggtaggtgt cac 483
 Leu Glu Ser
 120

<210> 396

<211> 120

<212> PRT

<213> Corynebacterium glutamicum

<400> 396

Met Ser Val Cys Glu Ala His Asn Pro Glu Asn Tyr Ser Thr Gly Gly
 1 5 10 15

Gly Asn Ile Ile Gly Gly Val Val Ser Pro Thr Leu Ala Ala Ser Glu
 20 25 30

Trp Gly Trp Gln Val Asp Pro Leu Gly Leu Arg Ile Val Leu Asn Asn
 35 40 45

Tyr Trp Glu Arg Trp Gln Lys Pro Leu Phe Ile Val Glu Asn Gly Leu
 50 55 60

Gly Ala Lys Asp Val Leu Ile Asp Gly Pro Ser Gly Pro Thr Val Asn
 65 70 75 80

Asp Asp Tyr Arg Ile Lys Tyr Leu Asp Asp Gly Gly Ser Gly Ile Leu
 85 90 95

Lys Arg Tyr Lys Lys Lys Ser Phe Asp Trp Cys Arg Asp Ile Ile Ala
 100 105 110

Thr Asn Gly Glu Ser Leu Glu Ser
 115 120

<210> 397

<211> 795

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(772)

<223> RXA01325

<400> 397

gcgcagcgct cggacgatta cgaacttcag gagaactcgg gggtcattcgt tgcattctac 60


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cctggaaatt ttcccacact aagtcagggtc taagtaggggt atg gat atg acg att 115
Met Asp Met Thr Ile
1 5

tcc cgc tcc acc atg gcc caa atc ctt gac tac acc ctc ctc gga cca 163
Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr Thr Leu Leu Gly Pro
10 15 20

gaa gta acc aac tcc gaa ctg gcc gca ttt ata gat tcc gca att gag 211
Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile Asp Ser Ala Ile Glu
25 30 35

ctg gga gtc ggc acg atc tgt gtc ccc aac agc atg gtc aac cta act 259
Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser Met Val Asn Leu Thr
40 45 50

gca aaa gcc caa gaa gct gga att cga gtg gcc acc gtc gca gga ttc 307
Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala Thr Val Ala Gly Phe
55 60 65

ccg cac ggc aaa acc ccc gcg ttg gtg aaa gcc gcc gaa gcg cgc ctt 355
Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala Ala Glu Ala Arg Leu
70 75 80 85

gcc gta cag tcc gga gct tcc gaa gta gat gtt gtt ttg gat att gcg 403
Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val Val Leu Asp Ile Ala
90 95 100

gta gtg aaa gag gga gat gcc aat agg ttg ctg cag gaa att gtg gca 451
Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu Gln Glu Ile Val Ala
105 110 115

atc agg gag gct gtt cca tct cct gtg gtg ctg aaa ttc atc ctc gaa 499
Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu Lys Phe Ile Leu Glu
120 125 130

aca gct gtt gtg agt gat gaa gca att gtg act gca gtg aat gcg ttg 547
Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr Ala Val Asn Ala Leu
135 140 145

att gct gct ggt gct gac ttc gct aaa act tcc acg gga ttc cac cca 595
Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser Thr Gly Phe His Pro
150 155 160 165

gcg gga ggg gca act gtt gag gct gtt cgg gtg atg gct tcg gct tct 643
Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val Met Ala Ser Ala Ser
170 175 180

cgg gga agg gtt gga att aag gct gcc ggt ggg gtg aaa act tgg gaa 691
Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly Val Lys Thr Trp Glu
185 190 195

gat gcg gtg gcg ttt gtt gaa gca ggg gct act cgc att gga act tct 739
Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr Arg Ile Gly Thr Ser
200 205 210

aat gcg gga gcc att ttg gag ggt gcg ccg gag tagtttggcg ttctaatacgg 792
Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
215 220

gac 795

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<210> 398

<211> 224

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 398

Met Asp Met Thr Ile Ser Arg Ser Thr Met Ala Gln Ile Leu Asp Tyr
 1 5 10 15

Thr Leu Leu Gly Pro Glu Val Thr Asn Ser Glu Leu Ala Ala Phe Ile
 20 25 30

Asp Ser Ala Ile Glu Leu Gly Val Gly Thr Ile Cys Val Pro Asn Ser
 35 40 45

Met Val Asn Leu Thr Ala Lys Ala Gln Glu Ala Gly Ile Arg Val Ala
 50 55 60

Thr Val Ala Gly Phe Pro His Gly Lys Thr Pro Ala Leu Val Lys Ala
 65 70 75 80

Ala Glu Ala Arg Leu Ala Val Gln Ser Gly Ala Ser Glu Val Asp Val
 85 90 95

Val Leu Asp Ile Ala Val Val Lys Glu Gly Asp Ala Asn Arg Leu Leu
 100 105 110

Gln Glu Ile Val Ala Ile Arg Glu Ala Val Pro Ser Pro Val Val Leu
 115 120 125

Lys Phe Ile Leu Glu Thr Ala Val Val Ser Asp Glu Ala Ile Val Thr
 130 135 140

Ala Val Asn Ala Leu Ile Ala Ala Gly Ala Asp Phe Ala Lys Thr Ser
 145 150 155 160

Thr Gly Phe His Pro Ala Gly Gly Ala Thr Val Glu Ala Val Arg Val
 165 170 175

Met Ala Ser Ala Ser Arg Gly Arg Val Gly Ile Lys Ala Ala Gly Gly
 180 185 190

Val Lys Thr Trp Glu Asp Ala Val Ala Phe Val Glu Ala Gly Ala Thr
 195 200 205

Arg Ile Gly Thr Ser Asn Ala Gly Ala Ile Leu Glu Gly Ala Pro Glu
 210 215 220

<210> 399

<211> 684

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(661)

<223> RXA00195

<400> 399

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tagtgggtgc gtttacccaa caagtgaag aatgggagtc gtg act aaa aag atc 115
                               Val Thr Lys Lys Ile
                               1           5

ctt att ttg gga agc act ggt tcg att gga act cag gcg ctg gac gtt 163
Leu Ile Leu Gly Ser Thr Gly Ser Ile Gly Thr Gln Ala Leu Asp Val
                10                15                20

att gct gat aat tca gac aag ttt gag gtg gtg ggt atc gct gcg ggc 211
Ile Ala Asp Asn Ser Asp Lys Phe Glu Val Val Gly Ile Ala Ala Gly
                25                30                35

ggg tct cag cca gac ctc gtt att tcg cag gcg cag cag ttg ggg ctg 259
Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala Gln Gln Leu Gly Leu
                40                45                50

gct gca gac aag gtt gcg gtt gct gat gca cag gct gcc gca gta att 307
Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln Ala Ala Ala Val Ile
                55                60                65

tcg aag gct ctc ggc ggc gag atc atc tct gga acc gat gct gcg aag 355
Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly Thr Asp Ala Ala Lys
                70                75                80                85

att ctg gtg gaa acc aca aag gcc gac act gtg ctt aat gct ctg gtt 403
Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val Leu Asn Ala Leu Val
                90                95                100

ggg tct ttg ggg ctt gcg gca acg ctg gcc act ctg gaa tct ggt gcg 451
Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr Leu Glu Ser Gly Ala
                105                110                115

cat ctt gcc ttg gct aac aaa gaa tcg ctg gtt gcc ggt ggt gag ttt 499
His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val Ala Gly Gly Glu Phe
                120                125                130

gtt acc tca aag gca aag ctg ggg cag atc att ccg gtc gat tcg gag 547
Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile Pro Val Asp Ser Glu
                135                140                145

cac tct gcc atg gcg cag tgt ttg cgt tcg ggt act cgt gat gag gtt 595
His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly Thr Arg Asp Glu Val
                150                155                160                165

gcg cgg att gtg ctg aca gct tcg ggc gga cct ttc agg gct gga cca 643
Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro Phe Arg Ala Gly Pro
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ggg aga aga tgt ggg agg tgactcccga gcaggcagca gcg 684
Gly Arg Arg Cys Gly Arg
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<212> PRT

<213> *Corynebacterium glutamicum*

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 20 25 30

Gly Ile Ala Ala Gly Gly Ser Gln Pro Asp Leu Val Ile Ser Gln Ala
 35 40 45

Gln Gln Leu Gly Leu Ala Ala Asp Lys Val Ala Val Ala Asp Ala Gln
 50 55 60

Ala Ala Ala Val Ile Ser Lys Ala Leu Gly Gly Glu Ile Ile Ser Gly
 65 70 75 80

Thr Asp Ala Ala Lys Ile Leu Val Glu Thr Thr Lys Ala Asp Thr Val
 85 90 95

Leu Asn Ala Leu Val Gly Ser Leu Gly Leu Ala Ala Thr Leu Ala Thr
 100 105 110

Leu Glu Ser Gly Ala His Leu Ala Leu Ala Asn Lys Glu Ser Leu Val
 115 120 125

Ala Gly Gly Glu Phe Val Thr Ser Lys Ala Lys Leu Gly Gln Ile Ile
 130 135 140

Pro Val Asp Ser Glu His Ser Ala Met Ala Gln Cys Leu Arg Ser Gly
 145 150 155 160

Thr Arg Asp Glu Val Ala Arg Ile Val Leu Thr Ala Ser Gly Gly Pro
 165 170 175

Phe Arg Ala Gly Pro Gly Arg Arg Cys Gly Arg
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<210> 401

<211> 738

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(715)

<223> RXA00196

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 Met Trp Glu Val Thr
 1 5

ccc gag cag gca gca gcg cac cca acg tgg gcg atg ggg cag atg aac 163
 Pro Glu Gln Ala Ala Ala His Pro Thr Trp Ala Met Gly Gln Met Asn
 10 15 20

acg ttg aac tcc gcc acc ctt att aat aaa ggc ctc gaa ctc atc gag 211
 Thr Leu Asn Ser Ala Thr Leu Ile Asn Lys Gly Leu Glu Leu Ile Glu
 25 30 35

gcg acc ctg ctg ttt gaa acg gat gcg gat ctc att gat gtg acg gtg 259
 Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu Ile Asp Val Thr Val
 40 45 50

cat ccg cag tcg atc atc cac tcc atg atc acg ttt acg gat ggt gcg 307
 His Pro Gln Ser Ile Ile His Ser Met Ile Thr Phe Thr Asp Gly Ala
 55 60 65

acc atc gcg cag gcg tcg cca cca tcg atg aaa ctg ccg atc gcg ttg 355
 Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys Leu Pro Ile Ala Leu
 70 75 80 85

gcg ctt gat tgg cca cat ccg gtg ccg aag gct cag ccg gcg ctg gat 403
 Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala Gln Pro Ala Leu Asp
 90 95 100

ttc acc gct gct cat acc tgg gct ttt gag ccg gtg gat gat gcc gca 451
 Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro Val Asp Asp Ala Ala
 105 110 115

ttc cct gcg gtg cag ctg gct agg cac gtc gca aag caa aaa ggc acg 499
 Phe Pro Ala Val Gln Leu Ala Arg His Val Ala Lys Gln Lys Gly Thr
 120 125 130

tac ccc gcg gtg tat aac gcc gcc aac gag gag gcg gct gag gcg ttt 547
 Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu Ala Ala Glu Ala Phe
 135 140 145

ttg cgc ggg cga atc aag ttt ccg cag atc gtg gac gtg gtg gac gag 595
 Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val Asp Val Val Asp Glu
 150 155 160 165

gtc ctc caa gga gct tct cag ttt gct ggt gta gca tca cac gtc gat 643
 Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val Ala Ser His Val Asp
 170 175 180

gat att ttg gca acc gaa tct gag gca cgc gcg cgt gcg aat gct ttg 691
 Asp Ile Leu Ala Thr Glu Ser Glu Ala Arg Ala Arg Ala Asn Ala Leu
 185 190 195

atc aac cgg ttg gca acc aac ttg taagctaagg agcttccgcc tcg 738
 Ile Asn Arg Leu Ala Thr Asn Leu
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<210> 402

<211> 205

<212> PRT

<213> Corynebacterium glutamicum

<400> 402

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 20 25 30

Leu Glu Leu Ile Glu Ala Thr Leu Leu Phe Glu Thr Asp Ala Asp Leu
 35 40 45
 Ile Asp Val Thr Val His Pro Gln Ser Ile Ile His Ser Met Ile Thr
 50 55 60
 Phe Thr Asp Gly Ala Thr Ile Ala Gln Ala Ser Pro Pro Ser Met Lys
 65 70 75 80
 Leu Pro Ile Ala Leu Ala Leu Asp Trp Pro His Arg Val Pro Lys Ala
 85 90 95
 Gln Pro Ala Leu Asp Phe Thr Ala Ala His Thr Trp Ala Phe Glu Pro
 100 105 110
 Val Asp Asp Ala Ala Phe Pro Ala Val Gln Leu Ala Arg His Val Ala
 115 120 125
 Lys Gln Lys Gly Thr Tyr Pro Ala Val Tyr Asn Ala Ala Asn Glu Glu
 130 135 140
 Ala Ala Glu Ala Phe Leu Arg Gly Arg Ile Lys Phe Pro Gln Ile Val
 145 150 155 160
 Asp Val Val Asp Glu Val Leu Gln Gly Ala Ser Gln Phe Ala Gly Val
 165 170 175
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 Arg Ala Asn Ala Leu Ile Asn Arg Leu Ala Thr Asn Leu
 195 200 205

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 <222> (101)..(2008)
 <223> RXN01562

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 Met Gly Ile Leu Asn
 1 5
 agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
 10 15 20
 gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
 25 30 35
 gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259

Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr	
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atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt	307
Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe	
55 60 65	
gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct	355
Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala	
70 75 80 85	
aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc	403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr	
90 95 100	
tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg	451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser	
105 110 115	
gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat	499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp	
120 125 130	
ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta	547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu	
135 140 145	
act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa	595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys	
150 155 160 165	
gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct	643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser	
170 175 180	
cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag	691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln	
185 190 195	
cct ttc tat gat cgc ttc atg gaa aag ggc aag acg tcc ctg aaa tcc	739
Pro Phe Tyr Asp Arg Phe Met Glu Lys Gly Lys Thr Ser Leu Lys Ser	
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atg ggg tgg gta ggg gag cgt act ttt gaa gcg ctc cat gca ttt aaa	787
Met Gly Trp Val Gly Glu Arg Thr Phe Glu Ala Leu His Ala Phe Lys	
215 220 225	
gaa ggt gtg aag agc acc gtc att ccc acc gaa atg ttc cct gaa ctg	835
Glu Gly Val Lys Ser Thr Val Ile Pro Thr Glu Met Phe Pro Glu Leu	
230 235 240 245	
ggc atg aaa tac gtg ggt ccg gtt gat gga cat aac caa aaa gct gtc	883
Gly Met Lys Tyr Val Gly Pro Val Asp Gly His Asn Gln Lys Ala Val	
250 255 260	
gac aat gcg ctg aaa tac gct cat gat tat gat ggc ccc atc atc gtg	931
Asp Asn Ala Leu Lys Tyr Ala His Asp Tyr Asp Gly Pro Ile Ile Val	
265 270 275	
cac atg gtc acc gaa aag ggt cgt ggt tac gcg cct gct gag cag gat	979
His Met Val Thr Glu Lys Gly Arg Gly Tyr Ala Pro Ala Glu Gln Asp	

280	285	290	
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gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg ttc agc gat Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val Phe Ser Asp 310 315 320 325			1075
gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt gcc atc acc Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val Ala Ile Thr 330 335 340			1123
gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa gcc aat ttc Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu Ala Asn Phe 345 350 355			1171
ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac gcg gta act Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His Ala Val Thr 360 365 370			1219
tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg gtg gct att Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val Val Ala Ile 375 380 385			1267
tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc atg gat gtg Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu Met Asp Val 390 395 400 405			1315
ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc tca ggt gtc Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg Ser Gly Val 410 415 420			1363
acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat atg gcg ctg Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp Met Ala Leu 425 430 435			1411
acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt gat gag gat Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg Asp Glu Asp 440 445 450			1459
tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat gat ggc ccc Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp Asp Gly Pro 455 460 465			1507
aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca att gtt gct Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro Ile Val Ala 470 475 480 485			1555
atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat gaa gac gcc Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr Glu Asp Ala 490 495 500			1603
act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc atc att gcg Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu Ile Ile Ala 505 510 515			1651
gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc agg att aaa Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser Arg Ile Lys 520 525 530			1699

cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg att gtc ccc 1747
 Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp Ile Val Pro
 535 540 545
 atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac ctc gtg atc 1795
 Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp Leu Val Ile
 550 555 560 565
 acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc ttg ctc tct 1843
 Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser Leu Leu Ser
 570 575 580
 gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga caa atc gcc 1891
 Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg Gln Ile Ala
 585 590 595
 gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa gtg ctc gcc 1939
 Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu Val Leu Ala
 600 605 610
 gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt gtt gga tgg 1987
 Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val Val Gly Trp
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 <212> PRT
 <213> Corynebacterium glutamicum

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 Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
 35 40 45
 Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
 50 55 60
 Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
 65 70 75 80
 Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
 85 90 95
 Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu
 100 105 110
 Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys
 115 120 125
 Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val

130					135					140						
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145					150					155					160	
Ile	Ala	Ala	Gly	Lys	Asp	Arg	Lys	Val	Val	Val	Val	Val	Val	Asn	Asp	Asn
				165					170					175		
Gly	Arg	Ser	Tyr	Ser	Pro	Thr	Ile	Gly	Gly	Phe	Ala	Glu	Asn	Leu	Ala	
			180					185					190			
Gly	Leu	Arg	Met	Gln	Pro	Phe	Tyr	Asp	Arg	Phe	Met	Glu	Lys	Gly	Lys	
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Thr	Ser	Leu	Lys	Ser	Met	Gly	Trp	Val	Gly	Glu	Arg	Thr	Phe	Glu	Ala	
	210					215					220					
Leu	His	Ala	Phe	Lys	Glu	Gly	Val	Lys	Ser	Thr	Val	Ile	Pro	Thr	Glu	
225					230					235					240	
Met	Phe	Pro	Glu	Leu	Gly	Met	Lys	Tyr	Val	Gly	Pro	Val	Asp	Gly	His	
				245					250					255		
Asn	Gln	Lys	Ala	Val	Asp	Asn	Ala	Leu	Lys	Tyr	Ala	His	Asp	Tyr	Asp	
			260					265					270			
Gly	Pro	Ile	Ile	Val	His	Met	Val	Thr	Glu	Lys	Gly	Arg	Gly	Tyr	Ala	
		275					280					285				
Pro	Ala	Glu	Gln	Asp	Leu	Asp	Glu	Leu	Met	His	Ser	Thr	Gly	Val	Ile	
	290					295					300					
Asp	Pro	Leu	Thr	Gly	Ala	Pro	Lys	Ser	Ala	Ser	Lys	Pro	Gly	Trp	Thr	
305					310					315					320	
Ser	Val	Phe	Ser	Asp	Glu	Leu	Val	Lys	Ile	Gly	Ala	Gln	Asn	Glu	Asn	
				325					330					335		
Val	Val	Ala	Ile	Thr	Ala	Ala	Met	Ala	Gly	Pro	Thr	Gly	Leu	Ser	Lys	
			340					345					350			
Phe	Glu	Ala	Asn	Phe	Pro	Asn	Arg	Phe	Phe	Asp	Val	Gly	Ile	Ala	Glu	
		355					360					365				
Gln	His	Ala	Val	Thr	Ser	Ala	Ala	Gly	Leu	Ala	Leu	Gly	Gly	Lys	His	
	370					375					380					
Pro	Val	Val	Ala	Ile	Tyr	Ser	Thr	Phe	Leu	Asn	Arg	Ala	Phe	Asp	Gln	
385					390					395					400	
Leu	Leu	Met	Asp	Val	Gly	Met	Leu	Asn	Gln	Pro	Val	Thr	Leu	Val	Leu	
				405					410					415		
Asp	Arg	Ser	Gly	Val	Thr	Gly	Ser	Asp	Gly	Ala	Ser	His	Asn	Gly	Val	
			420					425					430			
Trp	Asp	Met	Ala	Leu	Thr	Ser	Ile	Val	Pro	Gly	Val	Gln	Val	Ala	Ala	
		435					440					445				
Pro	Arg	Asp	Glu	Asp	Ser	Leu	Arg	Glu	Leu	Leu	Asn	Glu	Ala	Ile	Ser	
	450					455					460					

Ile Asp Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro
 465 470 475 480
 Thr Pro Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu
 485 490 495
 Ala Tyr Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser
 500 505 510
 Val Leu Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val
 515 520 525
 Ala Ser Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro
 530 535 540
 Arg Trp Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp
 545 550 555 560
 His Asp Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val
 565 570 575
 Gly Ser Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro
 580 585 590
 Arg Arg Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg
 595 600 605
 Asn Glu Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr
 610 615 620
 Thr Val Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
 625 630 635

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 <211> 1061
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 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(1038)
 <223> FRXA01562

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 ctc aca gga gct cct aaa tct gca tca aag ccc ggt tgg acc tct gtg 96
 Leu Thr Gly Ala Pro Lys Ser Ala Ser Lys Pro Gly Trp Thr Ser Val
 20 25 30
 ttc agc gat gag ctg gtc aag att ggt gcg cag aat gaa aac gtt gtt 144
 Phe Ser Asp Glu Leu Val Lys Ile Gly Ala Gln Asn Glu Asn Val Val
 35 40 45
 gcc atc acc gcc gcg atg gca ggt cct acc ggt ctg tcc aag ttc gaa 192
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60

gcc aat ttc ccc aac cga ttc ttt gat gtc ggc att gct gag cag cac	240
Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His	
65 70 75 80	
gcg gta act tct gcc gca ggc ctc gca ttg ggt gga aaa cac cct gtg	288
Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val	
85 90 95	
gtg gct att tac tcc acg ttc ttg aac cgc gct ttt gat cag ctg ctc	336
Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu	
100 105 110	
atg gat gtg ggc atg ctc aac cag cct gtt act ttg gtg ctt gat cgc	384
Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg	
115 120 125	
tca ggt gtc acg ggt tcg gat gga gcg agc cac aat ggc gtc tgg gat	432
Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp	
130 135 140	
atg gcg ctg acc tcg atc gtt cca ggc gtg cag gtg gcg gca cca cgt	480
Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg	
145 150 155 160	
gat gag gat tcc ttg cgt gag ctg ctc aat gag gct att tcc atc gat	528
Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp	
165 170 175	
gat ggc ccc aca gtt gtg cgt ttc ccc aag ggc gac ttg cca act cca	576
Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro	
180 185 190	
att gtt gct atc gac acc ttg gaa gac ggc gtg gat gtc ctc gca tat	624
Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr	
195 200 205	
gaa gac gcc act gac gtt gaa tca acc gac gat gcg cca tca gtt ctc	672
Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu	
210 215 220	
atc att gcg gta ggc gag cgc gca act gtt gca ctt gac gtt gct tcc	720
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser	
225 230 235 240	
agg att aaa cag cac ggc gtg aac gtc acg gtt gtt gac ccc cgc tgg	768
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp	
245 250 255	
att gtc ccc atc ccg cag tcc ttg gtc gcg ctg tct gat gat cat gac	816
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp	
260 265 270	
ctc gtg atc acc atc gaa gac ggc gtc atc cac ggc ggc gtg gga tcc	864
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser	
275 280 285	
ttg ctc tct gat gcg ctt aac gcc tct gag gtg gat acc cct cgc cga	912
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg	
290 295 300	

caa atc gcc gtg ccc cag aag tac ctg gat cac gcg tcc cgc aat gaa 960
 Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu
 305 310 315 320
 gtg ctc gcc gat tat ggc ctc gac gcc gac ggc att gaa acc act gtt 1008
 Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val
 325 330 335
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 Val Gly Trp Leu Asp Ser Leu Phe Gly Glu
 340 345
 ccg 1061

<210> 406
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 406
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 35 40 45
 Ala Ile Thr Ala Ala Met Ala Gly Pro Thr Gly Leu Ser Lys Phe Glu
 50 55 60
 Ala Asn Phe Pro Asn Arg Phe Phe Asp Val Gly Ile Ala Glu Gln His
 65 70 75 80
 Ala Val Thr Ser Ala Ala Gly Leu Ala Leu Gly Gly Lys His Pro Val
 85 90 95
 Val Ala Ile Tyr Ser Thr Phe Leu Asn Arg Ala Phe Asp Gln Leu Leu
 100 105 110
 Met Asp Val Gly Met Leu Asn Gln Pro Val Thr Leu Val Leu Asp Arg
 115 120 125
 Ser Gly Val Thr Gly Ser Asp Gly Ala Ser His Asn Gly Val Trp Asp
 130 135 140
 Met Ala Leu Thr Ser Ile Val Pro Gly Val Gln Val Ala Ala Pro Arg
 145 150 155 160
 Asp Glu Asp Ser Leu Arg Glu Leu Leu Asn Glu Ala Ile Ser Ile Asp
 165 170 175
 Asp Gly Pro Thr Val Val Arg Phe Pro Lys Gly Asp Leu Pro Thr Pro
 180 185 190
 Ile Val Ala Ile Asp Thr Leu Glu Asp Gly Val Asp Val Leu Ala Tyr
 195 200 205
 Glu Asp Ala Thr Asp Val Glu Ser Thr Asp Asp Ala Pro Ser Val Leu

210	215	220
Ile Ile Ala Val Gly Glu Arg Ala Thr Val Ala Leu Asp Val Ala Ser		
225	230	235 240
Arg Ile Lys Gln His Gly Val Asn Val Thr Val Val Asp Pro Arg Trp		
	245	250 255
Ile Val Pro Ile Pro Gln Ser Leu Val Ala Leu Ser Asp Asp His Asp		
	260	265 270
Leu Val Ile Thr Ile Glu Asp Gly Val Ile His Gly Gly Val Gly Ser		
	275	280 285
Leu Leu Ser Asp Ala Leu Asn Ala Ser Glu Val Asp Thr Pro Arg Arg		
	290	295 300
Gln Ile Ala Val Pro Gln Lys Tyr Leu Asp His Ala Ser Arg Asn Glu		
305	310	315 320
Val Leu Ala Asp Tyr Gly Leu Asp Ala Asp Gly Ile Glu Thr Thr Val		
	325	330 335
Val Gly Trp Leu Asp Ser Leu Phe Gly Glu		
	340	345

<210> 407
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(703)
 <223> FRXA01705

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 ccgtccgcat ccgagaagca aaggtgtctg actcgcgcca atg gga att ctg aac 115
 Met Gly Ile Leu Asn
 1 5
 agt att tca aca cct gct gac tta aag gcc ctt aat gat gag gat ttg 163
 Ser Ile Ser Thr Pro Ala Asp Leu Lys Ala Leu Asn Asp Glu Asp Leu
 10 15 20
 gac gct ctt gcc aaa gaa atc cga act ttc ctg gtc gat aaa gtc gca 211
 Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu Val Asp Lys Val Ala
 25 30 35
 gca act ggt ggc cac tta ggt cca aat ttg ggc gta gtg gaa tta acc 259
 Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly Val Val Glu Leu Thr
 40 45 50
 atc ggt ctt cat cga gtt ttc gat tcg cct caa gac ccg atc atc ttt 307
 Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln Asp Pro Ile Ile Phe
 55 60 65
 gat act tct cac cag tcc tat gtg cat aag atc ctg acg ggt cgc gct 355

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Asp Thr Ser His Gln Ser Tyr Val His Lys Ile Leu Thr Gly Arg Ala
70          75          80          85

aaa gat ttt gat tct ttg cgt caa aaa gat ggc ctt tct ggt tac acc 403
Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly Leu Ser Gly Tyr Thr
          90          95          100

tgc cgt gct gaa agt gag cac gat tgg act gag tct tcg cat gct tcg 451
Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu Ser Ser His Ala Ser
          105          110          115

gcg gcc ttg tct tat gcg gat ggt ttg tct aaa gcc aag cag ttg gat 499
Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys Ala Lys Gln Leu Asp
          120          125          130

ggc gat acc acg cat agt gtg gtt gct gtc gtt ggt gat ggc gct cta 547
Gly Asp Thr Thr His Ser Val Val Ala Val Val Gly Asp Gly Ala Leu
          135          140          145

act ggc ggc atg tgt tgg gaa gca ctg aac aat att gct gct ggt aaa 595
Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn Ile Ala Ala Gly Lys
          150          155          160          165

gac cgc aaa gtt gtt gtc gta gtc aat gac aat ggc cgg agt tat tct 643
Asp Arg Lys Val Val Val Val Val Asn Asp Asn Gly Arg Ser Tyr Ser
          170          175          180

cca acc att ggc gga ttt gcg gaa aac ctt gcg ggc ctt cgc atg cag 691
Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala Gly Leu Arg Met Gln
          185          190          195

cct ttc tat gat
Pro Phe Tyr Asp
          200

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<210> 408
<211> 201
<212> PRT
<213> Corynebacterium glutamicum

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<400> 408
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Asn Asp Glu Asp Leu Asp Ala Leu Ala Lys Glu Ile Arg Thr Phe Leu
          20          25          30

Val Asp Lys Val Ala Ala Thr Gly Gly His Leu Gly Pro Asn Leu Gly
          35          40          45

Val Val Glu Leu Thr Ile Gly Leu His Arg Val Phe Asp Ser Pro Gln
          50          55          60

Asp Pro Ile Ile Phe Asp Thr Ser His Gln Ser Tyr Val His Lys Ile
65          70          75          80

Leu Thr Gly Arg Ala Lys Asp Phe Asp Ser Leu Arg Gln Lys Asp Gly
          85          90          95

Leu Ser Gly Tyr Thr Cys Arg Ala Glu Ser Glu His Asp Trp Thr Glu

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100	105	110
Ser Ser His Ala Ser Ala Ala Leu Ser Tyr Ala Asp Gly Leu Ser Lys		
115	120	125
Ala Lys Gln Leu Asp Gly Asp Thr Thr His Ser Val Val Ala Val Val		
130	135	140
Gly Asp Gly Ala Leu Thr Gly Gly Met Cys Trp Glu Ala Leu Asn Asn		
145	150	155
Ile Ala Ala Gly Lys Asp Arg Lys Val Val Val Val Val Asn Asp Asn		
165	170	175
Gly Arg Ser Tyr Ser Pro Thr Ile Gly Gly Phe Ala Glu Asn Leu Ala		
180	185	190
Gly Leu Arg Met Gln Pro Phe Tyr Asp		
195	200	

<210> 409
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2218)
 <223> RXN00879

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 Val Thr Ala Arg Arg 5
 ttt ttg aat gaa ctc gcc gat ctc tac ggc gta gca act tcc tac act 163
 Phe Leu Asn Glu Leu Ala Asp Leu Tyr Gly Val Ala Thr Ser Tyr Thr 20
 gat tac aaa ggt gcc cat att gag gtc agc gat gac aca tta gtg aaa 211
 Asp Tyr Lys Gly Ala His Ile Glu Val Ser Asp Asp Thr Leu Val Lys 25 30 35
 atc ctg cgt gct ctg ggt gtg aat tta gat aca agc aac ctc ccc aac 259
 Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn 40 45 50
 gat gac gct atc caa cgc caa att gcc ctc ttc cat gat cga gag ttc 307
 Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe 55 60 65
 act cgc cca ctg cct cca tcg gtg gtt gca gtt gaa ggt gat gaa cta 355
 Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu 70 75 80 85
 gtt ttc ccg gtg cat gtg cac gac ggt tcc cct gca gat gtc cac atc 403
 Val Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile 90 95 100

gaa ttg gaa gac ggc acg cag cgg gat gtt tct cag gtg gaa aac tgg	451
Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp	
105 110 115	
aca gcg cca cgg gaa att gat ggg att agg tgg ggc gag gca tcg ttt	499
Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe	
120 125 130	
aag att cct ggt gat ctc ccc ttg ggt tgg cac aag ctt cac ctt aaa	547
Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys	
135 140 145	
tcc aat gaa cgc tca gct gag tgc ggt ttg atc atc acc ccg gct cgt	595
Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg	
150 155 160 165	
ctg tct act gct gat aag tat ctt gat tcc cct cgc agt ggt gtc atg	643
Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met	
170 175 180	
gcg cag atc tac tct gtg cgt tcc acg ttg tcg tgg ggc atg ggt gat	691
Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp	
185 190 195	
ttc aat gat tta gga aac ttg gca agt gtg gtt gcc cag gat gga gca	739
Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala	
200 205 210	
gac ttc ctg ctc atc aac ccc atg cac gct gca gag ccg ctg cct cct	787
Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro	
215 220 225	
act gag gac tct cct tat ctg ccc aca acc agg cgc ttt atc aac ccg	835
Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro	
230 235 240 245	
atc tac att cgg gta gaa gat att ccg gag ttt aat cag ctt gag att	883
Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile	
250 255 260	
gat cta cgc gat gat atc gca gag atg gct gcg gaa ttc cgc gaa cgc	931
Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg	
265 270 275	
aat ctg acc tca gac atc att gag cgc aat gac gtc tac gct gca aag	979
Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys	
280 285 290	
ctt caa gtg ctg cgc gcc att ttt gaa atg cct cgt tcc agc gaa cgt	1027
Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg	
295 300 305	
gaa gcc aac ttt gtc tcc ttc gtg caa cgg gaa ggc caa ggt ctt att	1075
Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile	
310 315 320 325	
gat ttc gcc acc tgg tgc gcg gac cgc gaa act gca cag tct gaa tct	1123
Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser	
330 335 340	

gtc	cac	gga	act	gag	cca	gac	cgc	gat	gag	ctg	acc	atg	ttc	tac	atg	1171
Val	His	Gly	Thr	Glu	Pro	Asp	Arg	Asp	Glu	Leu	Thr	Met	Phe	Tyr	Met	
			345					350					355			
tgg	ttg	cag	tgg	cta	tgt	gat	gag	cag	ctg	gcg	gca	gct	caa	aag	cgc	1219
Trp	Leu	Gln	Trp	Leu	Cys	Asp	Glu	Gln	Leu	Ala	Ala	Ala	Gln	Lys	Arg	
		360					365					370				
gct	gtc	gat	gcc	gga	atg	tcg	atc	ggc	atc	atg	gca	gac	ctg	gca	gtt	1267
Ala	Val	Asp	Ala	Gly	Met	Ser	Ile	Gly	Ile	Met	Ala	Asp	Leu	Ala	Val	
	375					380					385					
ggc	gtg	cat	cca	ggc	ggc	gct	gat	gcc	cag	aac	ctc	agc	cac	gta	ctt	1315
Gly	Val	His	Pro	Gly	Gly	Ala	Asp	Ala	Gln	Asn	Leu	Ser	His	Val	Leu	
390					395					400					405	
gct	ccg	gat	gcg	tca	gtg	ggc	gcc	cca	cca	gat	gga	tac	aac	cag	cag	1363
Ala	Pro	Asp	Ala	Ser	Val	Gly	Ala	Pro	Pro	Asp	Gly	Tyr	Asn	Gln	Gln	
			410					415						420		
ggc	caa	gac	tgg	tcc	cag	cca	cca	tgg	cat	cca	gtg	cgt	ctt	gca	gag	1411
Gly	Gln	Asp	Trp	Ser	Gln	Pro	Pro	Trp	His	Pro	Val	Arg	Leu	Ala	Glu	
			425					430					435			
gaa	ggc	tac	att	ccg	tgg	cgt	aat	ctg	ctg	cgc	act	gtg	ctg	cgt	cac	1459
Glu	Gly	Tyr	Ile	Pro	Trp	Arg	Asn	Leu	Leu	Arg	Thr	Val	Leu	Arg	His	
		440					445					450				
tcc	ggc	gga	atc	cgc	gtg	gac	cac	gtt	ctt	ggc	ttg	ttc	agg	ctc	ttt	1507
Ser	Gly	Gly	Ile	Arg	Val	Asp	His	Val	Leu	Gly	Leu	Phe	Arg	Leu	Phe	
	455					460					465					
gtc	atg	cca	cgc	atg	caa	tcc	cct	gct	acg	ggc	acc	tat	atc	cgc	ttc	1555
Val	Met	Pro	Arg	Met	Gln	Ser	Pro	Ala	Thr	Gly	Thr	Tyr	Ile	Arg	Phe	
470					475					480					485	
gac	cat	aat	gcg	ttg	gta	ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	1603
Asp	His	Asn	Ala	Leu	Val	Gly	Ile	Leu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	
			490					495						500		
ggc	gcc	gtt	gtc	att	ggt	gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	1651
Gly	Ala	Val	Val	Ile	Gly	Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	
		505						510					515			
caa	gat	gca	ttg	gct	cag	cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	1699
Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	
		520					525					530				
ttc	gag	cat	tcc	cca	agc	cag	ccg	ggt	cct	cgc	cgc	cag	gaa	gag	tat	1747
Phe	Glu	His	Ser	Pro	Ser	Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	
	535					540					545					
cgt	ccg	ctg	gcc	ttg	acc	act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	1795
Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	
550					555					560					565	
gct	ggt	tat	ttg	gag	ggc	gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	1843
Ala	Gly	Tyr	Leu	Glu	Gly	Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	
			570					575						580		
gtg	ctc	aac	act	gat	cct	gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	1891

Val Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp
 585 590 595

caa gcg gag atc ctt gat gtc gca gca tct gcc aac gca ttg cca gcc 1939
 Gln Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala
 600 605 610

cgg gaa tac gtg gga ctc gaa cgc gat cag cgc ggt gag ttg gct gag 1987
 Arg Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu
 615 620 625

ctg ttg gaa ggc ctg cac act ttc gtt gcg aaa acc cct tca gca ctg 2035
 Leu Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu
 630 635 640 645

acc tgt gtc tgc ttg gta gac atg gtc ggt gaa aag cgg gca cag aat 2083
 Thr Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn
 650 655 660

cag ccg ggc aca acg agg gat atg tat ccc aac tgg tgt atc cca ctg 2131
 Gln Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu
 665 670 675

tgt gac agc gaa ggc aac tcc gtg ctc att gaa tcg ctg cgt gaa aat 2179
 Cys Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn
 680 685 690

gag ctg tat cac cgt gtg gca aag gca agc aag cga gat taggtccgct 2228
 Glu Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp
 695 700 705

tcagttgtgg tgg 2241

<210> 410

<211> 706

<212> PRT

<213> Corynebacterium glutamicum

<400> 410

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 20 25 30

Asp Thr Leu Val Lys Ile Leu Arg Ala Leu Gly Val Asn Leu Asp Thr
 35 40 45

Ser Asn Leu Pro Asn Asp Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe
 50 55 60

His Asp Arg Glu Phe Thr Arg Pro Leu Pro Pro Ser Val Val Ala Val
 65 70 75 80

Glu Gly Asp Glu Leu Val Phe Pro Val His Val His Asp Gly Ser Pro
 85 90 95

Ala Asp Val His Ile Glu Leu Glu Asp Gly Thr Gln Arg Asp Val Ser
 100 105 110

Gln Val Glu Asn Trp Thr Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp
 115 120 125
 Gly Glu Ala Ser Phe Lys Ile Pro Gly Asp Leu Pro Leu Gly Trp His
 130 135 140
 Lys Leu His Leu Lys Ser Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile
 145 150 155 160
 Ile Thr Pro Ala Arg Leu Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro
 165 170 175
 Arg Ser Gly Val Met Ala Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser
 180 185 190
 Trp Gly Met Gly Asp Phe Asn Asp Leu Gly Asn Leu Ala Ser Val Val
 195 200 205
 Ala Gln Asp Gly Ala Asp Phe Leu Leu Ile Asn Pro Met His Ala Ala
 210 215 220
 Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg
 225 230 235 240
 Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe
 245 250 255
 Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile Ala Glu Met Ala Ala
 260 265 270
 Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp
 275 280 285
 Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala Ile Phe Glu Met Pro
 290 295 300
 Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser Phe Val Gln Arg Glu
 305 310 315 320
 Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr
 325 330 335
 Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro Asp Arg Asp Glu Leu
 340 345 350
 Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala
 355 360 365
 Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met Ser Ile Gly Ile Met
 370 375 380
 Ala Asp Leu Ala Val Gly Val His Pro Gly Gly Ala Asp Ala Gln Asn
 385 390 395 400
 Leu Ser His Val Leu Ala Pro Asp Ala Ser Val Gly Ala Pro Pro Asp
 405 410 415
 Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln Pro Pro Trp His Pro
 420 425 430
 Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg

435					440					445					
Thr	Val	Leu	Arg	His	Ser	Gly	Gly	Ile	Arg	Val	Asp	His	Val	Leu	Gly
450					455					460					
Leu	Phe	Arg	Leu	Phe	Val	Met	Pro	Arg	Met	Gln	Ser	Pro	Ala	Thr	Gly
465					470					475					480
Thr	Tyr	Ile	Arg	Phe	Asp	His	Asn	Ala	Leu	Val	Gly	Ile	Leu	Ala	Leu
485					490					495					
Glu	Ala	Glu	Leu	Ala	Gly	Ala	Val	Val	Ile	Gly	Glu	Asp	Leu	Gly	Thr
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Phe	Glu	Pro	Trp	Val	Gln	Asp	Ala	Leu	Ala	Gln	Arg	Gly	Ile	Met	Gly
515					520					525					
Thr	Ser	Ile	Leu	Trp	Phe	Glu	His	Ser	Pro	Ser	Gln	Pro	Gly	Pro	Arg
530					535					540					
Arg	Gln	Glu	Glu	Tyr	Arg	Pro	Leu	Ala	Leu	Thr	Thr	Val	Thr	Thr	His
545					550					555					560
Asp	Leu	Pro	Pro	Thr	Ala	Gly	Tyr	Leu	Glu	Gly	Glu	His	Ile	Ala	Leu
565					570					575					
Arg	Glu	Arg	Leu	Gly	Val	Leu	Asn	Thr	Asp	Pro	Ala	Ala	Glu	Leu	Ala
580					585					590					
Glu	Asp	Leu	Gln	Trp	Gln	Ala	Glu	Ile	Leu	Asp	Val	Ala	Ala	Ser	Ala
595					600					605					
Asn	Ala	Leu	Pro	Ala	Arg	Glu	Tyr	Val	Gly	Leu	Glu	Arg	Asp	Gln	Arg
610					615					620					
Gly	Glu	Leu	Ala	Glu	Leu	Leu	Glu	Gly	Leu	His	Thr	Phe	Val	Ala	Lys
625					630					635					640
Thr	Pro	Ser	Ala	Leu	Thr	Cys	Val	Cys	Leu	Val	Asp	Met	Val	Gly	Glu
645					650					655					
Lys	Arg	Ala	Gln	Asn	Gln	Pro	Gly	Thr	Thr	Arg	Asp	Met	Tyr	Pro	Asn
660					665					670					
Trp	Cys	Ile	Pro	Leu	Cys	Asp	Ser	Glu	Gly	Asn	Ser	Val	Leu	Ile	Glu
675					680					685					
Ser	Leu	Arg	Glu	Asn	Glu	Leu	Tyr	His	Arg	Val	Ala	Lys	Ala	Ser	Lys
690					695					700					
Arg Asp															
705															

<210> 411

<211> 2223

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

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200 205 210

ccc atg cac gct gca gag ccg ctg cct cct act gag gac tct cct tat	787
Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr Glu Asp Ser Pro Tyr	
215 220 225	
ctg ccc aca acc agg cgc ttt atc aac ccg atc tac att cgg gta gaa	835
Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile Tyr Ile Arg Val Glu	
230 235 240 245	
gat att ccg gag ttt aat cag ctt gag att gat cta cgc gat gat atc	883
Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp Leu Arg Asp Asp Ile	
250 255 260	
gca gag atg gct gcg gaa ttc cgc gaa cgc aat ctg acc tca gac atc	931
Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn Leu Thr Ser Asp Ile	
265 270 275	
att gag cgc aat gac gtc tac gct gca aag ctt caa gtg ctg cgc gcc	979
Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu Gln Val Leu Arg Ala	
280 285 290	
att ttt gaa atg cct cgt tcc agc gaa cgt gaa gcc aac ttt gtc tcc	1027
Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu Ala Asn Phe Val Ser	
295 300 305	
ttc gtg caa cgg gaa ggc caa ggt ctt att gat ttc gcc acc tgg tgc	1075
Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp Phe Ala Thr Trp Cys	
310 315 320 325	
gcg gac cgc gaa act gca cag tct gaa tct gtc cac gga act gag cca	1123
Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val His Gly Thr Glu Pro	
330 335 340	
gac cgc gat gag ctg acc atg ttc tac atg tgg ttg cag tgg cta tgt	1171
Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp Leu Gln Trp Leu Cys	
345 350 355	
gat gag cag ctg gcg gca gct caa aag cgc gct gtc gat gcc gga atg	1219
Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala Val Asp Ala Gly Met	
360 365 370	
tcg atc ggc atc atg gca gac ctg gca gtt ggt gtg cat cca ggt ggt	1267
Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly Val His Pro Gly Gly	
375 380 385	
gct gat gcc cag aac ctc agc cac gta ctt gct ccg gat gcg tca gtg	1315
Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala Pro Asp Ala Ser Val	
390 395 400 405	
ggc gcc cca cca gat gga tac aac cag cag ggc caa gac tgg tcc cag	1363
Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly Gln Asp Trp Ser Gln	
410 415 420	
cca cca tgg cat cca gtg cgt ctt gca gag gaa ggc tac att ccg tgg	1411
Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu Gly Tyr Ile Pro Trp	
425 430 435	
cgt aat ctg ctg cgc act gtg ctg cgt cac tcc ggc gga atc cgc gtg	1459
Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser Gly Gly Ile Arg Val	
440 445 450	

gac	cac	gtt	ctt	ggt	ttg	ttc	agg	ctc	ttt	gtc	atg	cca	cgc	atg	caa	1507
Asp	His	Val	Leu	Gly	Leu	Phe	Arg	Leu	Phe	Val	Met	Pro	Arg	Met	Gln	
	455					460					465					
tcc	cct	gct	acg	ggc	acc	tat	atc	cgc	ttc	gac	cat	aat	gcg	ttg	gta	1555
Ser	Pro	Ala	Thr	Gly	Thr	Tyr	Ile	Arg	Phe	Asp	His	Asn	Ala	Leu	Val	
470					475					480					485	
ggc	att	cta	gcc	cta	gaa	gca	gaa	ctc	gca	ggc	gcc	gtt	gtc	att	ggt	1603
Gly	Ile	Leu	Ala	Leu	Glu	Ala	Glu	Leu	Ala	Gly	Ala	Val	Val	Ile	Gly	
				490					495					500		
gaa	gat	ctg	gga	acg	ttt	gag	cct	tgg	gta	caa	gat	gca	ttg	gct	cag	1651
Glu	Asp	Leu	Gly	Thr	Phe	Glu	Pro	Trp	Val	Gln	Asp	Ala	Leu	Ala	Gln	
		505						510					515			
cgt	ggc	atc	atg	ggc	acc	tcg	atc	cta	tgg	ttc	gag	cat	tcc	cca	agc	1699
Arg	Gly	Ile	Met	Gly	Thr	Ser	Ile	Leu	Trp	Phe	Glu	His	Ser	Pro	Ser	
		520					525					530				
cag	ccg	ggt	cct	cgc	cgc	cag	gaa	gag	tat	cgt	ccg	ctg	gcc	ttg	acc	1747
Gln	Pro	Gly	Pro	Arg	Arg	Gln	Glu	Glu	Tyr	Arg	Pro	Leu	Ala	Leu	Thr	
	535					540					545					
act	gtg	acc	act	cat	gat	ctc	cct	ccg	act	gct	ggt	tat	ttg	gag	ggc	1795
Thr	Val	Thr	Thr	His	Asp	Leu	Pro	Pro	Thr	Ala	Gly	Tyr	Leu	Glu	Gly	
550					555					560					565	
gag	cac	att	gct	ctt	cgt	gag	cga	ttg	ggg	gtg	ctc	aac	act	gat	cct	1843
Glu	His	Ile	Ala	Leu	Arg	Glu	Arg	Leu	Gly	Val	Leu	Asn	Thr	Asp	Pro	
				570					575					580		
gct	gca	gaa	ctc	gct	gag	gat	ctg	cag	tgg	caa	gcg	gag	atc	ctt	gat	1891
Ala	Ala	Glu	Leu	Ala	Glu	Asp	Leu	Gln	Trp	Gln	Ala	Glu	Ile	Leu	Asp	
			585					590					595			
gtc	gca	gca	tct	gcc	aac	gca	ttg	cca	gcc	cgg	gaa	tac	gtg	gga	ctc	1939
Val	Ala	Ala	Ser	Ala	Asn	Ala	Leu	Pro	Ala	Arg	Glu	Tyr	Val	Gly	Leu	
		600					605					610				
gaa	cgc	gat	cag	cgc	ggt	gag	ttg	gct	gag	ctg	ttg	gaa	ggc	ctg	cac	1987
Glu	Arg	Asp	Gln	Arg	Gly	Glu	Leu	Ala	Glu	Leu	Leu	Glu	Gly	Leu	His	
	615					620					625					
act	ttc	gtt	gcg	aaa	acc	cct	tca	gca	ctg	acc	tgt	gtc	tgc	ttg	gta	2035
Thr	Phe	Val	Ala	Lys	Thr	Pro	Ser	Ala	Leu	Thr	Cys	Val	Cys	Leu	Val	
630					635					640					645	
gac	atg	gtc	ggt	gaa	aag	cgg	gca	cag	aat	cag	ccg	ggc	aca	acg	agg	2083
Asp	Met	Val	Gly	Glu	Lys	Arg	Ala	Gln	Asn	Gln	Pro	Gly	Thr	Thr	Arg	
				650					655					660		
gat	atg	tat	ccc	aac	tgg	tgt	atc	cca	ctg	tgt	gac	agc	gaa	ggc	aac	2131
Asp	Met	Tyr	Pro	Asn	Trp	Cys	Ile	Pro	Leu	Cys	Asp	Ser	Glu	Gly	Asn	
			665					670					675			
tcc	gtg	ctc	att	gaa	tcg	ctg	cgt	gaa	aat	gag	ctg	tat	cac	cgt	gtg	2179
Ser	Val	Leu	Ile	Glu	Ser	Leu	Arg	Glu	Asn	Glu	Leu	Tyr	His	Arg	Val	
		680					685					690				
gca	aag	gca	agc	aag	cga	gat	taggtccgct	tcagttgtgg	tg							2223

Ala Lys Ala Ser Lys Arg Asp
695 700

<210> 412

<211> 700

<212> PRT

<213> Corynebacterium glutamicum

<400> 412

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20 25 30

Leu Arg Ala Leu Gly Val Asn Leu Asp Thr Ser Asn Leu Pro Asn Asp
35 40 45

Asp Ala Ile Gln Arg Gln Ile Ala Leu Phe His Asp Arg Glu Phe Thr
50 55 60

Arg Pro Leu Pro Pro Ser Val Val Ala Val Glu Gly Asp Glu Leu Val
65 70 75 80

Phe Pro Val His Val His Asp Gly Ser Pro Ala Asp Val His Ile Glu
85 90 95

Leu Glu Asp Gly Thr Gln Arg Asp Val Ser Gln Val Glu Asn Trp Thr
100 105 110

Ala Pro Arg Glu Ile Asp Gly Ile Arg Trp Gly Glu Ala Ser Phe Lys
115 120 125

Ile Pro Gly Asp Leu Pro Leu Gly Trp His Lys Leu His Leu Lys Ser
130 135 140

Asn Glu Arg Ser Ala Glu Cys Gly Leu Ile Ile Thr Pro Ala Arg Leu
145 150 155 160

Ser Thr Ala Asp Lys Tyr Leu Asp Ser Pro Arg Ser Gly Val Met Ala
165 170 175

Gln Ile Tyr Ser Val Arg Ser Thr Leu Ser Trp Gly Met Gly Asp Phe
180 185 190

Asn Asp Leu Gly Asn Leu Ala Ser Val Val Ala Gln Asp Gly Ala Asp
195 200 205

Phe Leu Leu Ile Asn Pro Met His Ala Ala Glu Pro Leu Pro Pro Thr
210 215 220

Glu Asp Ser Pro Tyr Leu Pro Thr Thr Arg Arg Phe Ile Asn Pro Ile
225 230 235 240

Tyr Ile Arg Val Glu Asp Ile Pro Glu Phe Asn Gln Leu Glu Ile Asp
245 250 255

Leu Arg Asp Asp Ile Ala Glu Met Ala Ala Glu Phe Arg Glu Arg Asn
260 265 270

Leu Thr Ser Asp Ile Ile Glu Arg Asn Asp Val Tyr Ala Ala Lys Leu
 275 280 285
 Gln Val Leu Arg Ala Ile Phe Glu Met Pro Arg Ser Ser Glu Arg Glu
 290 295 300
 Ala Asn Phe Val Ser Phe Val Gln Arg Glu Gly Gln Gly Leu Ile Asp
 305 310 315 320
 Phe Ala Thr Trp Cys Ala Asp Arg Glu Thr Ala Gln Ser Glu Ser Val
 325 330 335
 His Gly Thr Glu Pro Asp Arg Asp Glu Leu Thr Met Phe Tyr Met Trp
 340 345 350
 Leu Gln Trp Leu Cys Asp Glu Gln Leu Ala Ala Ala Gln Lys Arg Ala
 355 360 365
 Val Asp Ala Gly Met Ser Ile Gly Ile Met Ala Asp Leu Ala Val Gly
 370 375 380
 Val His Pro Gly Gly Ala Asp Ala Gln Asn Leu Ser His Val Leu Ala
 385 390 395 400
 Pro Asp Ala Ser Val Gly Ala Pro Pro Asp Gly Tyr Asn Gln Gln Gly
 405 410 415
 Gln Asp Trp Ser Gln Pro Pro Trp His Pro Val Arg Leu Ala Glu Glu
 420 425 430
 Gly Tyr Ile Pro Trp Arg Asn Leu Leu Arg Thr Val Leu Arg His Ser
 435 440 445
 Gly Gly Ile Arg Val Asp His Val Leu Gly Leu Phe Arg Leu Phe Val
 450 455 460
 Met Pro Arg Met Gln Ser Pro Ala Thr Gly Thr Tyr Ile Arg Phe Asp
 465 470 475 480
 His Asn Ala Leu Val Gly Ile Leu Ala Leu Glu Ala Glu Leu Ala Gly
 485 490 495
 Ala Val Val Ile Gly Glu Asp Leu Gly Thr Phe Glu Pro Trp Val Gln
 500 505 510
 Asp Ala Leu Ala Gln Arg Gly Ile Met Gly Thr Ser Ile Leu Trp Phe
 515 520 525
 Glu His Ser Pro Ser Gln Pro Gly Pro Arg Arg Gln Glu Glu Tyr Arg
 530 535 540
 Pro Leu Ala Leu Thr Thr Val Thr Thr His Asp Leu Pro Pro Thr Ala
 545 550 555 560
 Gly Tyr Leu Glu Gly Glu His Ile Ala Leu Arg Glu Arg Leu Gly Val
 565 570 575
 Leu Asn Thr Asp Pro Ala Ala Glu Leu Ala Glu Asp Leu Gln Trp Gln
 580 585 590
 Ala Glu Ile Leu Asp Val Ala Ala Ser Ala Asn Ala Leu Pro Ala Arg

595	600	605
Glu Tyr Val Gly Leu Glu Arg Asp Gln Arg Gly Glu Leu Ala Glu Leu		
610	615	620
Leu Glu Gly Leu His Thr Phe Val Ala Lys Thr Pro Ser Ala Leu Thr		
625	630	635
Cys Val Cys Leu Val Asp Met Val Gly Glu Lys Arg Ala Gln Asn Gln		
645	650	655
Pro Gly Thr Thr Arg Asp Met Tyr Pro Asn Trp Cys Ile Pro Leu Cys		
660	665	670
Asp Ser Glu Gly Asn Ser Val Leu Ile Glu Ser Leu Arg Glu Asn Glu		
675	680	685
Leu Tyr His Arg Val Ala Lys Ala Ser Lys Arg Asp		
690	695	700

<210> 413
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1264)
 <223> RXN00043

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 Met Ala Glu Val Val 5
 1
 cat tat caa gaa aat gca ggt caa gca gtt aaa aaa att gaa gga aga 163
 His Tyr Gln Glu Asn Ala Gly Gln Ala Val Lys Lys Ile Glu Gly Arg 20
 10 15
 att gtt acc ccc cac ggg gtg att gat ggc ttt ctc caa ctc gaa aac 211
 Ile Val Thr Pro His Gly Val Ile Asp Gly Phe Leu Gln Leu Glu Asn 35
 25 30
 ggc atc atc acg gaa ctc tct gga gaa cca gca cct aaa aac gca gga 259
 Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala Pro Lys Asn Ala Gly 50
 40 45
 ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat 307
 Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His 65
 55 60
 aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag 355
 Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln 85
 70 75 80
 gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg 403
 Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met 100
 90 95

ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
105 110 115	
gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979
Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp	
280 285 290	
ggg gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc	1027
Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val	
295 300 305	
gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta	1075
Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu	
310 315 320 325	
gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac	1123
Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp	
330 335 340	

gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
 345 350 355

gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
 360 365 370

tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
 375 380 385

taaatacgag caaaactttc ctg 1287

<210> 414
 <211> 388
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 414
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 20 25 30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
 35 40 45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65 70 75 80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
 85 90 95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
 100 105 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
 115 120 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys
 130 135 140

Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu
 145 150 155 160

Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val
 165 170 175

Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala
 180 185 190

His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr
 195 200 205

Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr

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<210> 415
<211> 1287
<212> DNA
<213> Corynebacterium glutamicum
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<220>
<221> CDS
<222> (101)..(1264)
<223> FRXA00043
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ttc cac ccc gaa ctc ccc acg att gtt ccc agt ttt att gat ctt cat	307
Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser Phe Ile Asp Leu His	
55 60 65	
aat cac ggt gga aac ggt ggc gcg ttt cct acg gga acg cag gac cag	355
Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr Gly Thr Gln Asp Gln	
70 75 80 85	
gcg agg aat gcc gcg cag tat cac cgc gaa cat ggc acg acc gtg atg	403
Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His Gly Thr Thr Val Met	
90 95 100	
ttg gca agc atg gtt tcg gcg ccg gct gac gca ctg gca gcg cag gtg	451
Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala Leu Ala Ala Gln Val	
105 110 115	
gaa aac ctt att ccc ttg tgt gaa gag ggc ctg ctg tgc ggc att cac	499
Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu Leu Cys Gly Ile His	
120 125 130	
ctc gag ggt cct ttc atc aac gca tgc cgt tgt ggt gct caa aac ccg	547
Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys Gly Ala Gln Asn Pro	
135 140 145	
gat ttt att ttt ccc ggc aac cca aca gat ctt gcc cag gtg atc cat	595
Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu Ala Gln Val Ile His	
150 155 160 165	
gcg gga aaa ggt tgg atc aaa tcg atc aca gta gcg ccg gaa act gac	643
Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val Ala Pro Glu Thr Asp	
170 175 180	
aat ctt act gag ctt ctc gat ctc tgc gca gcg cac cac atc att gct	691
Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala His His Ile Ile Ala	
185 190 195	
tcc ttc ggg cac act gat gca gat ttt gat acc act acc agc gca att	739
Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr Thr Thr Ser Ala Ile	
200 205 210	
gcc ttg gct aaa gag aaa aat gtg acg gtc acg gct acg cat ttg ttc	787
Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr Ala Thr His Leu Phe	
215 220 225	
aat gcg atg cct ccg ctg cat cat agg gat ccc ggc agc gtg ggc gct	835
Asn Ala Met Pro Pro Leu His His Arg Asp Pro Gly Ser Val Gly Ala	
230 235 240 245	
ttg ctt gct gcg gca cgt gcc ggg gac gca tat gtt gag ttg atc gcc	883
Leu Leu Ala Ala Arg Ala Gly Asp Ala Tyr Val Glu Leu Ile Ala	
250 255 260	
gac ggc gtg cat ttg gcc gat gga acg gtc gat cta gct cgt tcc aac	931
Asp Gly Val His Leu Ala Asp Gly Thr Val Asp Leu Ala Arg Ser Asn	
265 270 275	
aac gcc ttt ttc atc acg gac gcc atg gaa gcc gcc gga atg cca gac	979

Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala Ala Gly Met Pro Asp
 280 285 290
 ggt gag tac att ttg ggc gtt ttg aac gtc acc gtc acc gat ggc gtc 1027
 Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr Val Thr Asp Gly Val
 295 300 305
 gcc cgt ctg cgc gat ggc ggc gcc atc gcc ggg ggt acc agc aca cta 1075
 Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly Gly Thr Ser Thr Leu
 310 315 320 325
 gcg agt cag ttc gtg cac cac gtg cgc agg ggt atg acg ctt atc gac 1123
 Ala Ser Gln Phe Val His His Val Arg Arg Gly Met Thr Leu Ile Asp
 330 335 340
 gcg acc ctc cac acc tca acc gtc gcc gcc aaa att ctc gga ctt agc 1171
 Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys Ile Leu Gly Leu Ser
 345 350 355
 gat cac gaa atc gtt aaa tcc aac cct gta aat ttt gtg gtc ttt gac 1219
 Asp His Glu Ile Val Lys Ser Asn Pro Val Asn Phe Val Val Phe Asp
 360 365 370
 tca aac ggc cag tta caa cag gtc cat tta gac cat caa gta att 1264
 Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp His Gln Val Ile
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<210> 416

<211> 388

<212> PRT

<213> Corynebacterium glutamicum

<400> 416

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 20 25 30

Leu Gln Leu Glu Asn Gly Ile Ile Thr Glu Leu Ser Gly Glu Pro Ala
 35 40 45

Pro Lys Asn Ala Gly Phe His Pro Glu Leu Pro Thr Ile Val Pro Ser
 50 55 60

Phe Ile Asp Leu His Asn His Gly Gly Asn Gly Gly Ala Phe Pro Thr
 65 70 75 80

Gly Thr Gln Asp Gln Ala Arg Asn Ala Ala Gln Tyr His Arg Glu His
 85 90 95

Gly Thr Thr Val Met Leu Ala Ser Met Val Ser Ala Pro Ala Asp Ala
 100 105 110

Leu Ala Ala Gln Val Glu Asn Leu Ile Pro Leu Cys Glu Glu Gly Leu
 115 120 125

Leu Cys Gly Ile His Leu Glu Gly Pro Phe Ile Asn Ala Cys Arg Cys

130	135	140
Gly Ala Gln Asn Pro Asp Phe Ile Phe Pro Gly Asn Pro Thr Asp Leu 145 150 155 160		
Ala Gln Val Ile His Ala Gly Lys Gly Trp Ile Lys Ser Ile Thr Val 165 170 175		
Ala Pro Glu Thr Asp Asn Leu Thr Glu Leu Leu Asp Leu Cys Ala Ala 180 185 190		
His His Ile Ile Ala Ser Phe Gly His Thr Asp Ala Asp Phe Asp Thr 195 200 205		
Thr Thr Ser Ala Ile Ala Leu Ala Lys Glu Lys Asn Val Thr Val Thr 210 215 220		
Ala Thr His Leu Phe Asn Ala Met Pro Pro Leu His His Arg Asp Pro 225 230 235 240		
Gly Ser Val Gly Ala Leu Leu Ala Ala Ala Arg Ala Gly Asp Ala Tyr 245 250 255		
Val Glu Leu Ile Ala Asp Gly Val His Leu Ala Asp Gly Thr Val Asp 260 265 270		
Leu Ala Arg Ser Asn Asn Ala Phe Phe Ile Thr Asp Ala Met Glu Ala 275 280 285		
Ala Gly Met Pro Asp Gly Glu Tyr Ile Leu Gly Val Leu Asn Val Thr 290 295 300		
Val Thr Asp Gly Val Ala Arg Leu Arg Asp Gly Gly Ala Ile Ala Gly 305 310 315 320		
Gly Thr Ser Thr Leu Ala Ser Gln Phe Val His His Val Arg Arg Gly 325 330 335		
Met Thr Leu Ile Asp Ala Thr Leu His Thr Ser Thr Val Ala Ala Lys 340 345 350		
Ile Leu Gly Leu Ser Asp His Glu Ile Val Lys Ser Asn Pro Val Asn 355 360 365		
Phe Val Val Phe Asp Ser Asn Gly Gln Leu Gln Gln Val His Leu Asp 370 375 380		
His Gln Val Ile 385		

<210> 417
 <211> 1584
 <212> DNA
 <213> Corynebacterium glutamicum

 <220>
 <221> CDS
 <222> (101)..(1561)
 <223> RXN01752

<400> 417

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                                         Met Met Glu Gln Asp
                                         1 5

ctc agc tac cgt gaa att ctt ccc ctc aac gcg agt gag gag aag aaa 163
Leu Ser Tyr Arg Glu Ile Leu Pro Leu Asn Ala Ser Glu Glu Lys Lys
                        10 15 20

aag gct gca ctg att gat gcc att gaa ggg tta agg gtg cgc gat ccg 211
Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu Arg Val Arg Asp Pro
                        25 30 35

cta ctc tct gcc tcg att gca ttt act aga ggg cag aaa gtc gcc ttc 259
Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly Gln Lys Val Ala Phe
                        40 45 50

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Ile Ala Val Val Val Gly Phe Ile Leu Met Leu Ile Phe Ala Arg Gln
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gca gca ctt att gga ctg tca gca acg tgt acg ttc atg tac ctc att 355
Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr Phe Met Tyr Leu Ile
                        70 75 80 85

aca ttg ttg gac aga ttt atc atg ttt tcc aga ggt atc cgc gcg gaa 403
Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg Gly Ile Arg Ala Glu
                        90 95 100

tcc atc atc cag gta tcg gat gaa gat gcg ctg gct ttc cct gag gac 451
Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu Ala Phe Pro Glu Asp
                        105 110 115

aag ctg aaa acc tac acg gtg ttg gtg ccc gcc tat ggc gaa cct gag 499
Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala Tyr Gly Glu Pro Glu
                        120 125 130

gtg att gcg cag ctg ctg gca tcc atg cac gct ttt gat tac ccc aag 547
Val Ile Ala Gln Leu Leu Ala Ser Met His Ala Phe Asp Tyr Pro Lys
                        135 140 145

cat ctt ctg cag gta ttg ctc atg ttg gag gaa gat gat ctg ccc acg 595
His Leu Leu Gln Val Leu Leu Met Leu Glu Glu Asp Asp Leu Pro Thr
                        150 155 160 165

atc gcc gcg gca gag gca gcg gga gtg gat cag gtg gca acg atc att 643
Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln Val Ala Thr Ile Ile
                        170 175 180

aag gtg ccg cca gcg cag ccc cgc acc aag ccg aag gcc tgt aac tat 691
Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro Lys Ala Cys Asn Tyr
                        185 190 195

gga ttg cac ttt gcc acg ggg gaa att gtc acg atc ttt gac gcg gaa 739
Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr Ile Phe Asp Ala Glu
                        200 205 210

gac atg cca gat ccc ctc caa ctg cgt cgc gtg gtg gtg gca ttt gaa 787
Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val Val Val Ala Phe Glu

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215	220	225	
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aac gcc agg cag aat ctg cta act gcg tgg ttc acc att gaa tat gac Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe Thr Ile Glu Tyr Asp 250 255 260			883
gtg tgg ttt aac ttc ctg ctg cca gcc gtc atg cgc atg aac gca cct Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met Arg Met Asn Ala Pro 265 270 275			931
gtc cca ttg ggc ggt acc tcc aac cat ctg ctc acg ggt gtc ctg aaa Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys 280 285 290			979
gat ctc ggc gcg tgg gat cct ttc aat gtc aca gaa aat gcc gac ctc Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr Glu Asn Ala Asp Leu 295 300 305			1027
ggc gta ccc atc gcg gca aaa gga tat tcc acc gcg gtg ttg gat tcg Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser 310 315 320 325			1075
gtg acg tgg gag gaa gca aac tcc gac acc atc aac tgg ttg cgc cag Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln 330 335 340			1123
cgt tct cgc tgg tac aag ggc tat ctg caa aca tgg ctt gtg tat atg Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met 345 350 355			1171
cgc agg cca aag tgg tta gtc caa gag ctt ggc atc att cct gct gtg Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val 360 365 370			1219
cgt ttt acc ttc ctc atg gca ggc acc ccg atc att gcg gtg ctc aat Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn 375 380 385			1267
ctg ctc ttt tgg tac ttg tcg ctc acg tgg att ctg ggc cag ccc ggc Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly 390 395 400 405			1315
acc att gag cag atg ttc cca cct gcg gtg tac tac cca gcg ttg gtg Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val 410 415 420			1363
tgt ttg gtg gtg gcc aat gct gcg acc atc ttt atg aat ctc att ggc Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly 425 430 435			1411
tgc cgg gaa ggc cgc gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile Ala Val Leu Thr Phe 440 445 450			1459
ccg ctg tat tgg ctg ctc atg agc att gca gcg ttg aaa ggc acg tgg Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp 455 460 465			1507

caa ttg atc acg cga cca tcc tat tgg gag aaa act gcc cac gga ttg 1555
 Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys Thr Ala His Gly Leu
 470 475 480 485

gag gcg taagcgggtgc ccatcgtaa acc 1584
 Glu Ala

<210> 418
 <211> 487
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 418
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 Ser Glu Glu Lys Lys Lys Ala Ala Leu Ile Asp Ala Ile Glu Gly Leu
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 Arg Val Arg Asp Pro Leu Leu Ser Ala Ser Ile Ala Phe Thr Arg Gly
 35 40 45
 Gln Lys Val Ala Phe Ile Ala Val Val Val Gly Phe Ile Leu Met Leu
 50 55 60
 Ile Phe Ala Arg Gln Ala Ala Leu Ile Gly Leu Ser Ala Thr Cys Thr
 65 70 75 80
 Phe Met Tyr Leu Ile Thr Leu Leu Asp Arg Phe Ile Met Phe Ser Arg
 85 90 95
 Gly Ile Arg Ala Glu Ser Ile Ile Gln Val Ser Asp Glu Asp Ala Leu
 100 105 110
 Ala Phe Pro Glu Asp Lys Leu Lys Thr Tyr Thr Val Leu Val Pro Ala
 115 120 125
 Tyr Gly Glu Pro Glu Val Ile Ala Gln Leu Leu Ala Ser Met His Ala
 130 135 140
 Phe Asp Tyr Pro Lys His Leu Leu Gln Val Leu Leu Met Leu Glu Glu
 145 150 155 160
 Asp Asp Leu Pro Thr Ile Ala Ala Ala Glu Ala Ala Gly Val Asp Gln
 165 170 175
 Val Ala Thr Ile Ile Lys Val Pro Pro Ala Gln Pro Arg Thr Lys Pro
 180 185 190
 Lys Ala Cys Asn Tyr Gly Leu His Phe Ala Thr Gly Glu Ile Val Thr
 195 200 205
 Ile Phe Asp Ala Glu Asp Met Pro Asp Pro Leu Gln Leu Arg Arg Val
 210 215 220
 Val Val Ala Phe Glu Arg Ser Ala Ser Asn Thr Val Cys Val Gln Ser
 225 230 235 240

Arg Leu Ser Tyr Arg Asn Ala Arg Gln Asn Leu Leu Thr Ala Trp Phe
 245 250 255
 Thr Ile Glu Tyr Asp Val Trp Phe Asn Phe Leu Leu Pro Gly Val Met
 260 265 270
 Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu Leu
 275 280 285
 Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val Thr
 290 295 300
 Glu Asn Ala Asp Leu Gly Val Pro Ile Ala Ala Lys Gly Tyr Ser Thr
 305 310 315 320
 Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr Ile
 325 330 335
 Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln Thr
 340 345 350
 Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu Gly
 355 360 365
 Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro Ile
 370 375 380
 Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp Ile
 385 390 395 400
 Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val Tyr
 405 410 415
 Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile Phe
 420 425 430
 Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu Ile
 435 440 445
 Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala Ala
 450 455 460
 Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu Lys
 465 470 475 480
 Thr Ala His Gly Leu Glu Ala
 485

<210> 419
 <211> 689
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (19) .. (666)
 <223> FRXA01839

<400> 419
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acc tcc aac cat ctg ctc acg ggt gtc ctg aaa gat ctc ggc gcg tgg 99												
Thr Ser Asn His Leu Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp												
	15				20					25		
gat cct ttc aat gtc aca gaa gat gcg gac ctc ggc gta cgc atc gcg 147												
Asp Pro Phe Asn Val Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala												
	30				35				40			
gca aag gga tat tcc acc gcg gtg ttg gat tcg gtg acg tgg gag gaa 195												
Ala Lys Gly Tyr Ser Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu												
	45				50				55			
gca aac tcc gac acc atc aac tgg ttg cgc cag cgt tct cgc tgg tac 243												
Ala Asn Ser Asp Thr Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr												
	60				65			70				75
aag ggc tat ctg caa aca tgg ctt gtg tat atg cgc agg cca aag tgg 291												
Lys Gly Tyr Leu Gln Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp												
			80					85				90
tta gtc caa gag ctt ggc atc att cct gct gtg cgt ttt acc ttc ctc 339												
Leu Val Gln Glu Leu Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu												
			95					100				105
atg gca ggc acc ccg atc att gcg gtg ctc aat ctg ctc ttt tgg tac 387												
Met Ala Gly Thr Pro Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr												
	110							115				120
ttg tcg ctc acg tgg att ctg ggc cag ccc ggc acc att gag cag atg 435												
Leu Ser Leu Thr Trp Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met												
	125							130				135
ttc cca cct gcg gtg tac tac cca gcg ttg gtg tgt ttg gtg gtg gcc 483												
Phe Pro Pro Ala Val Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala												
	140				145				150			155
aat gct gcg acc atc ttt atg aat ctc att ggc tgc cgg gaa ggc cgc 531												
Asn Ala Ala Thr Ile Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg												
			160					165				170
gac ccc ttg ctg ctc atc gcg gtt ctc acg ttc ccg ctg tat tgg ctg 579												
Asp Pro Leu Leu Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu												
			175					180				185
ctc atg agc att gca gcg ttg aaa ggc acg tgg caa ttg atc acg cga 627												
Leu Met Ser Ile Ala Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg												
	190							195				200
cca tcc tat tgg gag aaa act gcc cac gga ttg gag gcg taagcgggtgc 676												
Pro Ser Tyr Trp Glu Lys Act Ala His Gly Leu Glu Ala												
	205							210				215
ccatcgtcaa acc 689												

<210> 420

<211> 216

<212> PRT

<213> Corynebacterium glutamicum

<400> 420

Met Arg Met Asn Ala Pro Val Pro Leu Gly Gly Thr Ser Asn His Leu
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Leu Thr Gly Val Leu Lys Asp Leu Gly Ala Trp Asp Pro Phe Asn Val
20 25 30

Thr Glu Asp Ala Asp Leu Gly Val Arg Ile Ala Ala Lys Gly Tyr Ser
35 40 45

Thr Ala Val Leu Asp Ser Val Thr Trp Glu Glu Ala Asn Ser Asp Thr
50 55 60

Ile Asn Trp Leu Arg Gln Arg Ser Arg Trp Tyr Lys Gly Tyr Leu Gln
65 70 75 80

Thr Trp Leu Val Tyr Met Arg Arg Pro Lys Trp Leu Val Gln Glu Leu
85 90 95

Gly Ile Ile Pro Ala Val Arg Phe Thr Phe Leu Met Ala Gly Thr Pro
100 105 110

Ile Ile Ala Val Leu Asn Leu Leu Phe Trp Tyr Leu Ser Leu Thr Trp
115 120 125

Ile Leu Gly Gln Pro Gly Thr Ile Glu Gln Met Phe Pro Pro Ala Val
130 135 140

Tyr Tyr Pro Ala Leu Val Cys Leu Val Val Ala Asn Ala Ala Thr Ile
145 150 155 160

Phe Met Asn Leu Ile Gly Cys Arg Glu Gly Arg Asp Pro Leu Leu Leu
165 170 175

Ile Ala Val Leu Thr Phe Pro Leu Tyr Trp Leu Leu Met Ser Ile Ala
180 185 190

Ala Leu Lys Gly Thr Trp Gln Leu Ile Thr Arg Pro Ser Tyr Trp Glu
195 200 205

Lys Thr Ala His Gly Leu Glu Ala
210 215

<210> 421

<211> 1050

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1027)

<223> RXA01859

<400> 421

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ctcgagacga accaaaccgc tacctggggg taggaagaat atg aaa aag aag agc 115
Met Lys Lys Lys Ser

															1	5	
ttt	cca	atc	gca	aga	gtc	atc	ggg	atc	ggc	gtc	ctt	ggc	atc	gcc	ggg	163	
Phe	Pro	Ile	Ala	Arg	Val	Ile	Gly	Ile	Gly	Val	Leu	Gly	Ile	Ala	Gly		
				10					15					20			
atg	gga	ata	ttg	ttg	cta	tgg	ctt	gca	gtt	acc	ctg	tct	gat	cca	gca	211	
Met	Gly	Ile	Leu	Leu	Leu	Trp	Leu	Ala	Val	Thr	Leu	Ser	Asp	Pro	Ala		
				25					30					35			
tca	ccg	ggg	gcc	aaa	gaa	acc	gaa	gtc	ttt	gat	agg	tg	aaa	gtg	ctc	259	
Ser	Pro	Gly	Ala	Lys	Glu	Thr	Glu	Val	Phe	Asp	Arg	Trp	Lys	Val	Leu		
				40					45					50			
ttt	gat	gac	tat	att	cca	cca	gtc	agg	gta	ttg	gtt	gct	gcg	att	atc	307	
Phe	Asp	Asp	Tyr	Ile	Pro	Pro	Val	Arg	Val	Leu	Val	Ala	Ala	Ile	Ile		
				55					60					65			
gtt	gca	tta	att	ttc	gtc	ttt	atc	gct	gcc	aca	gtg	gaa	cga	acc	gta	355	
Val	Ala	Leu	Ile	Phe	Val	Phe	Ile	Ala	Ala	Thr	Val	Glu	Arg	Thr	Val		
				70					75					80			
acc	aac	cgc	tac	cga	agc	tcc	gta	gac	ggc	gaa	aga	gtg	cca	tta	gcg	403	
Thr	Asn	Arg	Tyr	Arg	Ser	Ser	Val	Asp	Gly	Glu	Arg	Val	Pro	Leu	Ala		
				90					95					100			
ccg	aag	att	gtg	atg	gca	gaa	acc	cga	ggg	gta	ttt	cat	gga	ccg	att	451	
Pro	Lys	Ile	Val	Met	Ala	Glu	Thr	Arg	Gly	Val	Phe	His	Gly	Pro	Ile		
				105					110					115			
acc	att	aac	gtg	ctc	gtg	cca	gca	cac	aat	gag	gcg	gaa	aga	att	act	499	
Thr	Ile	Asn	Val	Leu	Val	Pro	Ala	His	Asn	Glu	Ala	Glu	Arg	Ile	Thr		
				120					125					130			
gga	aca	att	cag	gca	ttg	aaa	tca	caa	cat	gag	cct	cca	gaa	cgc	atc	547	
Gly	Thr	Ile	Gln	Ala	Leu	Lys	Ser	Gln	His	Glu	Pro	Pro	Glu	Arg	Ile		
				135					140					145			
gtt	gta	gtt	gcc	gat	aat	tgc	act	gat	gaa	act	acg	gaa	tta	gcc	cgt	595	
Val	Val	Val	Ala	Asp	Asn	Cys	Thr	Asp	Glu	Thr	Thr	Glu	Leu	Ala	Arg		
				150					155					160			
gct	gag	gga	gtg	gag	gtc	ttg	gaa	aca	gtc	aat	aat	aag	ttt	aag	aag	643	
Ala	Glu	Gly	Val	Glu	Val	Leu	Glu	Thr	Val	Asn	Asn	Lys	Phe	Lys	Lys		
				170					175					180			
gcc	gga	gga	ctc	aat	cag	gct	ttg	agc	cgg	atg	ctt	ccc	aca	ttg	ggg	691	
Ala	Gly	Gly	Leu	Asn	Gln	Ala	Leu	Ser	Arg	Met	Leu	Pro	Thr	Leu	Gly		
				185					190					195			
gag	aat	gac	att	gtg	atg	atc	gtt	gac	gct	gat	aca	gca	ctt	gat	caa	739	
Glu	Asn	Asp	Ile	Val	Met	Ile	Val	Asp	Ala	Asp	Thr	Ala	Leu	Asp	Gln		
				200					205					210			
ggg	ttc	ctc	aag	gaa	gca	cgg	cgc	cgc	ttt	gag	tct	gat	cgc	gct	cta	787	
Gly	Phe	Leu	Lys	Glu	Ala	Arg	Arg	Arg	Phe	Glu	Ser	Asp	Arg	Ala	Leu		
				215					220					225			
atg	gcc	gtg	ggc	gga	ttg	ttc	tac	ggg	gag	tca	ggc	tcc	gga	tg	ctt	835	
Met	Ala	Val	Gly	Gly	Leu	Phe	Tyr	Gly	Glu	Ser	Gly	Ser	Gly	Trp	Leu		
				230					235					240			

ggc caa tat cag cgc aac gaa tac acc cgt tat agc cgt gac atc tat 883
 Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr Ser Arg Asp Ile Tyr
 250 255 260

 cga cgc cgc gga cgt gtg ttt gtt ttg act gga aca gcg tcg gct ttt 931
 Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly Thr Ala Ser Ala Phe
 265 270 275

 cgg cca cgc ggc ctg cgg aca gta gcg gaa tca cgc ggg aca ttg atc 979
 Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser Arg Gly Thr Leu Ile
 280 285 290

 ccc gga cgt aaa gcc gat gtt tat gac acc gcg ggc gtt gac cga aga 1027
 Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala Gly Val Asp Arg Arg
 295 300 305

 taatgagttg accctggctt tga 1050

<210> 422
 <211> 309
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 422
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 Leu Gly Ile Ala Gly Met Gly Ile Leu Leu Leu Trp Leu Ala Val Thr
 20 25 30

 Leu Ser Asp Pro Ala Ser Pro Gly Ala Lys Glu Thr Glu Val Phe Asp
 35 40 45

 Arg Trp Lys Val Leu Phe Asp Asp Tyr Ile Pro Pro Val Arg Val Leu
 50 55 60

 Val Ala Ala Ile Ile Val Ala Leu Ile Phe Val Phe Ile Ala Ala Thr
 65 70 75 80

 Val Glu Arg Thr Val Thr Asn Arg Tyr Arg Ser Ser Val Asp Gly Glu
 85 90 95

 Arg Val Pro Leu Ala Pro Lys Ile Val Met Ala Glu Thr Arg Gly Val
 100 105 110

 Phe His Gly Pro Ile Thr Ile Asn Val Leu Val Pro Ala His Asn Glu
 115 120 125

 Ala Glu Arg Ile Thr Gly Thr Ile Gln Ala Leu Lys Ser Gln His Glu
 130 135 140

 Pro Pro Glu Arg Ile Val Val Val Ala Asp Asn Cys Thr Asp Glu Thr
 145 150 155 160

 Thr Glu Leu Ala Arg Ala Glu Gly Val Glu Val Leu Glu Thr Val Asn
 165 170 175

 Asn Lys Phe Lys Lys Ala Gly Gly Leu Asn Gln Ala Leu Ser Arg Met
 180 185 190

Leu Pro Thr Leu Gly Glu Asn Asp Ile Val Met Ile Val Asp Ala Asp
 195 200 205
 Thr Ala Leu Asp Gln Gly Phe Leu Lys Glu Ala Arg Arg Arg Phe Glu
 210 215 220
 Ser Asp Arg Ala Leu Met Ala Val Gly Gly Leu Phe Tyr Gly Glu Ser
 225 230 235 240
 Gly Ser Gly Trp Leu Gly Gln Tyr Gln Arg Asn Glu Tyr Thr Arg Tyr
 245 250 255
 Ser Arg Asp Ile Tyr Arg Arg Arg Gly Arg Val Phe Val Leu Thr Gly
 260 265 270
 Thr Ala Ser Ala Phe Arg Pro Arg Gly Leu Arg Thr Val Ala Glu Ser
 275 280 285
 Arg Gly Thr Leu Ile Pro Gly Arg Lys Ala Asp Val Tyr Asp Thr Ala
 290 295 300
 Gly Val Asp Arg Arg
 305

<210> 423
 <211> 882
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(859)
 <223> RXA00042

<400> 423
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 atacgagcaa aactttcctg ataataaaaag gagtccgacc atg gac atc atc atc 115
 Met Asp Ile Ile Ile
 1 5
 tgc aaa gac gag caa gaa gtc ggc aaa gca gcg gca gcc ctg atc gca 163
 Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala Ala Leu Ile Ala
 10 15 20
 ccc ttc gca act aag ggc gga acc ttg ggg ctt gca act gga tcg tca 211
 Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu Ala Thr Gly Ser Ser
 25 30 35
 cct ttg agc acc tac caa gag ctc att cgc atg tat gaa gct ggg gaa 259
 Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met Tyr Glu Ala Gly Glu
 40 45 50
 gtg tca ttc aag aac tgc aag gca ttc ttg ttg gat gaa tac gtg gga 307
 Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu Asp Glu Tyr Val Gly
 55 60 65
 tta acg cgc gac gat gaa aac agc tac ttc aaa acc att cgt aaa gag 355
 Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys Thr Ile Arg Lys Glu

70	75	80	85	
ttc act gac cac atc gac atc gtt gat gaa gag gtc tac agc cca gat				403
Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu Val Tyr Ser Pro Asp				
	90	95	100	
ggt gca aac cct gat cca tac gaa gca gct gca gag tat gag gca aag				451
Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala Glu Tyr Glu Ala Lys				
	105	110	115	
atc gct gca gaa tcc gtt gat gtt caa atc ctt ggc atc ggc gga aac				499
Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu Gly Ile Gly Gly Asn				
	120	125	130	
ggc cac atc gct ttc aat gag cca tca tct tct ctg tca gga ctg aca				547
Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser Leu Ser Gly Leu Thr				
	135	140	145	
aag gtc cag gcg ctg cac cct aaa act gtg gag gac aac gct cga ttc				595
Lys Val Gln Ala Leu His Pro Lys Thr Val Glu Asp Asn Ala Arg Phe				
	150	155	160	165
ttc aac acc atc gaa gag gtc cca acc cac gcc ctc acc cag ggt ttg				643
Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala Leu Thr Gln Gly Leu				
	170	175	180	
ggc act ttg tcc cgc gcg caa aac atc gtg ttg gtg gca act ggt gaa				691
Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu Val Ala Thr Gly Glu				
	185	190	195	
gga aaa gcc gac gcc atc cgc gga act gtg gaa ggc cca ctg acc gcc				739
Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu Gly Pro Leu Thr Ala				
	200	205	210	
atg tgc cca ggt tcc atc ctg cag atg cac aac aat gcc acc atc atc				787
Met Cys Pro Gly Ser Ile Leu Gln Met His Asn Asn Ala Thr Ile Ile				
	215	220	225	
gtt gat gaa gca gca gca tcc aag ctg gaa aac gct gat cac tac cgt				835
Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn Ala Asp His Tyr Arg				
	230	235	240	245
ctc atg gag caa tta aag ctg cgc tagaaacaaa aaggaaagta gtg				882
Leu Met Glu Gln Leu Lys Leu Arg				
	250			

<210> 424

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 424

Met Asp Ile Ile Ile Cys Lys Asp Glu Gln Glu Val Gly Lys Ala Ala
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Ala Ala Leu Ile Ala Pro Phe Ala Thr Lys Gly Gly Thr Leu Gly Leu
20 25 30

Ala Thr Gly Ser Ser Pro Leu Ser Thr Tyr Gln Glu Leu Ile Arg Met
35 40 45

Tyr Glu Ala Gly Glu Val Ser Phe Lys Asn Cys Lys Ala Phe Leu Leu
 50 55 60
 Asp Glu Tyr Val Gly Leu Thr Arg Asp Asp Glu Asn Ser Tyr Phe Lys
 65 70 75 80
 Thr Ile Arg Lys Glu Phe Thr Asp His Ile Asp Ile Val Asp Glu Glu
 85 90 95
 Val Tyr Ser Pro Asp Gly Ala Asn Pro Asp Pro Tyr Glu Ala Ala Ala
 100 105 110
 Glu Tyr Glu Ala Lys Ile Ala Ala Glu Ser Val Asp Val Gln Ile Leu
 115 120 125
 Gly Ile Gly Gly Asn Gly His Ile Ala Phe Asn Glu Pro Ser Ser Ser
 130 135 140
 Leu Ser Gly Leu Thr Lys Val Gln Ala Leu His Pro Lys Thr Val Glu
 145 150 155 160
 Asp Asn Ala Arg Phe Phe Asn Thr Ile Glu Glu Val Pro Thr His Ala
 165 170 175
 Leu Thr Gln Gly Leu Gly Thr Leu Ser Arg Ala Gln Asn Ile Val Leu
 180 185 190
 Val Ala Thr Gly Glu Gly Lys Ala Asp Ala Ile Arg Gly Thr Val Glu
 195 200 205
 Gly Pro Leu Thr Ala Met Cys Pro Gly Ser Ile Leu Gln Met His Asn
 210 215 220
 Asn Ala Thr Ile Ile Val Asp Glu Ala Ala Ala Ser Lys Leu Glu Asn
 225 230 235 240
 Ala Asp His Tyr Arg Leu Met Glu Gln Leu Lys Leu Arg
 245 250

<210> 425
 <211> 1998
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1975)
 <223> RXA01482

<400> 425
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 ctgcgtccatt aagtgatcga gaaaaagttg ttgtaaagtc atg cgc atg tgt gga 115
 Met Arg Met Cys Gly
 1 5
 att gtt gga tat att ggc caa gcg ggc gac tcc cgt gat tac ttt gct 163
 Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser Arg Asp Tyr Phe Ala
 10 15 20

cta gat gta gtt gtt gaa gga cta cgt cgc ctg gaa tac cgc gga tat	211
Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu Glu Tyr Arg Gly Tyr	
25 30 35	
gac tcc gca ggt att gct att cac gcc aat ggt gag att agc tac cga	259
Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly Glu Ile Ser Tyr Arg	
40 45 50	
aag aag gcc gga aag gtt gct gca cta gat gca gaa atc gct aaa gca	307
Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala Glu Ile Ala Lys Ala	
55 60 65	
cct ctt cca gat tct att ttg gga att gga cac acc cgt tgg gca act	355
Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His Thr Arg Trp Ala Thr	
70 75 80 85	
cat ggt ggc cca acc gat gtc aac gct cac ccc cac gtt gtt tcc aat	403
His Gly Gly Pro Thr Asp Val Asn Ala His Pro His Val Val Ser Asn	
90 95 100	
ggc aag ctt gcc gta gta cac aac ggc atc atc gaa aac ttt gcg gaa	451
Gly Lys Leu Ala Val Val His Asn Gly Ile Ile Glu Asn Phe Ala Glu	
105 110 115	
ctg cgc tct gag ctt tcc gct aag ggc tac aac ttt gta tcc gat acc	499
Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn Phe Val Ser Asp Thr	
120 125 130	
gat acc gaa gtt gct gct tct ttg ctt gct gaa att tac aat act cag	547
Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu Ile Tyr Asn Thr Gln	
135 140 145	
gca aac ggt gac ctc acc ctt gct atg cag ctg acc ggt cag cgc ctt	595
Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu Thr Gly Gln Arg Leu	
150 155 160 165	
gag ggt gct ttc acc ctg cta gct att cat gct gat cac gat gac cgc	643
Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala Asp His Asp Asp Arg	
170 175 180	
atc gtt gca gct cgt cgt aac tct cct ttg gtt atc ggc gtc ggc gag	691
Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val Ile Gly Val Gly Glu	
185 190 195	
ggc gag aac ttc ctc gga tct gac gtt tct ggc ttt att gat tac acc	739
Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly Phe Ile Asp Tyr Thr	
200 205 210	
cgc aag gct gta gag ctg gct aat gac cag gtt gtt acc atc acc gct	787
Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val Val Thr Ile Thr Ala	
215 220 225	
gat gat tac gcc atc acc aac ttt gat gga tca gaa gca gtt ggc aag	835
Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser Glu Ala Val Gly Lys	
230 235 240 245	
cct ttc gac gtg gag tgg gac gct gca gct gct gaa aag ggt ggc ttc	883
Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Glu Lys Gly Gly Phe	
250 255 260	

ggt tcc ttc atg gag aag gaa atc cac gat cag cca gca gct gtt cgc	931
Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln Pro Ala Ala Val Arg	
265 270 275	
gat acc ctg atg ggc cgt ctt gat gaa gat ggc aag ctc gtt ctt gat	979
Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly Lys Leu Val Leu Asp	
280 285 290	
gag ctg cgc atc gat gaa gct att ctg cgt agt gtc gac aag atc gtc	1027
Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser Val Asp Lys Ile Val	
295 300 305	
att gtt gct tgt ggt act gca gct tat gca ggc cag gtt gct cgt tac	1075
Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly Gln Val Ala Arg Tyr	
310 315 320 325	
gcc att gag cac tgg tgc cgc atc cca acc gag gtg gag ctg gct cac	1123
Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu Val Glu Leu Ala His	
330 335 340	
gag ttc cgt tac cgc gac cca atc ctc aac gag aag acc ctt gtt gtg	1171
Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu Lys Thr Leu Val Val	
345 350 355	
gca ttg tcc cag tcc ggc gag acc atg gat acc ctc atg gct gtt cgc	1219
Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr Leu Met Ala Val Arg	
360 365 370	
cac gca cgt gag cag ggt gcc aag gtt gtt gct att tgt aac act gtt	1267
His Ala Arg Glu Gln Gly Ala Lys Val Val Ala Ile Cys Asn Thr Val	
375 380 385	
gga tcc act ctt cca cgt gaa gca gat gcg tcc ctg tac acc tac gct	1315
Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser Leu Tyr Thr Tyr Ala	
390 395 400 405	
ggc cct gag atc gct gtg gcg tcc acc aag gcg ttc ttg gct cag atc	1363
Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala Phe Leu Ala Gln Ile	
410 415 420	
act gct tct tac ttg ctt ggc ctg tac ttg gct cag ctg cgc ggc aac	1411
Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala Gln Leu Arg Gly Asn	
425 430 435	
aag ttc gct gat gag gtt tct tcc att ctg gac agc ctg cgt gag atg	1459
Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp Ser Leu Arg Glu Met	
440 445 450	
cct gag aag att cag cag gtc atc gat gca gaa gag cag atc aag aag	1507
Pro Glu Lys Ile Gln Gln Val Ile Asp Ala Glu Glu Gln Ile Lys Lys	
455 460 465	
ctt ggc caa gat atg gca gat gct aag tct gtg ctg ttc ctg ggc cgc	1555
Leu Gly Gln Asp Met Ala Asp Ala Lys Ser Val Leu Phe Leu Gly Arg	
470 475 480 485	
cac gtt ggt ttc cca gtt gcg ctt gag ggt gcg ttg aag ctc aag gag	1603
His Val Gly Phe Pro Val Ala Leu Glu Gly Ala Leu Lys Leu Lys Glu	
490 495 500	
atc gca tac ctg cac gct gaa ggt ttc gct gca ggc gag ctc aag cac	1651

Ile Ala Tyr Leu His Ala Glu Gly Phe Ala Ala Gly Glu Leu Lys His
505 510 515

ggc cca att gct ttg gtt gag gaa ggc cag ccg atc ttc gtt atc gtg 1699
Gly Pro Ile Ala Leu Val Glu Glu Gly Gln Pro Ile Phe Val Ile Val
520 525 530

cct tca cct cgt ggt cgc gat tcc ctg cac tcc aag gtt gtc tcc aac 1747
Pro Ser Pro Arg Gly Arg Asp Ser Leu His Ser Lys Val Val Ser Asn
535 540 545

att cag gag atc cgt gca cgt ggc gct gtc acc atc gtg att gca gag 1795
Ile Gln Glu Ile Arg Ala Arg Gly Ala Val Thr Ile Val Ile Ala Glu
550 555 560 565

gaa ggc gat gag gct gtc aac gat tac gcc aac ttc atc atc cgc att 1843
Glu Gly Asp Glu Ala Val Asn Asp Tyr Ala Asn Phe Ile Ile Arg Ile
570 575 580

cct cag gcc cca acc ctg atg cag cct ctg ctg tcc acc gtg cct ctg 1891
Pro Gln Ala Pro Thr Leu Met Gln Pro Leu Leu Ser Thr Val Pro Leu
585 590 595

cag atc ttt gcg tgc gct gtg gca acc gca aag ggc tac aac gtg gat 1939
Gln Ile Phe Ala Cys Ala Val Ala Thr Ala Lys Gly Tyr Asn Val Asp
600 605 610

cag cct cgt aac ctg gca aag tct gtc acc gtc gaa taaaaagatt 1985
Gln Pro Arg Asn Leu Ala Lys Ser Val Thr Val Glu
615 620 625

tcgcttctcg acg 1998

<210> 426

<211> 625

<212> PRT

<213> Corynebacterium glutamicum

<400> 426

Met Arg Met Cys Gly Ile Val Gly Tyr Ile Gly Gln Ala Gly Asp Ser
1 5 10 15

Arg Asp Tyr Phe Ala Leu Asp Val Val Val Glu Gly Leu Arg Arg Leu
20 25 30

Glu Tyr Arg Gly Tyr Asp Ser Ala Gly Ile Ala Ile His Ala Asn Gly
35 40 45

Glu Ile Ser Tyr Arg Lys Lys Ala Gly Lys Val Ala Ala Leu Asp Ala
50 55 60

Glu Ile Ala Lys Ala Pro Leu Pro Asp Ser Ile Leu Gly Ile Gly His
65 70 75 80

Thr Arg Trp Ala Thr His Gly Gly Pro Thr Asp Val Asn Ala His Pro
85 90 95

His Val Val Ser Asn Gly Lys Leu Ala Val Val His Asn Gly Ile Ile
100 105 110

Glu Asn Phe Ala Glu Leu Arg Ser Glu Leu Ser Ala Lys Gly Tyr Asn
 115 120 125
 Phe Val Ser Asp Thr Asp Thr Glu Val Ala Ala Ser Leu Leu Ala Glu
 130 135 140
 Ile Tyr Asn Thr Gln Ala Asn Gly Asp Leu Thr Leu Ala Met Gln Leu
 145 150 155 160
 Thr Gly Gln Arg Leu Glu Gly Ala Phe Thr Leu Leu Ala Ile His Ala
 165 170 175
 Asp His Asp Asp Arg Ile Val Ala Ala Arg Arg Asn Ser Pro Leu Val
 180 185 190
 Ile Gly Val Gly Glu Gly Glu Asn Phe Leu Gly Ser Asp Val Ser Gly
 195 200 205
 Phe Ile Asp Tyr Thr Arg Lys Ala Val Glu Leu Ala Asn Asp Gln Val
 210 215 220
 Val Thr Ile Thr Ala Asp Asp Tyr Ala Ile Thr Asn Phe Asp Gly Ser
 225 230 235 240
 Glu Ala Val Gly Lys Pro Phe Asp Val Glu Trp Asp Ala Ala Ala Ala
 245 250 255
 Glu Lys Gly Gly Phe Gly Ser Phe Met Glu Lys Glu Ile His Asp Gln
 260 265 270
 Pro Ala Ala Val Arg Asp Thr Leu Met Gly Arg Leu Asp Glu Asp Gly
 275 280 285
 Lys Leu Val Leu Asp Glu Leu Arg Ile Asp Glu Ala Ile Leu Arg Ser
 290 295 300
 Val Asp Lys Ile Val Ile Val Ala Cys Gly Thr Ala Ala Tyr Ala Gly
 305 310 315 320
 Gln Val Ala Arg Tyr Ala Ile Glu His Trp Cys Arg Ile Pro Thr Glu
 325 330 335
 Val Glu Leu Ala His Glu Phe Arg Tyr Arg Asp Pro Ile Leu Asn Glu
 340 345 350
 Lys Thr Leu Val Val Ala Leu Ser Gln Ser Gly Glu Thr Met Asp Thr
 355 360 365
 Leu Met Ala Val Arg His Ala Arg Glu Gln Gly Ala Lys Val Val Ala
 370 375 380
 Ile Cys Asn Thr Val Gly Ser Thr Leu Pro Arg Glu Ala Asp Ala Ser
 385 390 395 400
 Leu Tyr Thr Tyr Ala Gly Pro Glu Ile Ala Val Ala Ser Thr Lys Ala
 405 410 415
 Phe Leu Ala Gln Ile Thr Ala Ser Tyr Leu Leu Gly Leu Tyr Leu Ala
 420 425 430
 Gln Leu Arg Gly Asn Lys Phe Ala Asp Glu Val Ser Ser Ile Leu Asp

435	440	445
Ser Leu Arg Glu Met Pro	Glu Lys Ile Gln Gln Val	Ile Asp Ala Glu
450	455	460
Glu Gln Ile Lys Lys Leu	Gly Gln Asp Met Ala Asp	Ala Lys Ser Val
465	470	475
Leu Phe Leu Gly Arg His	Val Gly Phe Pro Val Ala	Leu Glu Gly Ala
485	490	495
Leu Lys Leu Lys Glu Ile	Ala Tyr Leu His Ala Glu	Gly Phe Ala Ala
500	505	510
Gly Glu Leu Lys His Gly	Pro Ile Ala Leu Val Glu	Glu Gly Gln Pro
515	520	525
Ile Phe Val Ile Val Pro	Ser Pro Arg Gly Arg Asp	Ser Leu His Ser
530	535	540
Lys Val Val Ser Asn Ile	Gln Glu Ile Arg Ala Arg	Gly Ala Val Thr
545	550	555
Ile Val Ile Ala Glu Glu	Gly Asp Glu Ala Val Asn	Asp Tyr Ala Asn
565	570	575
Phe Ile Ile Arg Ile Pro	Gln Ala Pro Thr Leu Met	Gln Pro Leu Leu
580	585	590
Ser Thr Val Pro Leu Gln	Ile Phe Ala Cys Ala Val	Ala Thr Ala Lys
595	600	605
Gly Tyr Asn Val Asp Gln	Pro Arg Asn Leu Ala Lys	Ser Val Thr Val
610	615	620
Glu		
625		

<210> 427
 <211> 666
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(666)
 <223> RXN03179

<400> 427	
gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca	48
Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala	
1 5 10 15	
gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc	96
Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe	
20 25 30	
ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac	144
Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp	
35 40 45	

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gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192
Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
    50                      55                      60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240
Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
    65                      70                      75                      80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288
Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
                      85                      90                      95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336
Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
                      100                      105                      110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384
Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
    115                      120                      125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432
Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
    130                      135                      140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480
Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
    145                      150                      155                      160

gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528
Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
                      165                      170                      175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
    180                      185                      190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt tcg cgg aaa tgt 624
Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
    195                      200                      205

cca aga aga cgg ctg gtc atg acc atc cac cag gtg tgt acc 666
Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
    210                      215                      220

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<210> 428

<211> 222

<212> PRT

<213> Corynebacterium glutamicum

<400> 428

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Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
  1                      5                      10                      15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
    20                      25                      30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
    35                      40                      45

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Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Ser Arg Lys Cys
 195 200 205

Pro Arg Arg Arg Leu Val Met Thr Ile His Gln Val Cys Thr
 210 215 220

<210> 429
 <211> 672
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(672)
 <223> FRXA02872

<400> 429
 gct cgt gag gca tgg cgc att ttc atg tcc cac tgg gat ctc tac gca 48
 Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

gga acc gca act ggc tac tgg gtg gag cag gaa ttt gag cac gtt ttc 96
 Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

ggc atc aac gcg gag cgc ctg aat gtt ggc acc cca gaa cat gct gac 144
 Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

gcc atc ttt gat gag ctg acc gat att ctt gcc aag cca gat ttc cga 192
 Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

cca cgc gca ctg gct gag cag ttc aac ttg gaa gtt cta gcc acc acc 240
 Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

gac gat ccg ctc gat gac ctg gca gat cac aag gca ctg gca gat gat 288
 Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95

cca acc ttc tcc cct cgt gtg ctc cct acc ttc cgc cca gac gca tac 336
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110

acc aag atg tac aac gct ggt tgg gca gaa aaa acc acc aag ctt atc 384
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125

gat acc gca ggt gac ggc aag gca ggc tgg gag ggt tac ctt cag gca 432
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140

atg cgc aac cgc cgc cag tac ttc atc aat cac ggt gca acc tcc gcg 480
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160

gac cac ggt ctc cac gac acc gac acc acc cca ctg agc cac aaa gat 528
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175

gcc cag aag atc ttg gac aag ggt ctc gct ggc aca gca acc ttg gct 576
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190

gaa atg cat gcc ttc gaa gcc aac acc acc tac cgt ttc gcg gaa atg 624
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205

tcc caa gaa gac ggc ctg gtc atg acc atc cac cca ggt gtg tac cgc 672
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 430

<211> 224

<212> PRT

<213> Corynebacterium glutamicum

<400> 430

Ala Arg Glu Ala Trp Arg Ile Phe Met Ser His Trp Asp Leu Tyr Ala
 1 5 10 15

Gly Thr Ala Thr Gly Tyr Trp Val Glu Gln Glu Phe Glu His Val Phe
 20 25 30

Gly Ile Asn Ala Glu Arg Leu Asn Val Gly Thr Pro Glu His Ala Asp
 35 40 45

Ala Ile Phe Asp Glu Leu Thr Asp Ile Leu Ala Lys Pro Asp Phe Arg
 50 55 60

Pro Arg Ala Leu Ala Glu Gln Phe Asn Leu Glu Val Leu Ala Thr Thr
 65 70 75 80

Asp Asp Pro Leu Asp Asp Leu Ala Asp His Lys Ala Leu Ala Asp Asp
 85 90 95
 Pro Thr Phe Ser Pro Arg Val Leu Pro Thr Phe Arg Pro Asp Ala Tyr
 100 105 110
 Thr Lys Met Tyr Asn Ala Gly Trp Ala Glu Lys Thr Thr Lys Leu Ile
 115 120 125
 Asp Thr Ala Gly Asp Gly Lys Ala Gly Trp Glu Gly Tyr Leu Gln Ala
 130 135 140
 Met Arg Asn Arg Arg Gln Tyr Phe Ile Asn His Gly Ala Thr Ser Ala
 145 150 155 160
 Asp His Gly Leu His Asp Thr Asp Thr Thr Pro Leu Ser His Lys Asp
 165 170 175
 Ala Gln Lys Ile Leu Asp Lys Gly Leu Ala Gly Thr Ala Thr Leu Ala
 180 185 190
 Glu Met His Ala Phe Glu Ala Asn Thr Thr Tyr Arg Phe Ala Glu Met
 195 200 205
 Ser Gln Glu Asp Gly Leu Val Met Thr Ile His Pro Gly Val Tyr Arg
 210 215 220

<210> 431
 <211> 533
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(510)
 <223> RXN03180

<400> 431
 ttc ggt gag aac aaa gat ctc atc tct gac agc agt ttc aac cgc tgg 48
 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15
 ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30
 gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45
 gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60
 ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe

65	70	75	80	
att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga				288
Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly				
	85	90	95	
ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc				336
Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu				
	100	105	110	
cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat				384
Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp				
	115	120	125	
gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa				432
Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln				
	130	135	140	
atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac				480
Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His				
	145	150	155	160
gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga				530
Val Arg Ile Ile Pro Asn Gly Lys Asp Gln				
	165	170		
tgt				533

<210> 432

<211> 170

<212> PRT

<213> Corynebacterium glutamicum

<400> 432

Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
1 5 10 15

Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
20 25 30

Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
35 40 45

Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
50 55 60

Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
65 70 75 80

Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
85 90 95

Leu Ser Glu Ala Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
100 105 110

Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
115 120 125

Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
130 135 140

Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160

Val Arg Ile Ile Pro Asn Gly Lys Asp Gln
 165 170

<210> 433

<211> 533

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(510)

<223> FRXA02873

<400> 433

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 Phe Gly Glu Asn Lys Asp Leu Ile Ser Asp Ser Ser Phe Asn Arg Trp
 1 5 10 15

ctg cgt acg gtt tcc ctc gga tcg acc cag gat gcc gat atg gct gca 96
 Leu Arg Thr Val Ser Leu Gly Ser Thr Gln Asp Ala Asp Met Ala Ala
 20 25 30

gct tcc aac ttg gca gcc aat tct aaa atg gcc cgc cag aac acc cgc 144
 Ala Ser Asn Leu Ala Ala Asn Ser Lys Met Ala Arg Gln Asn Thr Arg
 35 40 45

gat atc ctc gac gca gtc tct gat ggt ggc gtc atg ctc ggc cga aac 192
 Asp Ile Leu Asp Ala Val Ser Asp Gly Gly Val Met Leu Gly Arg Asn
 50 55 60

ggt gcc cta gtg ttg gga cct gtg gtt gga act ctc cac att aaa ttc 240
 Gly Ala Leu Val Leu Gly Pro Val Val Gly Thr Leu His Ile Lys Phe
 65 70 75 80

att gcg cct ttg aac aag cgt gtg gaa aga gtc atg tac aaa act gga 288
 Ile Ala Pro Leu Asn Lys Arg Val Glu Arg Val Met Tyr Lys Thr Gly
 85 90 95

ctc tca gaa gct gct gca gct gag caa tgt gct ttg gag gat cgt ctc 336
 Leu Ser Glu Ala Ala Ala Glu Gln Cys Ala Leu Glu Asp Arg Leu
 100 105 110

cgc gaa gag atg gcc cac gct ttg tat caa tgg aat ccg gga cgc gat 384
 Arg Glu Glu Met Ala His Ala Leu Tyr Gln Trp Asn Pro Gly Arg Asp
 115 120 125

gaa aac tat gac ctc gtg atc aac acc ggt tcg atg aca tac gaa caa 432
 Glu Asn Tyr Asp Leu Val Ile Asn Thr Gly Ser Met Thr Tyr Glu Gln
 130 135 140

atc gtt gat cta gtt gtg gaa act tac gcc agg aag tat ccg ctc cac 480
 Ile Val Asp Leu Val Val Glu Thr Tyr Ala Arg Lys Tyr Pro Leu His
 145 150 155 160

gtg aga atc att ccg aac gga aaa gac caa taaacataca gtccccgtga 530
 Val Arg Ile Ile Pro Asn Gly Lys Asp Gln

165 170

tgt 533

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<210> 434
<211> 170
<212> PRT
<213> Corynebacterium glutamicum
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<400> 434																
Phe	Gly	Glu	Asn	Lys	Asp	Leu	Ile	Ser	Asp	Ser	Ser	Phe	Asn	Arg	Trp	
1				5					10					15		
Leu	Arg	Thr	Val	Ser	Leu	Gly	Ser	Thr	Gln	Asp	Ala	Asp	Met	Ala	Ala	
			20					25					30			
Ala	Ser	Asn	Leu	Ala	Ala	Asn	Ser	Lys	Met	Ala	Arg	Gln	Asn	Thr	Arg	
		35					40					45				
Asp	Ile	Leu	Asp	Ala	Val	Ser	Asp	Gly	Gly	Val	Met	Leu	Gly	Arg	Asn	
	50					55					60					
Gly	Ala	Leu	Val	Leu	Gly	Pro	Val	Val	Gly	Thr	Leu	His	Ile	Lys	Phe	
65					70					75					80	
Ile	Ala	Pro	Leu	Asn	Lys	Arg	Val	Glu	Arg	Val	Met	Tyr	Lys	Thr	Gly	
				85					90					95		
Leu	Ser	Glu	Ala	Ala	Ala	Ala	Glu	Gln	Cys	Ala	Leu	Glu	Asp	Arg	Leu	
			100					105					110			
Arg	Glu	Glu	Met	Ala	His	Ala	Leu	Tyr	Gln	Trp	Asn	Pro	Gly	Arg	Asp	
		115					120					125				
Glu	Asn	Tyr	Asp	Leu	Val	Ile	Asn	Thr	Gly	Ser	Met	Thr	Tyr	Glu	Gln	
	130					135					140					
Ile	Val	Asp	Leu	Val	Val	Glu	Thr	Tyr	Ala	Arg	Lys	Tyr	Pro	Leu	His	
145					150					155					160	
Val	Arg	Ile	Ile	Pro	Asn	Gly	Lys	Asp	Gln							
				165					170							

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<210> 435
<211> 798
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(775)  
<223> RXA02292
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aaaagcgtag gcactaaagt tctcctgcac aatggaggat atg gac aat gac ttt 115
Met Asp Asn Asp Phe
1 5
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gaa tct atc gag aaa atg agc agc ggc gat tgg tac gtg gct acc ggc 163
 Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp Tyr Val Ala Thr Gly
 10 15 20

gcg gaa cgt gaa gaa gtg gca caa aaa aca gcg tta ctt ttc cac gaa 211
 Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala Leu Leu Phe His Glu
 25 30 35

tac aac caa att gga cct aca gac ccc gca cga act gcc gaa ata cta 259
 Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg Thr Ala Glu Ile Leu
 40 45 50

aga act gta cta aat cct gcc agc gga acc tgc acg atc aaa gcg cca 307
 Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys Thr Ile Lys Ala Pro
 55 60 65

gcc atc att gaa tac ggc ttc aac acc acg atc ggc gag cat gtg ttc 355
 Ala Ile Ile Glu Tyr Phe Asn Thr Thr Ile Gly Glu His Val Phe
 70 75 80 85

atc aac ttt ggc ctc acc att tta gat atc gca ccg gtt cgc atc ggg 403
 Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala Pro Val Arg Ile Gly
 90 95 100

gca cgc agc atg ctc ggg cca aac tgt cag ctc ttc acc gca ggt cac 451
 Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu Phe Thr Ala Gly His
 105 110 115

ccg gtc gat gac tgg gaa atg cgc tcc ggt ggg tgg gaa aat ggc gca 499
 Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly Trp Glu Asn Gly Ala
 120 125 130

ccc att tcc att ggc gag gat acg tgg ctg ggt gga aat gtc acc gtc 547
 Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly Gly Asn Val Thr Val
 135 140 145

gtt ggt ggc gtg agc att ggc gat agg tgt gtg att ggc gcg ggg ccc 595
 Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val Ile Gly Ala Gly Pro
 150 155 160 165

gtg gtg acc aag gat att ccg gat gat tct att gct gtg ggc aac cct 643
 Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile Ala Val Gly Asn Pro
 170 175 180

gcg cga gta gtg cgg aaa cgt gat gat agc cgg ctc gaa cgt tcg cag 691
 Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg Leu Glu Arg Ser Gln
 185 190 195

ctg cca gaa ggt gct tcc gtg gat gcg ttg ggg att ctt cct aca aaa 739
 Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly Ile Leu Pro Thr Lys
 200 205 210

tca cct agg ctg tca gaa aat att gcc gaa aaa tat taaatacgca 785
 Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys Tyr
 215 220 225

ggcaactaaga aga 798

<211> 225

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 436

Met Asp Asn Asp Phe Glu Ser Ile Glu Lys Met Ser Ser Gly Asp Trp
 1 5 10 15

Tyr Val Ala Thr Gly Ala Glu Arg Glu Glu Val Ala Gln Lys Thr Ala
 20 25 30

Leu Leu Phe His Glu Tyr Asn Gln Ile Gly Pro Thr Asp Pro Ala Arg
 35 40 45

Thr Ala Glu Ile Leu Arg Thr Val Leu Asn Pro Ala Ser Gly Thr Cys
 50 55 60

Thr Ile Lys Ala Pro Ala Ile Ile Glu Tyr Gly Phe Asn Thr Thr Ile
 65 70 75 80

Gly Glu His Val Phe Ile Asn Phe Gly Leu Thr Ile Leu Asp Ile Ala
 85 90 95

Pro Val Arg Ile Gly Ala Arg Ser Met Leu Gly Pro Asn Cys Gln Leu
 100 105 110

Phe Thr Ala Gly His Pro Val Asp Asp Trp Glu Met Arg Ser Gly Gly
 115 120 125

Trp Glu Asn Gly Ala Pro Ile Ser Ile Gly Glu Asp Thr Trp Leu Gly
 130 135 140

Gly Asn Val Thr Val Val Gly Gly Val Ser Ile Gly Asp Arg Cys Val
 145 150 155 160

Ile Gly Ala Gly Pro Val Val Thr Lys Asp Ile Pro Asp Asp Ser Ile
 165 170 175

Ala Val Gly Asn Pro Ala Arg Val Val Arg Lys Arg Asp Asp Ser Arg
 180 185 190

Leu Glu Arg Ser Gln Leu Pro Glu Gly Ala Ser Val Asp Ala Leu Gly
 195 200 205

Ile Leu Pro Thr Lys Ser Pro Arg Leu Ser Glu Asn Ile Ala Glu Lys
 210 215 220

Tyr

225

<210> 437

<211> 891

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(868)

<223> RXA02666

<400> 437

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tcttgacgat ctgagcttcg acgacgaaga ttagacgccc atg tcg tct aca cga 115
                                   Met Ser Ser Thr Arg
                                   1 5

atc ccc gtc atc gca ctc ctc gcg gcg gcg ggg cgc gga acc cgc ctc 163
Ile Pro Val Ile Ala Leu Leu Ala Ala Gly Arg Gly Thr Arg Leu
                                   10 15 20

ggc gga ccc atc ccc aaa gca ttc gtc acg ttg cgt gaa cgc aca ctt 211
Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu Arg Glu Arg Thr Leu
                                   25 30 35

tta gag cgc tcg ctc caa gcc atg ctc acc tcc gaa agc gtc gac gaa 259
Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser Glu Ser Val Asp Glu
                                   40 45 50

atc atc atc ctc gtc agc ccc gac atg gaa acc tac gcc cgc gat ttg 307
Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr Tyr Ala Arg Asp Leu
                                   55 60 65

ctg cgc aaa cgc ggt ctt ttg aac gac ccc gaa ggg gta cgc gta cgg 355
Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu Gly Val Arg Val Arg
                                   70 75 80 85

ctc gtg cac ggc ggc ggg gag cgc gcg gac tcg gtc tgg gca ggc ctt 403
Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser Val Trp Ala Gly Leu
                                   90 95 100

cag gca att tcg ctt gac gac gcc acc ccc gat gca att gtc tta atc 451
Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp Ala Ile Val Leu Ile
                                   105 110 115

cac gac agc gcc cga gcg ctc aca cca ccc ggc atg att gcg cgc gtg 499
His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly Met Ile Ala Arg Val
                                   120 125 130

gtg cgc aaa gtc cac gaa ggc gcc acc gca gtc atc cca gta ctg cca 547
Val Arg Lys Val His Glu Gly Ala Thr Ala Val Ile Pro Val Leu Pro
                                   135 140 145

gta tcg gac acc atc aaa cga gtg tcc cct gat ggc gga gta gtt gtc 595
Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp Gly Gly Val Val Val
                                   150 155 160 165

gac aca ccc aac cgt gca gaa ctt cgc gcc gtc caa acc cca caa ggc 643
Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val Gln Thr Pro Gln Gly
                                   170 175 180

ttc ctg ctg tcc gaa ctt gtt gca gcg aat gag aaa ttc ttc gcc gac 691
Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu Lys Phe Phe Ala Asp
                                   185 190 195

ccc aac cca ggc ttc atc cca acc gat gac gcc agc ttg atg gaa tgg 739
Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala Ser Leu Met Glu Trp
                                   200 205 210

tac ggc gca gat gta gtc tgc gta caa ggc gac cca atg gcg ttt aaa 787
Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp Pro Met Ala Phe Lys

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215 220 225
 gta aca acc ccc att gat atg atg ctg gca caa cgc atc acc gac gaa 835
 Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln Arg Ile Thr Asp Glu
 230 235 240 245
 gcc gaa ccc aca ata ttt gag gta cca ggt gac taacccaatc atccccgcg 888
 Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
 250 255
 tag 891

<210> 438
 <211> 256
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 438
 Met Ser Ser Thr Arg Ile Pro Val Ile Ala Leu Leu Ala Ala Ala Gly
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 Arg Gly Thr Arg Leu Gly Gly Pro Ile Pro Lys Ala Phe Val Thr Leu
 20 25 30
 Arg Glu Arg Thr Leu Leu Glu Arg Ser Leu Gln Ala Met Leu Thr Ser
 35 40 45
 Glu Ser Val Asp Glu Ile Ile Ile Leu Val Ser Pro Asp Met Glu Thr
 50 55 60
 Tyr Ala Arg Asp Leu Leu Arg Lys Arg Gly Leu Leu Asn Asp Pro Glu
 65 70 75 80
 Gly Val Arg Val Arg Leu Val His Gly Gly Gly Glu Arg Ala Asp Ser
 85 90 95
 Val Trp Ala Gly Leu Gln Ala Ile Ser Leu Asp Asp Ala Thr Pro Asp
 100 105 110
 Ala Ile Val Leu Ile His Asp Ser Ala Arg Ala Leu Thr Pro Pro Gly
 115 120 125
 Met Ile Ala Arg Val Val Arg Lys Val His Glu Gly Ala Thr Ala Val
 130 135 140
 Ile Pro Val Leu Pro Val Ser Asp Thr Ile Lys Arg Val Ser Pro Asp
 145 150 155 160
 Gly Gly Val Val Val Asp Thr Pro Asn Arg Ala Glu Leu Arg Ala Val
 165 170 175
 Gln Thr Pro Gln Gly Phe Leu Leu Ser Glu Leu Val Ala Ala Asn Glu
 180 185 190
 Lys Phe Phe Ala Asp Pro Asn Pro Gly Phe Ile Pro Thr Asp Asp Ala
 195 200 205
 Ser Leu Met Glu Trp Tyr Gly Ala Asp Val Val Cys Val Gln Gly Asp
 210 215 220

Pro Met Ala Phe Lys Val Thr Thr Pro Ile Asp Met Met Leu Ala Gln
 225 230 235 240
 Arg Ile Thr Asp Glu Ala Glu Pro Thr Ile Phe Glu Val Pro Gly Asp
 245 250 255

<210> 439
 <211> 1065
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1042)
 <223> RXA00202

<400> 439
 ctggcagcag attgtcatcg gttgtgtcat cgcgcttgcg gtgggcttcg atgtcatccg 60
 aaacaaaacc tctaagtaat tcctgaaagg aaattttcac atg tac gct cgt aaa 115
 Met Tyr Ala Arg Lys
 1 5
 ctt att gct ctg tcc gct tct gtc gtt ttg gct ttc agc ttg tct gct 163
 Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala Phe Ser Leu Ser Ala
 10 15 20
 tgc aac cgt gaa tct tct ggc acc agc gca gac ggc ggt tct gcg gat 211
 Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp Gly Gly Ser Ala Asp
 25 30 35
 ggg tcg atc acc ttg gct ctg tct acc cag acc aac ccg ttc ttt gtg 259
 Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr Asn Pro Phe Phe Val
 40 45 50
 cag ctt cgt gat ggt gcc cag gaa aag gct gat gaa ttg ggc gtg acc 307
 Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp Glu Leu Gly Val Thr
 55 60 65
 ctc aat gtt cag gat gct tcc gat gac gct gca acg cag gcc aac cag 355
 Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala Thr Gln Ala Asn Gln
 70 75 80 85
 ctc aac aac gct gtc acc acc ggt gct ggc gtg gtg att gtc aac cca 403
 Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val Val Ile Val Asn Pro
 90 95 100
 act gat tct gat gct gtg gtg ccg tcg gtg gaa gct ctc aac cag gct 451
 Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu Ala Leu Asn Gln Ala
 105 110 115
 gac att cct gtt gtg gct gtc gac cgt tcc tcc aat ggt ggc gag gtg 499
 Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser Asn Gly Gly Glu Val
 120 125 130
 gcg tcc ttc gtg gca tct gac aac gtt gct ggc ggc gcg cag gct gct 547
 Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly Gly Ala Gln Ala Ala

135	140	145	
gca gcc ctg gca gag gcg atc ggt ggc gaa ggt gaa atc ctc atg ctg			595
Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly Glu Ile Leu Met Leu			
150	155	160	165
caa ggc att gcg gga tcc tct gca tca cgt gat cgt gga cag gga ttt			643
Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp Arg Gly Gln Gly Phe			
	170	175	180
gaa gag gag atc gct aag cat gag ggc att tcc att gtg gct aag cag			691
Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser Ile Val Ala Lys Gln			
	185	190	195
acc gcc aac ttt gac cgc ggt gag ggc ctg gac gtg gca act aac ctg			739
Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp Val Ala Thr Asn Leu			
	200	205	210
ctg cag gca cac ccc aat gtg aag gcg atc ttc gcg gaa aac gat gag			787
Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe Ala Glu Asn Asp Glu			
	215	220	225
atg gcg ttg ggc gca atc gaa gcc ctg ggt gct cgt gct ggt gaa gat			835
Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala Arg Ala Gly Glu Asp			
230	235	240	245
gtc atc gtt gtc ggt ttc gat ggc acc aat gat ggt ctg gca gcg gtt			883
Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp Gly Leu Ala Ala Val			
	250	255	260
gaa gat gga cgc atg ttg gcc acc gtt gct cag cag cca gaa gag ctg			931
Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln Gln Pro Glu Glu Leu			
	265	270	275
gga gca aag gct gtg gaa gaa gca gct aag ctc ctg cgc ggt gag gac			979
Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu Leu Arg Gly Glu Asp			
	280	285	290
gct gaa aca gag gta cca gtt gag gtt gtc act gtg aag ctc gac aac			1027
Ala Glu Thr Glu Val Pro Val Glu Val Val Thr Val Lys Leu Asp Asn			
	295	300	305
gtc gcg gac ttc aag tagtcggcga tgaaaaagtc cgt			1065
Val Ala Asp Phe Lys			
310			

<210> 440

<211> 314

<212> PRT

<213> Corynebacterium glutamicum

<400> 440

Met Tyr Ala Arg Lys Leu Ile Ala Leu Ser Ala Ser Val Val Leu Ala
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Phe Ser Leu Ser Ala Cys Asn Arg Glu Ser Ser Gly Thr Ser Ala Asp
20 25 30

Gly Gly Ser Ala Asp Gly Ser Ile Thr Leu Ala Leu Ser Thr Gln Thr
35 40 45

Asn Pro Phe Phe Val Gln Leu Arg Asp Gly Ala Gln Glu Lys Ala Asp
 50 55 60
 Glu Leu Gly Val Thr Leu Asn Val Gln Asp Ala Ser Asp Asp Ala Ala
 65 70 75 80
 Thr Gln Ala Asn Gln Leu Asn Asn Ala Val Thr Thr Gly Ala Gly Val
 85 90 95
 Val Ile Val Asn Pro Thr Asp Ser Asp Ala Val Val Pro Ser Val Glu
 100 105 110
 Ala Leu Asn Gln Ala Asp Ile Pro Val Val Ala Val Asp Arg Ser Ser
 115 120 125
 Asn Gly Gly Glu Val Ala Ser Phe Val Ala Ser Asp Asn Val Ala Gly
 130 135 140
 Gly Ala Gln Ala Ala Ala Ala Leu Ala Glu Ala Ile Gly Gly Glu Gly
 145 150 155 160
 Glu Ile Leu Met Leu Gln Gly Ile Ala Gly Ser Ser Ala Ser Arg Asp
 165 170 175
 Arg Gly Gln Gly Phe Glu Glu Glu Ile Ala Lys His Glu Gly Ile Ser
 180 185 190
 Ile Val Ala Lys Gln Thr Ala Asn Phe Asp Arg Gly Glu Gly Leu Asp
 195 200 205
 Val Ala Thr Asn Leu Leu Gln Ala His Pro Asn Val Lys Ala Ile Phe
 210 215 220
 Ala Glu Asn Asp Glu Met Ala Leu Gly Ala Ile Glu Ala Leu Gly Ala
 225 230 235 240
 Arg Ala Gly Glu Asp Val Ile Val Val Gly Phe Asp Gly Thr Asn Asp
 245 250 255
 Gly Leu Ala Ala Val Glu Asp Gly Arg Met Leu Ala Thr Val Ala Gln
 260 265 270
 Gln Pro Glu Glu Leu Gly Ala Lys Ala Val Glu Glu Ala Ala Lys Leu
 275 280 285
 Leu Arg Gly Glu Asp Ala Glu Thr Glu Val Pro Val Glu Val Val Thr
 290 295 300
 Val Lys Leu Asp Asn Val Ala Asp Phe Lys
 305 310

<210> 441

<211> 963

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(940)

<400> 441

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Met Val Ser His Gly
1 5

gcg ccg ggc gat act ttt tgg gat ttg gtc cga aaa ggt gct gaa gac 163
Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg Lys Gly Ala Glu Asp
10 15 20

gcc gcc caa aaa gac aac gtt gaa ctc cgc tat tcc tct aat ccg gaa 211
Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr Ser Ser Asn Pro Glu
25 30 35

atc cct gaa caa tcc aac ctc gtg caa aat gcc atc gat tca cgc gtc 259
Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala Ile Asp Ser Arg Val
40 45 50

gac ggc atc gcc atg acc atg cct aat gct caa tca cta gga ccg gtc 307
Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln Ser Leu Gly Pro Val
55 60 65

gct caa aag gcc gtg gat gcg ggc att cct gtg gtt ggt ctc aac gct 355
Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val Val Gly Leu Asn Ala
70 75 80 85

gga atg aac gaa tac caa gat tat gga atg aca gga ttc ttt ggt caa 403
Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr Gly Phe Phe Gly Gln
90 95 100

gat gaa tcc gtc gca gga gca tcc gca gga gcg cgc ctt gcc gag gaa 451
Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala Arg Leu Ala Glu Glu
105 110 115

aac gca caa aaa gtt ttg tgt gtg atc cat gaa cag ggc aac tcc tcc 499
Asn Ala Gln Lys Val Leu Cys Val Ile His Glu Gln Gly Asn Ser Ser
120 125 130

cag gaa gct cgc tgt ggt ggc gtg tct gaa ggt ttg ggc aaa caa gta 547
Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly Leu Gly Lys Gln Val
135 140 145

gaa acc ctg tat gtc aac ggc atg gat ctc acc tca gtg aac tcc acc 595
Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr Ser Val Asn Ser Thr
150 155 160 165

ctg cag gca aaa ctt gct caa gac cgc agc att gat tgg gtt gtg gga 643
Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile Asp Trp Val Val Gly
170 175 180

ctc cag gct ggt gta tca atg gct att tct gat gcg gca gac gct gcg 691
Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp Ala Ala Asp Ala Ala
185 190 195

aac tca gaa gta aag atc gcc acc ttt gat aca aac gca cag ctc atg 739
Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr Asn Ala Gln Leu Met
200 205 210

acc gct att cgt gat ggc aag atc caa ttc gcc att gat cag caa cca 787
 Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala Ile Asp Gln Gln Pro
 215 220 225

tat ctg cag ggc tac atg gcc gtg gat tcg ctg tgg ttg gcg cac cga 835
 Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu Trp Leu Ala His Arg
 230 235 240 245

aac ggc acc act gtt ggt ggc gga cga ccc gtg tac aca gga cca gcc 883
 Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val Tyr Thr Gly Pro Ala
 250 255 260

att gtg gat gcc acc aac gtt gat gtc att gct gaa gcc gtt ggg gag 931
 Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala Glu Ala Val Gly Glu
 265 270 275

ggt ctg cga tgacaaaaat caagagtggg gag 963
 Gly Leu Arg
 280

<210> 442
 <211> 280
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 442
 Met Val Ser His Gly Ala Pro Gly Asp Thr Phe Trp Asp Leu Val Arg
 1 5 10 15

Lys Gly Ala Glu Asp Ala Ala Gln Lys Asp Asn Val Glu Leu Arg Tyr
 20 25 30

Ser Ser Asn Pro Glu Ile Pro Glu Gln Ser Asn Leu Val Gln Asn Ala
 35 40 45

Ile Asp Ser Arg Val Asp Gly Ile Ala Met Thr Met Pro Asn Ala Gln
 50 55 60

Ser Leu Gly Pro Val Ala Gln Lys Ala Val Asp Ala Gly Ile Pro Val
 65 70 75 80

Val Gly Leu Asn Ala Gly Met Asn Glu Tyr Gln Asp Tyr Gly Met Thr
 85 90 95

Gly Phe Phe Gly Gln Asp Glu Ser Val Ala Gly Ala Ser Ala Gly Ala
 100 105 110

Arg Leu Ala Glu Glu Asn Ala Gln Lys Val Leu Cys Val Ile His Glu
 115 120 125

Gln Gly Asn Ser Ser Gln Glu Ala Arg Cys Gly Gly Val Ser Glu Gly
 130 135 140

Leu Gly Lys Gln Val Glu Thr Leu Tyr Val Asn Gly Met Asp Leu Thr
 145 150 155 160

Ser Val Asn Ser Thr Leu Gln Ala Lys Leu Ala Gln Asp Arg Ser Ile
 165 170 175

Asp Trp Val Val Gly Leu Gln Ala Gly Val Ser Met Ala Ile Ser Asp

180	185	190
Ala Ala Asp Ala Ala Asn Ser Glu Val Lys Ile Ala Thr Phe Asp Thr		
195	200	205
Asn Ala Gln Leu Met Thr Ala Ile Arg Asp Gly Lys Ile Gln Phe Ala		
210	215	220
Ile Asp Gln Gln Pro Tyr Leu Gln Gly Tyr Met Ala Val Asp Ser Leu		
225	230	235
Trp Leu Ala His Arg Asn Gly Thr Thr Val Gly Gly Gly Arg Pro Val		
245	250	255
Tyr Thr Gly Pro Ala Ile Val Asp Ala Thr Asn Val Asp Val Ile Ala		
260	265	270
Glu Ala Val Gly Glu Gly Leu Arg		
275	280	

<210> 443
 <211> 1482
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1459)
 <223> RXN01569

<400> 443
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 agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
 Met Glu Tyr Gly Lys 5
 1
 caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
 Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp 20
 10 15
 ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
 Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln 35
 25 30
 cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
 Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln 50
 40 45
 aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
 Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His 65
 55 60
 gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
 Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe 85
 70 75 80
 gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc 403
 Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val 100
 90 95

gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt	451
Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly	
105 110 115	
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac	499
Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr	
120 125 130	
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac	547
Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn	
135 140 145	
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa	595
Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys	
150 155 160 165	
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc	643
Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg	
170 175 180	
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc	691
Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu Gly Thr Ala Leu Arg	
185 190 195	
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc	739
Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile	
200 205 210	
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc	787
Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile	
215 220 225	
ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc	835
Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg	
230 235 240 245	
gca gca gcg tgg gac atc aac gca gcg gca gtg gct aac ctc gcg acc	883
Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Asn Leu Ala Thr	
250 255 260	
atc gcg cgc gac aac aac ctc acc ctc gtg cac gtg tcc tca gat tat	931
Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His Val Ser Ser Asp Tyr	
265 270 275	
gtc ttc gac ggt gcg gcc gaa tcc tac gat gaa aac gca ccg ttt tcc	979
Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu Asn Ala Pro Phe Ser	
280 285 290	
cca ctc ggc gtg tac ggc caa tcc aaa gca gcc ggc gac atc gga gac	1027
Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala Gly Asp Ile Gly Asp	
295 300 305	
acc acc gca ccg cgc cac tac att gtg cgc acc agc tgg gtg att ggc	1075
Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly	
310 315 320 325	
gat ggc aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc	1123
Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly	
330 335 340	

atc gca cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc 1171
 Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr
 345 350 355

gaa gac atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca 1219
 Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala
 360 365 370

tat ggc acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc 1267
 Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala
 375 380 385

gat gtt gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg 1315
 Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val
 390 395 400 405

agc acc gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg 1363
 Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu
 410 415 420

aac tcc gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca 1411
 Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala
 425 430 435

ccg acc tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 1459
 Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 440 445 450

tgaaaggcat catcctcgca ggt 1482

<210> 444

<211> 453

<212> PRT

<213> Corynebacterium glutamicum

<400> 444

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
 1 5 10 15

Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
 130 135 140
 Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
 145 150 155 160
 Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
 165 170 175
 Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
 180 185 190
 Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
 195 200 205
 Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
 210 215 220
 Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
 225 230 235 240
 Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
 245 250 255
 Ala Asn Leu Ala Thr Ile Ala Arg Asp Asn Asn Leu Thr Leu Val His
 260 265 270
 Val Ser Ser Asp Tyr Val Phe Asp Gly Ala Ala Glu Ser Tyr Asp Glu
 275 280 285
 Asn Ala Pro Phe Ser Pro Leu Gly Val Tyr Gly Gln Ser Lys Ala Ala
 290 295 300
 Gly Asp Ile Gly Asp Thr Thr Ala Pro Arg His Tyr Ile Val Arg Thr
 305 310 315 320
 Ser Trp Val Ile Gly Asp Gly Asn Asn Phe Val Arg Thr Met Lys Ser
 325 330 335
 Leu Asp Glu Arg Gly Ile Ala Pro Ser Val Val Asp Asp Gln Ile Gly
 340 345 350
 Arg Leu Ser Phe Thr Glu Asp Ile Ala Ala Gly Ile Ala His Leu Leu
 355 360 365
 Glu Val Gly Ala Ala Tyr Gly Thr Tyr Asn Leu Thr Asn Thr Gly Glu
 370 375 380
 Pro Ala Ser Trp Ala Asp Val Ala Arg Ala Val Phe Ser Asp Pro Thr
 385 390 395 400
 Lys Val Thr Gly Val Ser Thr Ala Glu Tyr Phe Ala Asn Lys Asp Ala
 405 410 415
 Ala Pro Arg Pro Leu Asn Ser Val Leu Asp Leu Gly Lys Ile Glu Ala
 420 425 430
 Thr Gly Phe Ser Ala Pro Thr Trp Gln Thr Arg Leu Asn Asp Tyr Leu
 435 440 445
 Lys Glu Leu Ser Lys

450

<210> 445
 <211> 449
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(426)
 <223> FRXA01569

<400> 445
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 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
 1 5 10 15
 aat aat ttt gtc cgc acc atg aaa tcc ctc gac gaa cgc ggc atc gca 96
 Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
 20 25 30
 cca tca gta gtt gat gat caa atc ggc cgc cta tcc ttc acc gaa gac 144
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45
 atc gca gcc ggc atc gcg cac ctt ttg gaa gtg ggt gca gca tat ggc 192
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60
 acc tac aac ctc acc aac acc ggc gaa ccc gca agc tgg gcc gat gtt 240
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80
 gcc cgc gca gta ttt tcc gac ccc acc aaa gtt acc ggc gtg agc acc 288
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95
 gcc gag tac ttc gcc aac aaa gac gca gcg ccc cgc cca ctg aac tcc 336
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110
 gtt ttg gat ctc ggc aaa atc gaa gcc acc gga ttt agc gca ccg acc 384
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125
 tgg cag acc cgc ctc aac gac tac ctc aag gaa ctc tca aag 426
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140
 tgaaaggcat catcctcgca ggt 449

<210> 446
 <211> 142
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 446
 Ala Pro Arg His Tyr Ile Val Arg Thr Ser Trp Val Ile Gly Asp Gly
 1 5 10 15

Asn Asn Phe Val Arg Thr Met Lys Ser Leu Asp Glu Arg Gly Ile Ala
 20 25 30
 Pro Ser Val Val Asp Asp Gln Ile Gly Arg Leu Ser Phe Thr Glu Asp
 35 40 45
 Ile Ala Ala Gly Ile Ala His Leu Leu Glu Val Gly Ala Ala Tyr Gly
 50 55 60
 Thr Tyr Asn Leu Thr Asn Thr Gly Glu Pro Ala Ser Trp Ala Asp Val
 65 70 75 80
 Ala Arg Ala Val Phe Ser Asp Pro Thr Lys Val Thr Gly Val Ser Thr
 85 90 95
 Ala Glu Tyr Phe Ala Asn Lys Asp Ala Ala Pro Arg Pro Leu Asn Ser
 100 105 110
 Val Leu Asp Leu Gly Lys Ile Glu Ala Thr Gly Phe Ser Ala Pro Thr
 115 120 125
 Trp Gln Thr Arg Leu Asn Asp Tyr Leu Lys Glu Leu Ser Lys
 130 135 140

<210> 447
 <211> 1028
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1021)
 <223> FRXA02055

<400> 447
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 agaacaacgt cgaagctacc tacgctaagc agggacaata atg gaa tac ggt aaa 115
 Met Glu Tyr Gly Lys
 1 5
 caa ctc acc tcc cac acc acc gac atc gaa ggc cta ctg gtt ttc gat 163
 Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly Leu Leu Val Phe Asp
 10 15 20
 ttc ccc gtc cac ggc gac aac cgc ggc tgg ttc aag gaa aat tgg cag 211
 Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe Lys Glu Asn Trp Gln
 25 30 35
 cgc acc aag atg acc aac ctg ggg ctg ccc gat ttt ggc ccc gtc caa 259
 Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp Phe Gly Pro Val Gln
 40 45 50
 aac aac atg agt ttc aac gcc acc gcc ggc acg act cgc ggc atg cac 307
 Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr Thr Arg Gly Met His
 55 60 65
 gct gag ccg tgg gat aaa ttt gtg tcc gtc gcg gtg ggt tcc gtt ttc 355
 Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala Val Gly Ser Val Phe

70	75	80	85	
gga gct tgg gtg gat ctg cgc gcg ggc tcg agc acg tac ggt aac gtc Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser Thr Tyr Gly Asn Val 90 95 100				403
gta acg caa aaa att acc cct gac gtg gga gtt tac gtc ccg cgt ggt Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val Tyr Val Pro Arg Gly 105 110 115				451
gtg gca aac ggc ttc cag gcg ctc gag gac ggc acg ctg tac acc tac Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly Thr Leu Tyr Thr Tyr 120 125 130				499
ctc gtc aac gat cat tgg tcc ccc gac gcg cat tac gcc aac gtc aac Leu Val Asn Asp His Trp Ser Pro Asp Ala His Tyr Ala Asn Val Asn 135 140 145				547
ctc aac atg atc gac tgg ccg ctg ccc atc acc gag atc tcc gaa aaa Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr Glu Ile Ser Glu Lys 150 155 160 165				595
gat aaa aaa cat cca gcg ctt atc gac gcc acc ccc ctg ccc gcc cgc Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr Pro Leu Pro Ala Arg 170 175 180				643
aag gtt ctc gtg gtc ggc gcc ggc gga caa ctg gga acc gcg cta cgc Lys Val Leu Val Val Gly Ala Gly Gln Leu Gly Thr Ala Leu Arg 185 190 195				691
gcg cag ttc cca gac gcg gaa ttt gtc acg cgc caa gaa ctc gat atc Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg Gln Glu Leu Asp Ile 200 205 210				739
acc tca gat ctc acc gag gct cgc gcg tgg aaa caa tac tcc acc atc Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys Gln Tyr Ser Thr Ile 215 220 225				787
ata aac gcc gcc gcc tac act gcc gtt gac cag gca gaa cac gac cgc Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln Ala Glu His Asp Arg 230 235 240 245				835
gca gca gcg tgg gac att aac gca gcg gca gtg gct acc tcg cga cca Ala Ala Ala Trp Asp Ile Asn Ala Ala Val Ala Thr Ser Arg Pro 250 255 260				883
tcg cgc gcg aca aca acc tca ccc tcg tgc acg tgt cct cag att atg Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr Cys Pro Gln Ile Met 265 270 275				931
tct tcg acg gtg cgg gcg aat cct acg atg aaa acg cac cgt ttt ccc Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys Thr His Arg Phe Pro 280 285 290				979
cac tcg gcg tgt acg gcc aat cca aag cag ccg gcg aca tcg His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro Ala Thr Ser 295 300 305				1021
taagcac				1028

<210> 448

<211> 307

<212> PRT

<213> Corynebacterium glutamicum

<400> 448

Met Glu Tyr Gly Lys Gln Leu Thr Ser His Thr Thr Asp Ile Glu Gly
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Leu Leu Val Phe Asp Phe Pro Val His Gly Asp Asn Arg Gly Trp Phe
 20 25 30

Lys Glu Asn Trp Gln Arg Thr Lys Met Thr Asn Leu Gly Leu Pro Asp
 35 40 45

Phe Gly Pro Val Gln Asn Asn Met Ser Phe Asn Ala Thr Ala Gly Thr
 50 55 60

Thr Arg Gly Met His Ala Glu Pro Trp Asp Lys Phe Val Ser Val Ala
 65 70 75 80

Val Gly Ser Val Phe Gly Ala Trp Val Asp Leu Arg Ala Gly Ser Ser
 85 90 95

Thr Tyr Gly Asn Val Val Thr Gln Lys Ile Thr Pro Asp Val Gly Val
 100 105 110

Tyr Val Pro Arg Gly Val Ala Asn Gly Phe Gln Ala Leu Glu Asp Gly
 115 120 125

Thr Leu Tyr Thr Tyr Leu Val Asn Asp His Trp Ser Pro Asp Ala His
 130 135 140

Tyr Ala Asn Val Asn Leu Asn Met Ile Asp Trp Pro Leu Pro Ile Thr
 145 150 155 160

Glu Ile Ser Glu Lys Asp Lys Lys His Pro Ala Leu Ile Asp Ala Thr
 165 170 175

Pro Leu Pro Ala Arg Lys Val Leu Val Val Gly Ala Gly Gly Gln Leu
 180 185 190

Gly Thr Ala Leu Arg Ala Gln Phe Pro Asp Ala Glu Phe Val Thr Arg
 195 200 205

Gln Glu Leu Asp Ile Thr Ser Asp Leu Thr Glu Ala Arg Ala Trp Lys
 210 215 220

Gln Tyr Ser Thr Ile Ile Asn Ala Ala Ala Tyr Thr Ala Val Asp Gln
 225 230 235 240

Ala Glu His Asp Arg Ala Ala Ala Trp Asp Ile Asn Ala Ala Ala Val
 245 250 255

Ala Thr Ser Arg Pro Ser Arg Ala Thr Thr Thr Ser Pro Ser Cys Thr
 260 265 270

Cys Pro Gln Ile Met Ser Ser Thr Val Arg Ala Asn Pro Thr Met Lys
 275 280 285

Thr His Arg Phe Pro His Ser Ala Cys Thr Ala Asn Pro Lys Gln Pro

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290                               295                               300

Ala Thr Ser
305

<210> 449
<211> 1056
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> RXA00825

<400> 449
cccgttcacg ctgggctttg gtgcggtgat ggcaactatt tgtctgatca ttgtgagttt 60

tagtgcacgc cgattctgag aaacaactaa agtgagccac atg cgc aca gta gtt 115
                               Met Arg Thr Val Val
                               1                               5

acc ggc ggt gcc ggc ttc atc gga tcc cat ctc gtt gac ctt ttg atc 163
Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu Val Asp Leu Leu Ile
                               10                               15                               20

aag gaa ggc cac gag gtc gtt gtg atc gat aac ctc tcc cgc gga cgc 211
Lys Glu Gly His Glu Val Val Val Ile Asp Asn Leu Ser Arg Gly Arg
                               25                               30                               35

ctg gag aat ctc tcc gat gcg gaa gcc acc gga aaa ctc acc ttt gtg 259
Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly Lys Leu Thr Phe Val
                               40                               45                               50

gaa gcc gat ctt ctc gac gtt gat ttc aac gag ttt cta gga acc cac 307
Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu Phe Leu Gly Thr His
                               55                               60                               65

aag cct gag gtt att ttc cac ctg gca gcg caa atc gat gtg cgc cac 355
Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln Ile Asp Val Arg His
                               70                               75                               80                               85

tct gtt gta gat cct ctt cac gac gcc gaa acc aac att ttg tcc acc 403
Ser Val Val Asp Pro Leu His Asp Ala Glu Thr Asn Ile Leu Ser Thr
                               90                               95                               100

atc cgc atc gct gac gct gcc cgc cag cac ggt gtt cgc aag gtt gtc 451
Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly Val Arg Lys Val Val
                               105                               110                               115

ttt acc tcc tca ggc ggt tcc att tac ggt gag cct tcg gaa ttc cca 499
Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu Pro Ser Glu Phe Pro
                               120                               125                               130

gtt gat gaa acc gtg cca gtg gat cca cat tcc cct tat gcg gca tcc 547
Val Asp Glu Thr Val Pro Val Asp Pro His Ser Pro Tyr Ala Ala Ser
                               135                               140                               145

aag gtg tcc ggt gaa att tac ctg aac acc ttc cgc cac ctg tac ggc 595
Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe Arg His Leu Tyr Gly

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150	155	160	165	
tta gac tgt tct cac atc gca ccg gca aat gtt tac ggc cca cgc caa				643
Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val Tyr Gly Pro Arg Gln				
	170	175	180	
gat cca cac ggt gaa gca gga gtt gtg gcc att ttc gcg ctg cga ctt				691
Asp Pro His Gly Glu Ala Gly Val Val Ala Ile Phe Ala Leu Arg Leu				
	185	190	195	
ctg gga ggc ctg gac acc aag gta ttc ggc gac ggc gga aac acc cgc				739
Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp Gly Gly Asn Thr Arg				
	200	205	210	
gac tac gtc tac gtc ggt gac gta gtt cgt gct ttc tac ctg gct tct				787
Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala Phe Tyr Leu Ala Ser				
	215	220	225	
ggg gaa atc ggt ggg gga gag cgc ttc aac att ggc acc tct gtg gaa				835
Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile Gly Thr Ser Val Glu				
	230	235	240	245
acc tct gac cgc cag ctg cac acc ctc gtg gcc act gcg gca ggt tcc				883
Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala Thr Ala Ala Gly Ser				
	250	255	260	
aaa gat gat cct gaa tat gca cct gca cgt ctc ggc gat gtg cca cgc				931
Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu Gly Asp Val Pro Arg				
	265	270	275	
agt gca ctc agc ttc ggc aag gcc aaa gag gtg ctt ggt tgg gag cct				979
Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val Leu Gly Trp Glu Pro				
	280	285	290	
gag gtg aac atc gaa caa ggt gtg gcc aag act gtg gag tac ttc cgc				1027
Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr Val Glu Tyr Phe Arg				
	295	300	305	
act cac taggggaaaaa tccaccacaa atc				1056
Thr His				
310				

<210> 450

<211> 311

<212> PRT

<213> Corynebacterium glutamicum

<400> 450

Met Arg Thr Val Val Thr Gly Gly Ala Gly Phe Ile Gly Ser His Leu	
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Val Asp Leu Leu Ile Lys Glu Gly His Glu Val Val Val Ile Asp Asn	
20 25 30	

Leu Ser Arg Gly Arg Leu Glu Asn Leu Ser Asp Ala Glu Ala Thr Gly	
35 40 45	

Lys Leu Thr Phe Val Glu Ala Asp Leu Leu Asp Val Asp Phe Asn Glu	
50 55 60	

Phe Leu Gly Thr His Lys Pro Glu Val Ile Phe His Leu Ala Ala Gln
 65 70 75 80
 Ile Asp Val Arg His Ser Val Val Asp Pro Leu His Asp Ala Glu Thr
 85 90 95
 Asn Ile Leu Ser Thr Ile Arg Ile Ala Asp Ala Ala Arg Gln His Gly
 100 105 110
 Val Arg Lys Val Val Phe Thr Ser Ser Gly Gly Ser Ile Tyr Gly Glu
 115 120 125
 Pro Ser Glu Phe Pro Val Asp Glu Thr Val Pro Val Asp Pro His Ser
 130 135 140
 Pro Tyr Ala Ala Ser Lys Val Ser Gly Glu Ile Tyr Leu Asn Thr Phe
 145 150 155 160
 Arg His Leu Tyr Gly Leu Asp Cys Ser His Ile Ala Pro Ala Asn Val
 165 170 175
 Tyr Gly Pro Arg Gln Asp Pro His Gly Glu Ala Gly Val Val Ala Ile
 180 185 190
 Phe Ala Leu Arg Leu Leu Gly Gly Leu Asp Thr Lys Val Phe Gly Asp
 195 200 205
 Gly Gly Asn Thr Arg Asp Tyr Val Tyr Val Gly Asp Val Val Arg Ala
 210 215 220
 Phe Tyr Leu Ala Ser Gly Glu Ile Gly Gly Gly Glu Arg Phe Asn Ile
 225 230 235 240
 Gly Thr Ser Val Glu Thr Ser Asp Arg Gln Leu His Thr Leu Val Ala
 245 250 255
 Thr Ala Ala Gly Ser Lys Asp Asp Pro Glu Tyr Ala Pro Ala Arg Leu
 260 265 270
 Gly Asp Val Pro Arg Ser Ala Leu Ser Phe Gly Lys Ala Lys Glu Val
 275 280 285
 Leu Gly Trp Glu Pro Glu Val Asn Ile Glu Gln Gly Val Ala Lys Thr
 290 295 300
 Val Glu Tyr Phe Arg Thr His
 305 310

<210> 451
 <211> 1140
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1117)
 <223> RXA02054

<400> 451
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	Met Thr Ser Leu Leu	
	1 5	
gtg acc gga ggt gcc gga ttt atc ggc gcc aac ttc gtc cgc caa acc	163	
Val Thr Gly Gly Ala Gly Phe Ile Gly Ala Asn Phe Val Arg Gln Thr		
	10 15 20	
gta gag cag cac cct gaa tac acc cac atc acg gtg ctg gat aaa ctc	211	
Val Glu Gln His Pro Glu Tyr Thr His Ile Thr Val Leu Asp Lys Leu		
	25 30 35	
acc tac gca gga aac gcc gac aat ctc aaa ggc ctc ccc gac agc aaa	259	
Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly Leu Pro Asp Ser Lys		
	40 45 50	
gta acc ctc atc gaa ggc gat atc tgc gat gct gaa tta gtc gac tcc	307	
Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala Glu Leu Val Asp Ser		
	55 60 65	
ctg gtc aaa gac cac gac atc aca gtc cac ttc gca gca gaa tcc cac	355	
Leu Val Lys Asp His Asp Ile Thr Val His Phe Ala Ala Glu Ser His		
	70 75 80 85	
aac gac aac tcc ctc aac gac ccc tcc ccg ttt gtt cac act aac ctc	403	
Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe Val His Thr Asn Leu		
	90 95 100	
atc ggc acc ttt gtc ctg cta gaa gca gtc cgc aag cac aac aaa cgc	451	
Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg Lys His Asn Lys Arg		
	105 110 115	
ttc cac cac atc tcc acc gat gaa gtc ttc ggc gat cta gag ctg gat	499	
Phe His His Ile Ser Thr Asp Glu Val Phe Gly Asp Leu Glu Leu Asp		
	120 125 130	
gat cca aac cgc ttc act gaa acc acc gcc tac aag cca tcg tct cca	547	
Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr Lys Pro Ser Ser Pro		
	135 140 145	
tat tct gca acc aag gca ggg tct gat cac ttg gta cac gca tgg atc	595	
Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu Val His Ala Trp Ile		
	150 155 160 165	
cgc tcc ttc gga atc cag gca acc atg tct aac tgc tcc aac aat tac	643	
Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn Cys Ser Asn Asn Tyr		
	170 175 180	
ggc ccc tac cag cac att gaa aag ttc atc ccc cgc cag atc acc aat	691	
Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro Arg Gln Ile Thr Asn		
	185 190 195	
att ctg gcc ggc ctg aca cca aaa ctt tat gga acc ggc gag cag gtc	739	
Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly Thr Gly Glu Gln Val		
	200 205 210	
cgc gac tgg atc cac gtc gat gat cac aat gac gcc gtc cac ctg atc	787	
Arg Asp Trp Ile His Val Asp Asp His Asn Asp Ala Val His Leu Ile		
	215 220 225	

ctg agt aag ggc aag atc ggc gaa acc tac atc atc ggc gcc gac aac 835
 Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile Ile Gly Ala Asp Asn
 230 235 240 245
 gat cat gtg aat aac aag cag gtc atc gag ctt att tgt gaa ctc atg 883
 Asp His Val Asn Asn Lys Gln Val Ile Glu Leu Ile Cys Glu Leu Met
 250 255 260
 ggc ctc gac aaa aac gca tac gag cac gtc gca gac cgc ccc ggc cac 931
 Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala Asp Arg Pro Gly His
 265 270 275
 gat atg cgt tac gcc atg gat tcc acc aag ctg cgc acc gag ctc ggc 979
 Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu Arg Thr Glu Leu Gly
 280 285 290
 tgg gca cct aaa tac acc gac gtt gat tcc ggc atg cgc aaa ggc cta 1027
 Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly Met Arg Lys Gly Leu
 295 300 305
 gag cag acc atc gat tgg tac cgc gaa aac gag gcc tgg tgg cgc cct 1075
 Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu Ala Trp Trp Arg Pro
 310 315 320 325
 gcc aag aac aac gtc gaa gct acc tac gct aag cag gga caa 1117
 Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys Gln Gly Gln
 330 335
 taatggaata cggtaaacaa ctc 1140

<210> 452
 <211> 339
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 452
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 1 5 10 15
 Phe Val Arg Gln Thr Val Glu Gln His Pro Glu Tyr Thr His Ile Thr
 20 25 30
 Val Leu Asp Lys Leu Thr Tyr Ala Gly Asn Ala Asp Asn Leu Lys Gly
 35 40 45
 Leu Pro Asp Ser Lys Val Thr Leu Ile Glu Gly Asp Ile Cys Asp Ala
 50 55 60
 Glu Leu Val Asp Ser Leu Val Lys Asp His Asp Ile Thr Val His Phe
 65 70 75 80
 Ala Ala Glu Ser His Asn Asp Asn Ser Leu Asn Asp Pro Ser Pro Phe
 85 90 95
 Val His Thr Asn Leu Ile Gly Thr Phe Val Leu Leu Glu Ala Val Arg
 100 105 110
 Lys His Asn Lys Arg Phe His His Ile Ser Thr Asp Glu Val Phe Gly
 115 120 125

Asp Leu Glu Leu Asp Asp Pro Asn Arg Phe Thr Glu Thr Thr Ala Tyr
 130 135 140
 Lys Pro Ser Ser Pro Tyr Ser Ala Thr Lys Ala Gly Ser Asp His Leu
 145 150 155 160
 Val His Ala Trp Ile Arg Ser Phe Gly Ile Gln Ala Thr Met Ser Asn
 165 170 175
 Cys Ser Asn Asn Tyr Gly Pro Tyr Gln His Ile Glu Lys Phe Ile Pro
 180 185 190
 Arg Gln Ile Thr Asn Ile Leu Ala Gly Leu Thr Pro Lys Leu Tyr Gly
 195 200 205
 Thr Gly Glu Gln Val Arg Asp Trp Ile His Val Asp Asp His Asn Asp
 210 215 220
 Ala Val His Leu Ile Leu Ser Lys Gly Lys Ile Gly Glu Thr Tyr Ile
 225 230 235 240
 Ile Gly Ala Asp Asn Asp His Val Asn Asn Lys Gln Val Ile Glu Leu
 245 250 255
 Ile Cys Glu Leu Met Gly Leu Asp Lys Asn Ala Tyr Glu His Val Ala
 260 265 270
 Asp Arg Pro Gly His Asp Met Arg Tyr Ala Met Asp Ser Thr Lys Leu
 275 280 285
 Arg Thr Glu Leu Gly Trp Ala Pro Lys Tyr Thr Asp Val Asp Ser Gly
 290 295 300
 Met Arg Lys Gly Leu Glu Gln Thr Ile Asp Trp Tyr Arg Glu Asn Glu
 305 310 315 320
 Ala Trp Trp Arg Pro Ala Lys Asn Asn Val Glu Ala Thr Tyr Ala Lys
 325 330 335

Gln Gly Gln

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 <213> Corynebacterium glutamicum

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 <222> (101)..(886)
 <223> RXN00427

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 aatcaaacct atccggtgaa acacattgtg gtgggtgata atg ggg cgg atc cta 115
 Met Gly Arg Ile Leu
 1 5
 gta ttc tat agt gtc act tta gag gtg gcg gga gac cgt ccc gtt tac 163

Val	Phe	Tyr	Ser	Val	Thr	Leu	Glu	Val	Ala	Gly	Asp	Arg	Pro	Val	Tyr		
				10					15					20			
acg	cct	tcg	cgc	acc	aat	ttg	ggc	gac	ggg	ggc	ggg	ttt	gct	ttt	ggg	211	
Thr	Pro	Ser	Arg	Thr	Asn	Leu	Gly	Asp	Gly	Gly	Gly	Phe	Ala	Phe	Gly		
			25					30					35				
ttt	ttg	acg	gcg	ttg	gcg	ctg	ggg	gcg	aac	gcg	gtg	tgg	tgc	aca	gac	259	
Phe	Leu	Thr	Ala	Leu	Ala	Leu	Gly	Ala	Asn	Ala	Val	Trp	Cys	Thr	Asp		
			40				45					50					
gat	gac	ggc	cgg	ccg	gag	ggg	cca	ggg	gtg	ttg	aag	acg	ctt	atc	gac	307	
Asp	Asp	Gly	Arg	Pro	Glu	Gly	Pro	Gly	Val	Leu	Lys	Thr	Leu	Ile	Asp		
	55					60					65						
gcc	gct	tct	cgg	cat	aat	ctg	gag	gag	gtt	tct	ccg	gtg	gta	tgc	aat	355	
Ala	Ala	Ser	Arg	His	Asn	Leu	Glu	Glu	Val	Ser	Pro	Val	Val	Cys	Asn		
	70				75				80						85		
gct	gat	gat	ccg	gag	cgg	ttg	gca	ttt	ccg	ctg	cgt	cgg	ggc	ttg	gag	403	
Ala	Asp	Asp	Pro	Glu	Arg	Leu	Ala	Phe	Pro	Leu	Arg	Arg	Gly	Leu	Glu		
			90						95					100			
tgg	cgt	cgg	atg	cgc	agt	gag	ttg	att	gat	cca	gcc	aac	ccg	gag	gat	451	
Trp	Arg	Arg	Met	Arg	Ser	Glu	Leu	Ile	Asp	Pro	Ala	Asn	Pro	Glu	Asp		
			105					110					115				
gat	ttg	ctg	ccg	ggc	atc	gcc	tcc	ttg	ttc	aat	ggg	gcc	ctg	atc	agc	499	
Asp	Leu	Leu	Pro	Gly	Ile	Ala	Ser	Leu	Phe	Asn	Gly	Ala	Leu	Ile	Ser		
			120				125					130					
gct	tat	gca	atg	gag	cgc	att	ggc	gtg	ccg	gac	tat	cga	ctg	ttt	att	547	
Ala	Tyr	Ala	Met	Glu	Arg	Ile	Gly	Val	Pro	Asp	Tyr	Arg	Leu	Phe	Ile		
	135					140					145						
cgc	ggc	gat	gag	gtg	gag	tat	cac	cgc	cgt	ttg	gtg	cgt	tcc	ggg	ttg	595	
Arg	Gly	Asp	Glu	Val	Glu	Tyr	His	Arg	Arg	Leu	Val	Arg	Ser	Gly	Leu		
	150				155					160					165		
ccg	ttt	ggg	acg	tgt	ttg	acc	acg	gcg	tat	ttg	cac	ccg	gat	ggg	tct	643	
Pro	Phe	Gly	Thr	Cys	Leu	Thr	Thr	Ala	Tyr	Leu	His	Pro	Asp	Gly	Ser		
			170					175						180			
gat	gag	ttc	aag	ccg	att	ctg	ggg	ggg	cgg	atg	cat	acg	cag	tat	ccg	691	
Asp	Glu	Phe	Lys	Pro	Ile	Leu	Gly	Gly	Arg	Met	His	Thr	Gln	Tyr	Pro		
			185				190						195				
gat	aat	gat	ttc	aag	agg	ttt	ttc	acc	tac	cgc	aac	cgt	ggc	tac	ctg	739	
Asp	Asn	Asp	Phe	Lys	Arg	Phe	Phe	Thr	Tyr	Arg	Asn	Arg	Gly	Tyr	Leu		
			200				205					210					
atg	agc	cag	ccg	gga	atg	cgc	aag	ctt	ctc	cct	cag	gaa	tat	gcg	cgc	787	
Met	Ser	Gln	Pro	Gly	Met	Arg	Lys	Leu	Leu	Pro	Gln	Glu	Tyr	Ala	Arg		
	215					220					225						
ttt	gcg	tgg	ttc	ttc	ctg	gtt	cag	aaa	cgg	gat	gtg	aag	gga	ttc	cgg	835	
Phe	Ala	Trp	Phe	Phe	Leu	Val	Gln	Lys	Arg	Asp	Val	Lys	Gly	Phe	Arg		
	230				235					240					245		
gag	tgg	ctg	cgc	ctg	cac	aaa	ctg	ggc	cgc	gac	gag	aaa	ttc	aat	agg	883	
Glu	Trp	Leu	Arg	Leu	His	Lys	Leu	Gly	Arg	Asp	Glu	Lys	Phe	Asn	Arg		

250

255

260

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Pro

909

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<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 454

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Gly Phe Ala Phe Gly Phe Leu Thr Ala Leu Ala Leu Gly Ala Asn Ala
35 40 45

Val Trp Cys Thr Asp Asp Asp Gly Arg Pro Glu Gly Pro Gly Val Leu
50 55 60

Lys Thr Leu Ile Asp Ala Ala Ser Arg His Asn Leu Glu Glu Val Ser
65 70 75 80

Pro Val Val Cys Asn Ala Asp Asp Pro Glu Arg Leu Ala Phe Pro Leu
85 90 95

Arg Arg Gly Leu Glu Trp Arg Arg Met Arg Ser Glu Leu Ile Asp Pro
100 105 110

Ala Asn Pro Glu Asp Asp Leu Leu Pro Gly Ile Ala Ser Leu Phe Asn
115 120 125

Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg Ile Gly Val Pro Asp
130 135 140

Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu Tyr His Arg Arg Leu
145 150 155 160

Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu
165 170 175

His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile Leu Gly Gly Arg Met
180 185 190

His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg
195 200 205

Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met Arg Lys Leu Leu Pro
210 215 220

Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu Val Gln Lys Arg Asp
225 230 235 240

Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His Lys Leu Gly Arg Asp
245 250 255

Glu Lys Phe Asn Arg Pro
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<222> (101)..(532)
<223> FRXA00427

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Leu Leu Pro Gly Ile
1 5
gcc tcc ttg ttc aat ggt gcc ctg atc agc gct tat gca atg gag cgc 163
Ala Ser Leu Phe Asn Gly Ala Leu Ile Ser Ala Tyr Ala Met Glu Arg
10 15 20
att ggc gtg ccg gac tat cga ctg ttt att cgc ggc gat gag gtg gag 211
Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg Gly Asp Glu Val Glu
25 30 35
tat cac cgc cgt ttg gtg cgt tcc ggt ttg ccg ttt ggt acg tgt ttg 259
Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro Phe Gly Thr Cys Leu
40 45 50
acc acg gcg tat ttg cac ccg gat ggt tct gat gag ttc aag ccg att 307
Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp Glu Phe Lys Pro Ile
55 60 65
ctg ggt ggg cgg atg cat acg cag tat ccg gat aat gat ttc aag agg 355
Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp Asn Asp Phe Lys Arg
70 75 80 85
ttt ttc acc tac cgc aac cgt ggc tac ctg atg agc cag ccg gga atg 403
Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met Ser Gln Pro Gly Met
90 95 100
cgc aag ctt ctc cct cag gaa tat gcg cgc ttt gcg tgg ttc ttc ctg 451
Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe Ala Trp Phe Phe Leu
105 110 115
gtt cag aaa cgg gat gtg aag gga ttc cgg gag tgg ctg cgc ctg cac 499
Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu Trp Leu Arg Leu His
120 125 130
aaa ctg ggc cgc gac gag aaa ttc aat agg ccc tagatcagtt ttagtagttc 552
Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
135 140
ctc 555

<210> 456

<211> 144

<212> PRT

<213> Corynebacterium glutamicum

<400> 456

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Tyr Ala Met Glu Arg Ile Gly Val Pro Asp Tyr Arg Leu Phe Ile Arg
 20 25 30

Gly Asp Glu Val Glu Tyr His Arg Arg Leu Val Arg Ser Gly Leu Pro
 35 40 45

Phe Gly Thr Cys Leu Thr Thr Ala Tyr Leu His Pro Asp Gly Ser Asp
 50 55 60

Glu Phe Lys Pro Ile Leu Gly Gly Arg Met His Thr Gln Tyr Pro Asp
 65 70 75 80

Asn Asp Phe Lys Arg Phe Phe Thr Tyr Arg Asn Arg Gly Tyr Leu Met
 85 90 95

Ser Gln Pro Gly Met Arg Lys Leu Leu Pro Gln Glu Tyr Ala Arg Phe
 100 105 110

Ala Trp Phe Phe Leu Val Gln Lys Arg Asp Val Lys Gly Phe Arg Glu
 115 120 125

Trp Leu Arg Leu His Lys Leu Gly Arg Asp Glu Lys Phe Asn Arg Pro
 130 135 140

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<211> 507

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(484)

<223> RXA00327

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 Met Ile Gln Ala Ala
 1 5

ttg tgg atc gtg ctc ttt tta ttc gct gat cgc ctg tcc aat ccg ctg 163
 Leu Trp Ile Val Leu Phe Leu Phe Ala Asp Arg Leu Ser Asn Pro Leu
 10 15 20

gtt ttt gtc agc gcc atc atg ttc gcg att tcc ttt agc tcc ccc gtg 211
 Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser Phe Ser Ser Pro Val
 25 30 35

gcg aac ttc ggt ttc gat acg atc tgc gaa aaa ctc gac cgc cgc gtc 259
 Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys Leu Asp Arg Arg Val
 40 45 50
 atg gtc gcc ggc acc ggc atg gcc aac atg agc gcc tac att tgc gcg 307
 Met Val Ala Gly Thr Gly Met Ala Asn Met Ser Ala Tyr Ile Cys Ala
 55 60 65
 atg ctg gcc aca caa atc atc gga ttt tta ctc gac tgg aac gcc gac 355
 Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu Asp Trp Asn Ala Asp
 70 75 80 85
 ggc cac gcc tac acc tgg tcg aat ttc cag gtg gcg tgg ctt ggt ctg 403
 Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val Ala Trp Leu Gly Leu
 90 95 100
 ggc gcg gtg tgg ctg gca ggc atg atc ggg ctt gca gtc tgc ctc ctg 451
 Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu Ala Val Cys Leu Leu
 105 110 115
 ctg cag cgt cga aaa aat att gct ttt cga cgc taaaacccga ccgtaaccgc 504
 Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
 120 125
 tag 507

<210> 458
 <211> 128
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 458
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 Leu Ser Asn Pro Leu Val Phe Val Ser Ala Ile Met Phe Ala Ile Ser
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 Phe Ser Ser Pro Val Ala Asn Phe Gly Phe Asp Thr Ile Cys Glu Lys
 35 40 45
 Leu Asp Arg Arg Val Met Val Ala Gly Thr Gly Met Ala Asn Met Ser
 50 55 60
 Ala Tyr Ile Cys Ala Met Leu Ala Thr Gln Ile Ile Gly Phe Leu Leu
 65 70 75 80
 Asp Trp Asn Ala Asp Gly His Ala Tyr Thr Trp Ser Asn Phe Gln Val
 85 90 95
 Ala Trp Leu Gly Leu Gly Ala Val Trp Leu Ala Gly Met Ile Gly Leu
 100 105 110
 Ala Val Cys Leu Leu Leu Gln Arg Arg Lys Asn Ile Ala Phe Arg Arg
 115 120 125

<210> 460

<211> 164
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 460
 Val Gly Val Glu Arg Gly Lys Val Ser Ala Lys Ala Leu Val Val Trp
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 20 25 30
 Phe Gly Val Ala Gly Val His Ala Ile Asp Arg Phe Asp Ile Asp Ala
 35 40 45
 Ser Arg Leu Ala Val Phe Thr Ser Val Gln Val Gly Val Tyr Val Leu
 50 55 60
 Ala Gln Ile Pro Met Gly Met Leu Val Asp Arg Phe Asp Ala Arg Lys
 65 70 75 80
 Leu Leu Leu Ala Gly Ala Leu Ile Leu Ala Ala Gly Gln Leu Ile Leu
 85 90 95
 Gly Phe Thr Asp Ser Tyr Met Ile Ala Ile Phe Ala Arg Val Leu Ile
 100 105 110
 Ser Val Gly Asp Ser Ser Ala Phe Leu Ser Val Met Arg Leu Leu Pro
 115 120 125
 Asn Trp Phe Pro Met Ser Trp Thr Pro Val Leu Gln Gln Leu Thr Gly
 130 135 140
 Ala Phe Gly Phe Val Gly Gln Phe Ser Pro Arg Cys Arg Phe Cys Thr
 145 150 155 160
 Tyr Ser Thr Pro

<210> 461
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1324)
 <223> RXA00329

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 Met Ala Ala Ile Thr
 1 5
 agc cgc acc agc ttt ggt gtg gct gga gtg gag gcc att gat cgt ttt 163
 Ser Arg Thr Ser Phe Gly Val Ala Gly Val Glu Ala Ile Asp Arg Phe
 10 15 20
 cag gta gac gcc aca cgc att gca gta ttc act tct gtt cag gtt ggt 211

Gln	Val	Asp	Ala	Thr	Arg	Ile	Ala	Val	Phe	Thr	Ser	Val	Gln	Val	Gly	
			25					30					35			
gtg	tac	gcg	ttt	gct	cag	att	ccg	atg	ggc	att	ttg	atc	gat	aag	ttt	259
Val	Tyr	Ala	Phe	Ala	Gln	Ile	Pro	Met	Gly	Ile	Leu	Ile	Asp	Lys	Phe	
		40					45					50				
ggc	cct	cg	aag	ctc	ctt	gcc	att	ggc	gct	ttg	gtg	atg	ggc	atc	ggc	307
Gly	Pro	Arg	Lys	Leu	Leu	Ala	Ile	Gly	Ala	Leu	Val	Met	Gly	Ile	Gly	
	55					60					65					
cag	ctc	att	ttg	ggc	ttt	acg	gat	agc	tat	tcc	atc	gcg	att	att	gcc	355
Gln	Leu	Ile	Leu	Gly	Phe	Thr	Asp	Ser	Tyr	Ser	Ile	Ala	Ile	Ile	Ala	
	70				75					80					85	
cg	gtg	ttt	atc	ggc	gcc	ggc	gat	gca	tgc	atc	ttc	ctt	tgc	gtt	atg	403
Arg	Val	Phe	Ile	Gly	Ala	Gly	Asp	Ala	Ser	Ile	Phe	Leu	Ser	Val	Met	
				90					95					100		
cg	atc	ctg	ccg	ttt	tgg	ttc	cca	ctg	aag	cac	acc	cct	att	ttc	acg	451
Arg	Ile	Leu	Pro	Phe	Trp	Phe	Pro	Leu	Lys	His	Thr	Pro	Ile	Phe	Thr	
			105					110					115			
cag	tta	act	acc	tgc	ctt	ggc	cag	ttg	ggc	cag	ttc	ttt	tct	gcg	gtg	499
Gln	Leu	Thr	Thr	Cys	Leu	Gly	Gln	Leu	Gly	Gln	Phe	Phe	Ser	Ala	Val	
		120					125					130				
cct	ttc	atg	gcg	ttg	ttg	ggc	gcg	cag	ggc	tgg	cct	gtg	gcg	ttt	gtc	547
Pro	Phe	Met	Ala	Leu	Leu	Gly	Ala	Gln	Gly	Trp	Pro	Val	Ala	Phe	Val	
	135					140					145					
agc	ctt	ggc	tcc	gtg	gtg	gca	ctc	att	gcg	atc	gca	gcg	ctg	gtg	gcc	595
Ser	Leu	Gly	Ser	Val	Val	Ala	Leu	Ile	Ala	Ile	Ala	Ala	Leu	Val	Ala	
	150				155				160						165	
gtt	cg	gat	act	cca	gat	cct	cag	cca	aaa	cct	gtc	gaa	tca	gct	cag	643
Val	Arg	Asp	Thr	Pro	Asp	Pro	Gln	Pro	Lys	Pro	Val	Glu	Ser	Ala	Gln	
				170					175					180		
gaa	gca	gat	aaa	cca	agc	ctg	cg	gcg	agt	ttg	aag	ttg	att	gtc	cg	691
Glu	Ala	Asp	Lys	Pro	Ser	Leu	Arg	Ala	Ser	Leu	Lys	Leu	Ile	Val	Arg	
			185					190					195			
aat	ccg	att	acg	tgg	cag	ggc	ttc	ttc	att	cac	tac	gta	ttg	atg	gtg	739
Asn	Pro	Ile	Thr	Trp	Gln	Gly	Phe	Phe	Ile	His	Tyr	Val	Leu	Met	Val	
		200					205					210				
tgg	cag	acc	gtg	ttc	tcc	atg	atg	tgg	ggc	gtc	ccg	ctg	atg	act	ttg	787
Trp	Gln	Thr	Val	Phe	Ser	Met	Met	Trp	Gly	Val	Pro	Leu	Met	Thr	Leu	
	215					220					225					
ggc	atg	gga	ctg	tct	gca	acg	acg	gct	ggc	ttg	gtg	ttg	agc	atc	aac	835
Gly	Met	Gly	Leu	Ser	Ala	Thr	Thr	Ala	Gly	Leu	Val	Leu	Ser	Ile	Asn	
	230				235					240					245	
acg	ctg	tgc	atg	gtg	gta	tgc	gcg	cca	atc	atc	gga	ata	att	tcc	gca	883
Thr	Leu	Cys	Met	Val	Val	Ser	Ala	Pro	Ile	Ile	Gly	Ile	Ile	Ser	Ala	
				250					255					260		
cg	ctt	ggg	tat	cg	cgt	gac	gtg	gtc	gcc	att	gcg	ctg	tgc	ttt	gtt	931
Arg	Leu	Gly	Tyr	Arg	Arg	Asp	Val	Val	Ala	Ile	Ala	Leu	Ser	Phe	Val	

265	270	275	
caa tcc gca gta tgg ctg gtg ttc ttg gcc tcc gat gca cct cgt ggt			979
Gln Ser Ala Val Trp Leu Val Phe Leu Ala Ser Asp Ala Pro Arg Gly			
280	285	290	
ttg atg gct atc atc ttg gtc aac atc gtc atg ggt ctg act act gcg			1027
Leu Met Ala Ile Ile Leu Val Asn Ile Val Met Gly Leu Thr Thr Ala			
295	300	305	
gct tct ggt tat ggc ttt gac acc att cgt gag cgc cta gat cgc aag			1075
Ala Ser Gly Tyr Gly Phe Asp Thr Ile Arg Glu Arg Leu Asp Arg Lys			
310	315	320	325
att ttg gct gcg ggc acg gga ctg gca aac atg ggt gga ttc ttg tca			1123
Ile Leu Ala Ala Gly Thr Gly Leu Ala Asn Met Gly Gly Phe Leu Ser			
330	335	340	
tcg atg gtt gca gcg cag gtt atg ggg ttc ctt ctt gat cac agc gcg			1171
Ser Met Val Ala Ala Gln Val Met Gly Phe Leu Leu Asp His Ser Ala			
345	350	355	
cat ggt agc acc tat act tgg gtg gac ttc cgt ttt ggt ttc ctt gcg			1219
His Gly Ser Thr Tyr Thr Trp Val Asp Phe Arg Phe Gly Phe Leu Ala			
360	365	370	
att ctt gtc aca tgg gcc gtc gga gtc acg gga ttt gtt gta gcc cga			1267
Ile Leu Val Thr Trp Ala Val Gly Val Thr Gly Phe Val Val Ala Arg			
375	380	385	
ctc aag ggt gga ccg gcc cgc aga tta ctc gcc cag att agg tct acc			1315
Leu Lys Gly Gly Pro Gly Arg Arg Leu Leu Ala Gln Ile Arg Ser Thr			
390	395	400	405
aag gac ttt taaagatcgg gtaaaacctg tgg			1347
Lys Asp Phe			

<210> 462

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 462

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Ala	Ile	Asp	Arg	Phe	Gln	Val	Asp	Ala	Thr	Arg	Ile	Ala	Val	Phe	Thr
		20						25					30		

Ser	Val	Gln	Val	Gly	Val	Tyr	Ala	Phe	Ala	Gln	Ile	Pro	Met	Gly	Ile
		35					40					45			

Leu	Ile	Asp	Lys	Phe	Gly	Pro	Arg	Lys	Leu	Leu	Ala	Ile	Gly	Ala	Leu
	50					55					60				

Val	Met	Gly	Ile	Gly	Gln	Leu	Ile	Leu	Gly	Phe	Thr	Asp	Ser	Tyr	Ser
65					70					75					80

Ile	Ala	Ile	Ile	Ala	Arg	Val	Phe	Ile	Gly	Ala	Gly	Asp	Ala	Ser	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

					85			90					95		
Phe	Leu	Ser	Val	Met	Arg	Ile	Leu	Pro	Phe	Trp	Phe	Pro	Leu	Lys	His
			100				105						110		
Thr	Pro	Ile	Phe	Thr	Gln	Leu	Thr	Thr	Cys	Leu	Gly	Gln	Leu	Gly	Gln
		115				120						125			
Phe	Phe	Ser	Ala	Val	Pro	Phe	Met	Ala	Leu	Leu	Gly	Ala	Gln	Gly	Trp
130					135						140				
Pro	Val	Ala	Phe	Val	Ser	Leu	Gly	Ser	Val	Val	Ala	Leu	Ile	Ala	Ile
145				150						155				160	
Ala	Ala	Leu	Val	Ala	Val	Arg	Asp	Thr	Pro	Asp	Pro	Gln	Pro	Lys	Pro
			165				170						175		
Val	Glu	Ser	Ala	Gln	Glu	Ala	Asp	Lys	Pro	Ser	Leu	Arg	Ala	Ser	Leu
			180				185						190		
Lys	Leu	Ile	Val	Arg	Asn	Pro	Ile	Thr	Trp	Gln	Gly	Phe	Phe	Ile	His
		195				200						205			
Tyr	Val	Leu	Met	Val	Trp	Gln	Thr	Val	Phe	Ser	Met	Met	Trp	Gly	Val
210					215						220				
Pro	Leu	Met	Thr	Leu	Gly	Met	Gly	Leu	Ser	Ala	Thr	Thr	Ala	Gly	Leu
225				230						235				240	
Val	Leu	Ser	Ile	Asn	Thr	Leu	Cys	Met	Val	Val	Ser	Ala	Pro	Ile	Ile
			245				250						255		
Gly	Ile	Ile	Ser	Ala	Arg	Leu	Gly	Tyr	Arg	Arg	Asp	Val	Val	Ala	Ile
			260				265						270		
Ala	Leu	Ser	Phe	Val	Gln	Ser	Ala	Val	Trp	Leu	Val	Phe	Leu	Ala	Ser
		275				280						285			
Asp	Ala	Pro	Arg	Gly	Leu	Met	Ala	Ile	Ile	Leu	Val	Asn	Ile	Val	Met
290					295						300				
Gly	Leu	Thr	Thr	Ala	Ala	Ser	Gly	Tyr	Gly	Phe	Asp	Thr	Ile	Arg	Glu
305				310						315				320	
Arg	Leu	Asp	Arg	Lys	Ile	Leu	Ala	Ala	Gly	Thr	Gly	Leu	Ala	Asn	Met
			325				330						335		
Gly	Gly	Phe	Leu	Ser	Ser	Met	Val	Ala	Ala	Gln	Val	Met	Gly	Phe	Leu
		340				345						350			
Leu	Asp	His	Ser	Ala	His	Gly	Ser	Thr	Tyr	Thr	Trp	Val	Asp	Phe	Arg
		355				360						365			
Phe	Gly	Phe	Leu	Ala	Ile	Leu	Val	Thr	Trp	Ala	Val	Gly	Val	Thr	Gly
370					375						380				
Phe	Val	Val	Ala	Arg	Leu	Lys	Gly	Gly	Pro	Gly	Arg	Arg	Leu	Leu	Ala
385				390						395				400	
Gln	Ile	Arg	Ser	Thr	Lys	Asp	Phe								
			405												

atg caa aac ggt gaa cag gcg tgt tcc tca gca acc aac aat ggc ctc 643
Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala Thr Asn Asn Gly Leu

170	175	180	
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aac ggc acc aac cgt gca cct cgt gaa ctt aaa cta gat gag tca ctc Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys Leu Asp Glu Ser Leu 215 220 225			787
gat ggc gtg gag cac acc tgg act gtg agc acc acc cgc gac ggc gtt Asp Gly Val Glu His Thr Trp Thr Val Ser Thr Thr Arg Asp Gly Val 230 235 240 245			835
gag tac ttc att gat gat gag gcg att aac cgc cag tca tgg cgc aac Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg Gln Ser Trp Arg Asn 250 255 260			883
gat gtc act ttg ggg cat gcc gaa att gat gat ttc ggg atc tcc gcg Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp Phe Gly Ile Ser Ala 265 270 275			931
cag acg ttt gat gag atc gtc gac cgc gaa tgg act ctc act ctt aat Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp Thr Leu Thr Leu Asn 280 285 290			979
caa aag gta gaa agc gcc gac tgg gca aaa cca cgt tcc tct gag gaa Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro Arg Ser Ser Glu Glu 295 300 305			1027
gat ttc cca gtc cgg tcc atg gtg att gac cgc atc gag gtc acc gga Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg Ile Glu Val Thr Gly 310 315 320 325			1075
tct ccc gca gta tct gaa gac acc ccc atg cca gat acc acc cag ctt Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro Asp Thr Thr Gln Leu 330 335 340			1123
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cgc tac gag cca gca agt gct gat ttt gcc gat ggc cgc agg cct tcc Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp Gly Arg Arg Pro Ser 360 365 370			1219
tgg aac tac ttc aat ttg aag gaa tcg tgg cag aat cca gaa ctc gag Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln Asn Pro Glu Leu Glu 375 380 385			1267
caa cgc cca gaa gct gtc gaa ttc gtt gat gga cgc atg gat atc gtg Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly Arg Met Asp Ile Val 390 395 400 405			1315
acc cgt cgc cac tgt ctg gcc acc act gat gac atc gcc act ccg gaa Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp Ile Ala Thr Pro Glu 410 415 420			1363

aac gca cag gag gaa ccg tgc gcg ccg ggt gag gtg aca cgc tac agc	1411
Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu Val Thr Arg Tyr Ser	
425 430 435	
tca gcg cgt gtc cac ctt cca gag atc ccc gcc ggc aac ttc cgg ctc	1459
Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala Gly Asn Phe Arg Leu	
440 445 450	
acc gtg cgc gca cgg gcg cag tcc gaa gag ctt gtc gac ggc gtc cgc	1507
Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu Val Asp Gly Val Arg	
455 460 465	
ccc gct atc tgg atg cag aac aat acc aac ttc tgt gct gac aac gat	1555
Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe Cys Ala Asp Asn Asp	
470 475 480 485	
gga cgc cct tat ggt gaa ctg gat att act gag ttc tac agc tct cgt	1603
Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu Phe Tyr Ser Ser Arg	
490 495 500	
gtg aac acc cag tac tcg gca gta cac ctt gga tgt gct ggc aac cgc	1651
Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly Cys Ala Gly Asn Arg	
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cca gag atg aag ctt cgc caa atg gaa atg gaa gag tcc atg ttt ggg	1699
Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu Glu Ser Met Phe Gly	
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Asp Trp His Asp Trp Gly Val Glu Val Phe Asp Gly Gln Ile Val Phe	
535 540 545	
acc att gac ggc aag gca gta act tcc tct ggc aaa gat gtc ttt ggc	1795
Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly Lys Asp Val Phe Gly	
550 555 560 565	
aac tct gtt acc cca gcc gct gca cct ctt cgc ccc gcg cac ttc aag	1843
Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg Pro Ala His Phe Lys	
570 575 580	
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Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly Gln Pro Trp His Leu	
585 590 595	
att ttg aac acc atg gtg gag cag tct ggc aaa gac agc tgg att aca	1939
Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys Asp Ser Trp Ile Thr	
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gcg gtc gac aat aac gag gcg ttc cca gaa cac cgc ttc caa att gac	1987
Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His Arg Phe Gln Ile Asp	
615 620 625	
cat gtg gca gta gat atc gag tct gac tct gtg gac aat gta tgg cct	2035
His Val Ala Val Asp Ile Glu Ser Asp Ser Val Asp Asn Val Trp Pro	
630 635 640 645	
gac gct gcg aat gaa atc cca gac aat gtt ggt att gaa gac tct gat	2083
Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly Ile Glu Asp Ser Asp	
650 655 660	

gat ggc agc gac ctg gag gtt ggt tcg acc gga agc tct aca gct gag 2131
Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly Ser Ser Thr Ala Glu
665 670 675

acc gtg agc tgg atc tcg ttg ttc acc gcg ttg agc tcg ctg gtc ttc 2179
Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu Ser Ser Leu Val Phe
680 685 690

aca ctg gct ctc aat caa gaa gca ttg cag aat ttg att aat cag ttc 2227
Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn Leu Ile Asn Gln Phe
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Met Arg Gln Phe Lys
710

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<211> 714

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 464

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20 25 30

Gln Val Ala Asn Pro Ala Pro Asp Leu Ser Ala Pro Tyr Thr Trp Val
35 40 45

Glu Glu Phe Asp Ser Glu Asp Ala Leu Lys Gly Trp Asn Ile Phe Arg
50 55 60

Gln Pro Asp Tyr Gly Ser Asp Lys Val Leu Tyr Thr Glu Asp Ala Leu
65 70 75 80

Ser Ile Glu Asp Gly Lys Leu Thr Ile Thr Thr Gln Arg His Cys Val
85 90 95

Asp Glu Asp Phe Ala Ile Ser Asp Pro Val Asn Arg Gly Lys Leu Asn
100 105 110

Asp Ser Thr Ala Gln Val Glu Pro Cys Ala Pro Gly Gln Phe Glu Lys
115 120 125

Phe Thr Ser Ala Arg Ile Val Thr Pro Lys Ile Ala Arg Gly Glu Phe
130 135 140

Asp Leu Ser Val Thr Ala Thr Leu Asn Thr Gly Gly Val Glu Gly Val
145 150 155 160

Arg Ser Ala Ile Trp Met Gln Asn Gly Glu Gln Ala Cys Ser Ser Ala
165 170 175

Thr Asn Asn Gly Leu Tyr Gly Glu Leu Asp Leu Val Glu His Phe Ser
180 185 190

Tyr Asp Leu Arg Ser Pro Trp Ser Pro Ser Asn Thr His Leu Gly Cys
195 200 205

Asp Pro Glu Ser Val Asn Gly Thr Asn Arg Ala Pro Arg Glu Leu Lys
 210 215 220
 Leu Asp Glu Ser Leu Asp Gly Val Glu His Thr Trp Thr Val Ser Thr
 225 230 235 240
 Thr Arg Asp Gly Val Glu Tyr Phe Ile Asp Asp Glu Ala Ile Asn Arg
 245 250 255
 Gln Ser Trp Arg Asn Asp Val Thr Leu Gly His Ala Glu Ile Asp Asp
 260 265 270
 Phe Gly Ile Ser Ala Gln Thr Phe Asp Glu Ile Val Asp Arg Glu Trp
 275 280 285
 Thr Leu Thr Leu Asn Gln Lys Val Glu Ser Ala Asp Trp Ala Lys Pro
 290 295 300
 Arg Ser Ser Glu Glu Asp Phe Pro Val Arg Ser Met Val Ile Asp Arg
 305 310 315 320
 Ile Glu Val Thr Gly Ser Pro Ala Val Ser Glu Asp Thr Pro Met Pro
 325 330 335
 Asp Thr Thr Gln Leu Leu Thr Gln Asp Thr Leu Glu Tyr Leu Gly Arg
 340 345 350
 Met Pro Val Leu Glu Arg Tyr Glu Pro Ala Ser Ala Asp Phe Ala Asp
 355 360 365
 Gly Arg Arg Pro Ser Trp Asn Tyr Phe Asn Leu Lys Glu Ser Trp Gln
 370 375 380
 Asn Pro Glu Leu Glu Gln Arg Pro Glu Ala Val Glu Phe Val Asp Gly
 385 390 395 400
 Arg Met Asp Ile Val Thr Arg Arg His Cys Leu Ala Thr Thr Asp Asp
 405 410 415
 Ile Ala Thr Pro Glu Asn Ala Gln Glu Glu Pro Cys Ala Pro Gly Glu
 420 425 430
 Val Thr Arg Tyr Ser Ser Ala Arg Val His Leu Pro Glu Ile Pro Ala
 435 440 445
 Gly Asn Phe Arg Leu Thr Val Arg Ala Arg Ala Gln Ser Glu Glu Leu
 450 455 460
 Val Asp Gly Val Arg Pro Ala Ile Trp Met Gln Asn Asn Thr Asn Phe
 465 470 475 480
 Cys Ala Asp Asn Asp Gly Arg Pro Tyr Gly Glu Leu Asp Ile Thr Glu
 485 490 495
 Phe Tyr Ser Ser Arg Val Asn Thr Gln Tyr Ser Ala Val His Leu Gly
 500 505 510
 Cys Ala Gly Asn Arg Pro Glu Met Lys Leu Arg Gln Met Glu Met Glu
 515 520 525

Glu Ser Met Phe Gly Asp Trp His Asp Trp Gly Val Glu Val Phe Asp
 530 535 540
 Gly Gln Ile Val Phe Thr Ile Asp Gly Lys Ala Val Thr Ser Ser Gly
 545 550 555 560
 Lys Asp Val Phe Gly Asn Ser Val Thr Pro Ala Ala Ala Pro Leu Arg
 565 570 575
 Pro Ala His Phe Lys Leu Ser Glu Glu Glu Tyr Arg Glu Val Ile Gly
 580 585 590
 Gln Pro Trp His Leu Ile Leu Asn Thr Met Val Glu Gln Ser Gly Lys
 595 600 605
 Asp Ser Trp Ile Thr Ala Val Asp Asn Asn Glu Ala Phe Pro Glu His
 610 615 620
 Arg Phe Gln Ile Asp His Val Ala Val Asp Ile Glu Ser Asp Ser Val
 625 630 635 640
 Asp Asn Val Trp Pro Asp Ala Ala Asn Glu Ile Pro Asp Asn Val Gly
 645 650 655
 Ile Glu Asp Ser Asp Asp Gly Ser Asp Leu Glu Val Gly Ser Thr Gly
 660 665 670
 Ser Ser Thr Ala Glu Thr Val Ser Trp Ile Ser Leu Phe Thr Ala Leu
 675 680 685
 Ser Ser Leu Val Phe Thr Leu Ala Leu Asn Gln Glu Ala Leu Gln Asn
 690 695 700
 Leu Ile Asn Gln Phe Met Arg Gln Phe Lys
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 <211> 389
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(382)
 <223> RXN03015

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 Leu Gly Val Gly Thr
 1 5
 cct cag cag aag ggt act tat gcg gcg gat ctg acg tat gtt cgt cag 163
 Pro Gln Gln Lys Gly Thr Tyr Ala Ala Asp Leu Thr Tyr Val Arg Gln
 10 15 20
 gtt gtt gag gat ttg gtg ccg ctg ctt gag ggc gag cac att att ttc 211
 Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly Glu His Ile Ile Phe
 25 30 35

ggc aag tct acg gtt ccg gtt ggt act gct gag cag ttg cag gag ctt 259
 Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu Gln Leu Gln Glu Leu
 40 45 50
 gct gat tct ctg gtc aag cct ggt tcg cac gtg gag atc gcg tgg aat 307
 Ala Asp Ser Leu Val Lys Pro Gly Ser His Val Glu Ile Ala Trp Asn
 55 60 65
 ccg gag ttc ttg cgt gag ggc tac gcg gtc aaa gac acc atc act ccg 355
 Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys Asp Thr Ile Thr Pro
 70 75 80 85
 gac cgc atc gtg gtg ggt gtg cgt gaa taagaca 389
 Asp Arg Ile Val Val Gly Val Arg Glu
 90

<210> 466
 <211> 94
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 466
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 Thr Tyr Val Arg Gln Val Val Glu Asp Leu Val Pro Leu Leu Glu Gly
 20 25 30
 Glu His Ile Ile Phe Gly Lys Ser Thr Val Pro Val Gly Thr Ala Glu
 35 40 45
 Gln Leu Gln Glu Leu Ala Asp Ser Leu Val Lys Pro Gly Ser His Val
 50 55 60
 Glu Ile Ala Trp Asn Pro Glu Phe Leu Arg Glu Gly Tyr Ala Val Lys
 65 70 75 80
 Asp Thr Ile Thr Pro Asp Arg Ile Val Val Gly Val Arg Glu
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<210> 467
 <211> 801
 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(778)
 <223> RXN03056

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 Leu Asp Ala Ala Gly
 1 5
 att tca ctt tca gcc gtt gga tcc gac ttc ggc aag atc aac atc acc 163

Ile Ser Leu Ser Ala Val Gly Ser Asp Phe Gly Lys Ile Asn Ile Thr	
10 15 20	
gat cct ttt gaa gat cac ttg gag cgc gca cgc cac ggt gtt gag gtc	211
Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg His Gly Val Glu Val	
25 30 35	
gct aag ctc ttc ggc gcg aaa tac atc cgc atg ttc tcc ttc ttt att	259
Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met Phe Ser Phe Phe Ile	
40 45 50	
gca gaa ggc gac aac cct gaa agc ttc cgc aaa gaa gta ctc tcc cgc	307
Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys Glu Val Leu Ser Arg	
55 60 65	
acc cac gca atg gtc gaa ctc gca gaa gcc ggc ggc atc acc ctc ctc	355
Thr His Ala Met Val Glu Leu Ala Glu Ala Gly Gly Ile Thr Leu Leu	
70 75 80 85	
cac gaa aat gaa aag gga atc tat ggc gac tcc ccg cag cgc gtg aag	403
His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser Pro Gln Arg Val Lys	
90 95 100	
gat tta atc acc agc atc gac tcc cct aac tac cgc gca atc tac gac	451
Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr Arg Ala Ile Tyr Asp	
105 110 115	
gca gct aac tac gtg caa acc gga ttc aag cct ttt gat gag gca tgg	499
Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro Phe Asp Glu Ala Trp	
120 125 130	
ccg atc gtt aag gac tac gtc gac tac gtc cac atc aag gac gcg acc	547
Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His Ile Lys Asp Ala Thr	
135 140 145	
att cca gat gca gag cac ccc atc gga atc atc aag cca gca gga caa	595
Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile Lys Pro Ala Gly Gln	
150 155 160 165	
ggc gac ggc caa tac cca gag ctc ctt gcc gcg cta aac gcc gac ggt	643
Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala Leu Asn Ala Asp Gly	
170 175 180	
tac aac gga ttc gtc tcc atc gag cct cac ctg ggt gac ttc gat gaa	691
Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu Gly Asp Phe Asp Glu	
185 190 195	
ttc ggc gga ctc tgc gga cct gac ctg tgg acc agc gca tgc gac gct	739
Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr Ser Ala Cys Asp Ala	
200 205 210	
ctc gca gga atc ctg aac aac atc aac gcc gag tac aac taaggacaac	788
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<210> 468

<211> 226

<212> PRT

<213> Corynebacterium glutamicum

<400> 468

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Lys Ile Asn Ile Thr Asp Pro Phe Glu Asp His Leu Glu Arg Ala Arg
20 25 30

His Gly Val Glu Val Ala Lys Leu Phe Gly Ala Lys Tyr Ile Arg Met
35 40 45

Phe Ser Phe Phe Ile Ala Glu Gly Asp Asn Pro Glu Ser Phe Arg Lys
50 55 60

Glu Val Leu Ser Arg Thr His Ala Met Val Glu Leu Ala Glu Ala Gly
65 70 75 80

Gly Ile Thr Leu Leu His Glu Asn Glu Lys Gly Ile Tyr Gly Asp Ser
85 90 95

Pro Gln Arg Val Lys Asp Leu Ile Thr Ser Ile Asp Ser Pro Asn Tyr
100 105 110

Arg Ala Ile Tyr Asp Ala Ala Asn Tyr Val Gln Thr Gly Phe Lys Pro
115 120 125

Phe Asp Glu Ala Trp Pro Ile Val Lys Asp Tyr Val Asp Tyr Val His
130 135 140

Ile Lys Asp Ala Thr Ile Pro Asp Ala Glu His Pro Ile Gly Ile Ile
145 150 155 160

Lys Pro Ala Gly Gln Gly Asp Gly Gln Tyr Pro Glu Leu Leu Ala Ala
165 170 175

Leu Asn Ala Asp Gly Tyr Asn Gly Phe Val Ser Ile Glu Pro His Leu
180 185 190

Gly Asp Phe Asp Glu Phe Gly Gly Leu Cys Gly Pro Asp Leu Trp Thr
195 200 205

Ser Ala Cys Asp Ala Leu Ala Gly Ile Leu Asn Asn Ile Asn Ala Glu
210 215 220

Tyr Asn
225

<210> 469

<211> 687

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(664)

<223> RXN03030

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                                         Met Ala Arg Phe Ser
                                           1             5

cca caa gat ctc gca gac cac ctc aag gat gga ctg ctc tct ttc ccg      163
Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly Leu Leu Ser Phe Pro
                10                      15                        20

gcc acc gct ttc caa gat gac ctc gaa gta gat gaa gct gct tat gtc      211
Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp Glu Ala Ala Tyr Val
                25                      30                        35
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		40					45					50				
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Ala	Gly	Gly	Thr	Gly	Glu	Gly	Phe	Ser	Leu	Thr	Val	Glu	Glu	Asn	His	
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cgt	gtc	act	caa	ctt	gca	gtt	cag	gcg	tcc	agc	ccg	gaa	gtt	ccc	gtg	355
Arg	Val	Thr	Gln	Leu	Ala	Val	Gln	Ala	Ser	Ser	Pro	Glu	Val	Pro	Val	
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Leu	Gly	Ser	Ala	Thr	Gly	Ser	Thr	Lys	Ser	Ala	Ile	Ala	Asn	Ala	Gln	
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ggc	gca	gag	gca	gca	ggc	gct	gaa	ggg	gtc	ctc	ctg	ctt	cct	ccc	tac	451
Gly	Ala	Glu	Ala	Ala	Gly	Ala	Glu	Gly	Val	Leu	Leu	Leu	Pro	Pro	Tyr	
			105					110					115			
ctc	acc	gaa	tgc	gac	gca	gaa	ggc	ctg	tac	aac	cat	gca	gcc	gca	gtc	499
Leu	Thr	Glu	Cys	Asp	Ala	Glu	Gly	Leu	Tyr	Asn	His	Ala	Ala	Ala	Val	
		120					125					130				
tgt	gaa	tcc	act	tct	ctt	ggg	gtc	atc	gtg	tac	aac	cgt	gcc	aat	gcc	547
Cys	Glu	Ser	Thr	Ser	Leu	Gly	Val	Ile	Val	Tyr	Asn	Arg	Ala	Asn	Ala	
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atc	tac	tcc	cca	gag	gtt	atc	gct	cga	ctc	tct	gag	cgc	tac	ccc	aac	595
Ile	Tyr	Ser	Pro	Glu	Val	Ile	Ala	Arg	Leu	Ser	Glu	Arg	Tyr	Pro	Asn	
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Phe	Ile	Gly	Phe	Lys	Asp	Gly	Thr	Gly	Asn	Ile	Glu	His	Leu	Ala	Lys	
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atc	acc	acg	cta	tgc	gga	gat	cgc	ctg	ttc	tac	ctc	ggg	gga	ctt	ccc	691
Ile	Thr	Thr	Leu	Cys	Gly	Asp	Arg	Leu	Phe	Tyr	Leu	Gly	Gly	Leu	Pro	
			185					190					195			
acc	gct	gag	acc	ttt	gca	cta	cca	ctg	ctt	cag	atg	ggc	atg	agc	acc	739
Thr	Ala	Glu	Thr	Phe	Ala	Leu	Pro	Leu	Leu	Gln	Met	Gly	Met	Ser	Thr	
		200					205					210				
tac	tcc	tct	gca	atg	ttc	aac	ttc	att	cca	gat	ttc	gca	ctg	agc	ttc	787
Tyr	Ser	Ser	Ala	Met	Phe	Asn	Phe	Ile	Pro	Asp	Phe	Ala	Leu	Ser	Phe	
	215					220					225					
tac	gcc	gat	gtt	cgt	gcg	cag	gac	agc	gca	gca	gta	aag	cag	aag	ctg	835
Tyr	Ala	Asp	Val	Arg	Ala	Gln	Asp	Ser	Ala	Ala	Val	Lys	Gln	Lys	Leu	
	230				235				240						245	
agc	gat	ttt	gtg	ctc	ccc	tac	ttg	gat	atc	cgc	gat	cgc	gca	caa	ggc	883
Ser	Asp	Phe	Val	Leu	Pro	Tyr	Leu	Asp	Ile	Arg	Asp	Arg	Ala	Gln	Gly	
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tac	ggg	gtc	tcc	att	ggg	aag	ggc	gga	ctc	aag	gct	gtt	ggc	cgc	aac	931
Tyr	Gly	Val	Ser	Ile	Gly	Lys	Gly	Gly	Leu	Lys	Ala	Val	Gly	Arg	Asn	
			265				270						275			
gct	ggc	ggc	gtt	cgc	cca	cca	ctg	cgt	aac	ctt	tcc	gag	caa	gat	atc	979

Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu Ser Glu Gln Asp Ile
 280 285 290

gcg gac ctg tcg gat ttg ctt gcc acc tct ggc gca ggt tcc tac cgc 1027
 Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly Ala Gly Ser Tyr Arg
 295 300 305

ctt cag ttg agg tgaaagcatg atcaccgcaa cgc 1062
 Leu Gln Leu Arg
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<210> 472

<211> 313

<212> PRT

<213> Corynebacterium glutamicum

<400> 472

Met Ala Arg Phe Ser Pro Gln Asp Leu Ala Asp His Leu Lys Asp Gly
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Leu Leu Ser Phe Pro Ala Thr Ala Phe Gln Asp Asp Leu Glu Val Asp
 20 25 30

Glu Ala Ala Tyr Val Glu His Ile Glu Trp Gln Ser Ser Tyr Pro Val
 35 40 45

Ala Gly Leu Phe Ala Ala Gly Gly Thr Gly Glu Gly Phe Ser Leu Thr
 50 55 60

Val Glu Glu Asn His Arg Val Thr Gln Leu Ala Val Gln Ala Ser Ser
 65 70 75 80

Pro Glu Val Pro Val Leu Gly Ser Ala Thr Gly Ser Thr Lys Ser Ala
 85 90 95

Ile Ala Asn Ala Gln Gly Ala Glu Ala Ala Gly Ala Glu Gly Val Leu
 100 105 110

Leu Leu Pro Pro Tyr Leu Thr Glu Cys Asp Ala Glu Gly Leu Tyr Asn
 115 120 125

His Ala Ala Ala Val Cys Glu Ser Thr Ser Leu Gly Val Ile Val Tyr
 130 135 140

Asn Arg Ala Asn Ala Ile Tyr Ser Pro Glu Val Ile Ala Arg Leu Ser
 145 150 155 160

Glu Arg Tyr Pro Asn Phe Ile Gly Phe Lys Asp Gly Thr Gly Asn Ile
 165 170 175

Glu His Leu Ala Lys Ile Thr Thr Leu Cys Gly Asp Arg Leu Phe Tyr
 180 185 190

Leu Gly Gly Leu Pro Thr Ala Glu Thr Phe Ala Leu Pro Leu Leu Gln
 195 200 205

Met Gly Met Ser Thr Tyr Ser Ser Ala Met Phe Asn Phe Ile Pro Asp
 210 215 220

Phe Ala Leu Ser Phe Tyr Ala Asp Val Arg Ala Gln Asp Ser Ala Ala

225		230		235		240
Val Lys Gln Lys Leu Ser Asp Phe Val Leu Pro Tyr Leu Asp Ile Arg						
		245		250		255
Asp Arg Ala Gln Gly Tyr Gly Val Ser Ile Gly Lys Gly Gly Leu Lys						
		260		265		270
Ala Val Gly Arg Asn Ala Gly Gly Val Arg Pro Pro Leu Arg Asn Leu						
		275		280		285
Ser Glu Gln Asp Ile Ala Asp Leu Ser Asp Leu Leu Ala Thr Ser Gly						
		290		295		300
Ala Gly Ser Tyr Arg Leu Gln Leu Arg						
305		310				

<210> 473
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(901)
 <223> RXN02125

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 Met Val Ala Thr Ser
 1 5
 cag ttt atc gat gac agc gag gct gcc cag gcg gta cgc gca gct att 163
 Gln Phe Ile Asp Asp Ser Glu Ala Ala Gln Ala Val Arg Ala Ala Ile
 10 15 20
 gtt gca gga tac cga aac att gat act gcc cta gcg tat gga aac gag 211
 Val Ala Gly Tyr Arg Asn Ile Asp Thr Ala Leu Ala Tyr Gly Asn Glu
 25 30 35
 cgc gcc gtt gcc gaa gcc att cgc acc gct gga gtg ccc cgc gag gag 259
 Arg Gly Val Gly Glu Gly Ile Arg Thr Ala Gly Val Pro Arg Glu Glu
 40 45 50
 ctc ttt att tcc acc aag cta gct gca gaa atc aaa gat tac gat gga 307
 Leu Phe Ile Ser Thr Lys Leu Ala Ala Glu Ile Lys Asp Tyr Asp Gly
 55 60 65
 gca gtc gcc gcg att gat gag tct ttg gcg aaa att gcc ttg gat tat 355
 Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys Ile Gly Leu Asp Tyr
 70 75 80 85
 gtc gat ctg atg ctc att cac tcc cca caa cca tgg agt gat ttc cgt 403
 Val Asp Leu Met Leu Ile His Ser Pro Gln Pro Trp Ser Asp Phe Arg
 90 95 100
 ggt ggg gac tat tca gag gga aac cgt gaa gcg tgg cgc gcg ctg gaa 451
 Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala Trp Arg Ala Leu Glu

105	110	115	
gat gcc tac aaa gcc gga aag att cga tcc att ggt gtc tcg aac ttc			499
Asp Ala Tyr Lys Ala Gly Lys	Ile Arg Ser Ile Gly Val Ser Asn Phe		
120	125	130	
ctg gag gcc gat ctg gag aat atc tta gac tcc gcg acg gtt gct cct			547
Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser Ala Thr Val Ala Pro			
135	140	145	
cac gtt aat cag ctt ctt gtg cat gtt gga aac acc cca agc gag tta			595
His Val Asn Gln Leu Leu Val His Val Gly Asn Thr Pro Ser Glu Leu			
150	155	160	165
atc agt ttc tgc gat tcc aag ggc att ctg gtc gaa gca tat tca ccc			643
Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val Glu Ala Tyr Ser Pro			
170	175	180	
atc gcc cac gga gag atg ctg aag aac cag cag gtc aag gcg att gct			691
Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln Val Lys Ala Ile Ala			
185	190	195	
gac aag tac aac gtg agc att ccg cag cta tgc att cgg tac aca att			739
Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys Ile Arg Tyr Thr Ile			
200	205	210	
caa ctg gga acg gtg tct ttg cca aag act gcc aac cca gat cat atg			787
Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala Asn Pro Asp His Met			
215	220	225	
agc tcc aat gcg cag atc gac ttt gaa att tcc gag gaa gac atg gcg			835
Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser Glu Glu Asp Met Ala			
230	235	240	245
gca ctt caa gaa gtg acc gcc cgc gat tat ggc gag cac agc ggt ttt			883
Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly Glu His Ser Gly Phe			
250	255	260	
cct gtg tat tcc ggc aag tagaaagatt tttatcatgg gac			924
Pro Val Tyr Ser Gly Lys			
265			

<210> 474

<211> 267

<212> PRT

<213> Corynebacterium glutamicum

<400> 474

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		20					25					30			

Ala	Tyr	Gly	Asn	Glu	Arg	Gly	Val	Gly	Glu	Gly	Ile	Arg	Thr	Ala	Gly
		35					40				45				

Val	Pro	Arg	Glu	Glu	Leu	Phe	Ile	Ser	Thr	Lys	Leu	Ala	Ala	Glu	Ile
	50					55					60				

Lys Asp Tyr Asp Gly Ala Val Ala Ala Ile Asp Glu Ser Leu Ala Lys
 65 70 75 80
 Ile Gly Leu Asp Tyr Val Asp Leu Met Leu Ile His Ser Pro Gln Pro
 85 90 95
 Trp Ser Asp Phe Arg Gly Gly Asp Tyr Ser Glu Gly Asn Arg Glu Ala
 100 105 110
 Trp Arg Ala Leu Glu Asp Ala Tyr Lys Ala Gly Lys Ile Arg Ser Ile
 115 120 125
 Gly Val Ser Asn Phe Leu Glu Ala Asp Leu Glu Asn Ile Leu Asp Ser
 130 135 140
 Ala Thr Val Ala Pro His Val Asn Gln Leu Leu Val His Val Gly Asn
 145 150 155 160
 Thr Pro Ser Glu Leu Ile Ser Phe Cys Asp Ser Lys Gly Ile Leu Val
 165 170 175
 Glu Ala Tyr Ser Pro Ile Ala His Gly Glu Met Leu Lys Asn Gln Gln
 180 185 190
 Val Lys Ala Ile Ala Asp Lys Tyr Asn Val Ser Ile Pro Gln Leu Cys
 195 200 205
 Ile Arg Tyr Thr Ile Gln Leu Gly Thr Val Ser Leu Pro Lys Thr Ala
 210 215 220
 Asn Pro Asp His Met Ser Ser Asn Ala Gln Ile Asp Phe Glu Ile Ser
 225 230 235 240
 Glu Glu Asp Met Ala Ala Leu Gln Glu Val Thr Ala Arg Asp Tyr Gly
 245 250 255
 Glu His Ser Gly Phe Pro Val Tyr Ser Gly Lys
 260 265

<210> 475
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<220>
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 <222> (101)..(3538)
 <223> RXN00200

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 Met Arg Gln Val Gly
 1 5
 ggt aat ggg ggc cat caa cta gac tcg atc aac gtg tca gat gta gtt 163
 Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn Val Ser Asp Val Val
 10 15 20

gag tcg aag aaa cta aag ggt tct gcg caa gaa ccc ccg cag gtt gcc	211
Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu Pro Pro Gln Val Ala	
25 30 35	
ccg ggc tgg ctg aag aaa ctg gct atc tca tca ggt ctg ctt ggc ctg	259
Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser Gly Leu Leu Gly Leu	
40 45 50	
ttg atg ttt gtg ctg ttg cct ttc ctg cca gtg aac cag gtg cag tct	307
Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val Asn Gln Val Gln Ser	
55 60 65	
tcg ctg tca tgg cca caa aat ggt gag ctt tcc agc gtt aac gcc ccg	355
Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser Ser Val Asn Ala Pro	
70 75 80 85	
ctg att tcc tac gca ccg cag tcg atg gat gcg tcc atc cct gtg tcc	403
Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala Ser Ile Pro Val Ser	
90 95 100	
gcg ctg gac agt ctc aat gac aat cag tcg ttg gtg atg ggc acg ttg	451
Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu Val Met Gly Thr Leu	
105 110 115	
cct ctg gac agt acg gac gcc acc aac cgt ggt ctg ttt gtg cgc acc	499
Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly Leu Phe Val Arg Thr	
120 125 130	
atc gac ggt aac ctt gac gtg att gtt cgc ggt gag gtg ctg ttg gat	547
Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly Glu Val Leu Leu Asp	
135 140 145	
ctt tca cca aca gag gtg aac cgt ctg cca gat gat gcg atc cta gag	595
Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp Asp Ala Ile Leu Glu	
150 155 160 165	
att tcc tcc acc gag gaa acc acc agc gcg gaa atc acc ggc acg gca	643
Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu Ile Thr Gly Thr Ala	
170 175 180	
ttc agc ggc gag acc gaa ggc gat gag cgg cct cag gtc acc ggc gtt	691
Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro Gln Val Thr Gly Val	
185 190 195	
tac acc gag ctt gtc gac gac ccc tcc acc gca tcg gcc ctg gcc tca	739
Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala Ser Ala Leu Ala Ser	
200 205 210	
gcg ggc tta aac gtt gat att gag atc aac tcc cgc ttc act tca tcc	787
Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser Arg Phe Thr Ser Ser	
215 220 225	
ccc agc ctt cta aag tac gca gcc atc ttc att ggc ctt gcg tct gtg	835
Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile Gly Leu Ala Ser Val	
230 235 240 245	
ttg gtc tcc ctg tgg aca ctg cac cgc atg gat att ttg gat ggt cga	883
Leu Val Ser Leu Trp Thr Leu His Arg Met Asp Ile Leu Asp Gly Arg	
250 255 260	
aaa gca cac cgc ttc ctg cct gcc aac tgg tac aag ctg aag cca ctt	931

Lys	Ala	His	Arg	Phe	Leu	Pro	Ala	Asn	Trp	Tyr	Lys	Leu	Lys	Pro	Leu		
			265					270					275				
gat	ggt	gtt	gtc	gta	gcg	att	ttg	gtg	ttc	tgg	cac	ttc	ctt	ggc	gcc	979	
Asp	Gly	Val	Val	Val	Ala	Ile	Leu	Val	Phe	Trp	His	Phe	Leu	Gly	Ala		
		280					285					290					
aac	acc	tct	gac	gac	ggc	ttc	atc	atg	acc	atg	gcc	cgc	gtg	tcc	cag	1027	
Asn	Thr	Ser	Asp	Asp	Gly	Phe	Ile	Met	Thr	Met	Ala	Arg	Val	Ser	Gln		
		295				300					305						
aac	gcg	gat	tat	atg	gcc	aac	tac	tac	cgc	tgg	ttc	ggt	gtc	cca	gaa	1075	
Asn	Ala	Asp	Tyr	Met	Ala	Asn	Tyr	Tyr	Arg	Trp	Phe	Gly	Val	Pro	Glu		
310					315					320					325		
tca	cca	ttc	ggc	gca	cca	tat	tac	gac	ttg	ctg	gct	ctg	atg	gcc	tac	1123	
Ser	Pro	Phe	Gly	Ala	Pro	Tyr	Tyr	Asp	Leu	Leu	Ala	Leu	Met	Ala	Tyr		
				330					335					340			
atc	tca	acc	tca	tca	atc	tgg	ctt	cgt	cta	ccc	gca	ttg	ctc	gct	gga	1171	
Ile	Ser	Thr	Ser	Ser	Ile	Trp	Leu	Arg	Leu	Pro	Ala	Leu	Leu	Ala	Gly		
			345					350					355				
ctg	atc	atg	tgg	ttc	gtg	atc	acc	aga	gag	gtc	atg	cca	cgg	ttt	ggc	1219	
Leu	Ile	Met	Trp	Phe	Val	Ile	Thr	Arg	Glu	Val	Met	Pro	Arg	Phe	Gly		
		360					365					370					
tca	ttg	gtt	aac	ggt	cgc	cgc	gtt	gcg	cac	tgg	tct	gca	gcc	atg	gtg	1267	
Ser	Leu	Val	Asn	Gly	Arg	Arg	Val	Ala	His	Trp	Ser	Ala	Ala	Met	Val		
	375					380					385						
ttc	ctg	gcg	ttc	tgg	ctt	cca	tac	aac	aac	ggc	act	cgc	cca	gag	cca	1315	
Phe	Leu	Ala	Phe	Trp	Leu	Pro	Tyr	Asn	Asn	Gly	Thr	Arg	Pro	Glu	Pro		
390					395					400					405		
atc	atc	gcg	atg	gga	gct	cta	ctt	gcg	tgg	gtt	tcc	ttc	gag	cgc	gct	1363	
Ile	Ile	Ala	Met	Gly	Ala	Leu	Leu	Ala	Trp	Val	Ser	Phe	Glu	Arg	Ala		
				410					415					420			
atc	gct	acc	tcc	agg	ttg	ttg	ccc	gct	gcc	att	ggt	gtc	att	atc	gcc	1411	
Ile	Ala	Thr	Ser	Arg	Leu	Leu	Pro	Ala	Ala	Ile	Gly	Val	Ile	Ile	Ala		
			425				430						435				
acc	att	tcc	ctg	gca	tca	ggc	ccc	acc	ggt	cta	atg	gca	gtt	gct	gcg	1459	
Thr	Ile	Ser	Leu	Ala	Ser	Gly	Pro	Thr	Gly	Leu	Met	Ala	Val	Ala	Ala		
		440				445						450					
ttg	ctg	gtc	agt	ttg	tcc	gcg	ttg	att	cgc	att	ctt	tat	agg	cgc	ttg	1507	
Leu	Leu	Val	Ser	Leu	Ser	Ala	Leu	Ile	Arg	Ile	Leu	Tyr	Arg	Arg	Leu		
	455					460					465						
ccg	ctt	att	ggg	gcg	tcg	agg	ggg	gcg	tcg	aaa	agc	aaa	gtc	ttt	ggc	1555	
Pro	Leu	Ile	Gly	Ala	Ser	Arg	Gly	Ala	Ser	Lys	Ser	Lys	Val	Phe	Gly		
470					475					480					485		
gct	tcg	atg	gct	atg	ctt	gcc	cca	ttc	ctt	gcg	tct	ggc	acc	gcg	att	1603	
Ala	Ser	Met	Ala	Met	Leu	Ala	Pro	Phe	Leu	Ala	Ser	Gly	Thr	Ala	Ile		
				490					495					500			
ctc	atc	gcc	gtt	ttt	ggc	gat	cag	act	ctg	tca	acc	gtc	atg	gaa	tcc	1651	
Leu	Ile	Ala	Val	Phe	Gly	Asp	Gln	Thr	Leu	Ser	Thr	Val	Met	Glu	Ser		

505					510					515						
atc	agc	gtg	cgc	tcc	gcg	aag	ggc	ccg	gca	ctg	acc	tgg	tac	cac	gaa	1699
Ile	Ser	Val	Arg	Ser	Ala	Lys	Gly	Pro	Ala	Leu	Thr	Trp	Tyr	His	Glu	
		520					525					530				
tat	gtg	cgc	tac	caa	acc	gtc	atg	gaa	caa	acc	gtt	gat	ggt	tcc	ttc	1747
Tyr	Val	Arg	Tyr	Gln	Thr	Val	Met	Glu	Gln	Thr	Val	Asp	Gly	Ser	Phe	
		535					540					545				
acc	cgc	cgt	ttt	gct	gtg	ctg	atg	ctc	atg	gcg	tgt	ctg	gct	att	gtg	1795
Thr	Arg	Arg	Phe	Ala	Val	Leu	Met	Leu	Met	Ala	Cys	Leu	Ala	Ile	Val	
		550					555				560				565	
gtc	atc	gcg	atc	ctg	cgt	tac	ggc	cgc	att	cca	ggc	gct	gcg	aag	gga	1843
Val	Ile	Ala	Ile	Leu	Arg	Tyr	Gly	Arg	Ile	Pro	Gly	Ala	Ala	Lys	Gly	
				570					575					580		
cca	tca	ctg	cgt	ttg	atg	atg	gtc	att	ttc	ggc	acc	atg	ttc	ttc	atg	1891
Pro	Ser	Leu	Arg	Leu	Met	Met	Val	Ile	Phe	Gly	Thr	Met	Phe	Phe	Met	
			585						590					595		
atg	ttc	acc	cca	acc	aag	tgg	act	cac	cac	ttc	ggt	gtc	tac	gca	gga	1939
Met	Phe	Thr	Pro	Thr	Lys	Trp	Thr	His	His	Phe	Gly	Val	Tyr	Ala	Gly	
		600					605					610				
ctt	gcc	ggc	gca	ttg	gcc	gga	ctt	gct	gcc	gtg	ggg	ctg	tcc	tat	gtt	1987
Leu	Ala	Gly	Ala	Leu	Ala	Gly	Leu	Ala	Ala	Val	Gly	Leu	Ser	Tyr	Val	
		615					620				625					
gcg	gtg	aaa	tca	cca	cgc	atg	cgc	acc	att	tcc	atc	ggt	gcg	ttc	ctc	2035
Ala	Val	Lys	Ser	Pro	Arg	Met	Arg	Thr	Ile	Ser	Ile	Gly	Ala	Phe	Leu	
		630					635				640				645	
ttc	ctg	ctg	gcg	ctg	gct	ctc	gca	ggc	gtg	aac	gga	ttc	tgg	tac	acc	2083
Phe	Leu	Leu	Ala	Leu	Ala	Leu	Ala	Gly	Val	Asn	Gly	Phe	Trp	Tyr	Thr	
				650					655					660		
tcc	agc	tac	gcc	gtg	cca	tgg	tgg	gat	aaa	acc	atc	cag	atc	aag	ggc	2131
Ser	Ser	Tyr	Ala	Val	Pro	Trp	Trp	Asp	Lys	Thr	Ile	Gln	Ile	Lys	Gly	
			665					670					675			
atc	gaa	gca	tcc	acc	gta	gtg	ctc	gtg	atc	gcc	gtg	atc	gtg	ctg	atc	2179
Ile	Glu	Ala	Ser	Thr	Val	Val	Leu	Val	Ile	Ala	Val	Ile	Val	Leu	Ile	
			680					685				690				
atc	ggt	gtt	att	caa	tcc	ttt	gtc	cac	gat	gtg	aaa	acc	gcg	caa	gcc	2227
Ile	Gly	Val	Ile	Gln	Ser	Phe	Val	His	Asp	Val	Lys	Thr	Ala	Gln	Ala	
		695					700					705				
gaa	acc	aat	cac	tcc	atg	ggc	gaa	ctc	gtg	gcg	gaa	gat	gaa	gca	aag	2275
Glu	Thr	Asn	His	Ser	Met	Gly	Glu	Leu	Val	Ala	Glu	Asp	Glu	Ala	Lys	
		710					715				720				725	
cgc	gag	cgt	gcc	tcc	agg	ttc	acc	ggc	ctt	gcg	gcc	tcc	cct	atc	gca	2323
Arg	Glu	Arg	Ala	Ser	Arg	Phe	Thr	Gly	Leu	Ala	Ala	Ser	Pro	Ile	Ala	
				730					735					740		
gga	gtg	tcc	gcc	ctc	gtt	gtg	ctg	att	acc	tgc	gca	tcc	atg	ggc	aaa	2371
Gly	Val	Ser	Ala	Leu	Val	Val	Leu	Ile	Thr	Cys	Ala	Ser	Met	Gly	Lys	
			745					750						755		

ggc ttt gtg gac caa tac ccc gcg tac tcc gtg ggt ctt ggc aac ctc Gly Phe Val Asp Gln Tyr Pro Ala Tyr Ser Val Gly Leu Gly Asn Leu 760 765 770	2419
cgc tcc ctg acc ggc aac aca tgt ggc ctt gcc tcc gac gcc atg ctg Arg Ser Leu Thr Gly Asn Thr Cys Gly Leu Ala Ser Asp Ala Met Leu 775 780 785	2467
gaa acc aac tcc aac gat tcc ttc ctc act cca gtg aac tcc aca ctt Glu Thr Asn Ser Asn Asp Ser Phe Leu Thr Pro Val Asn Ser Thr Leu 790 795 800 805	2515
ggc gag tcc ctg gaa tcc gaa gat att cgc ggc ttt agt gct gcc ggc Gly Glu Ser Leu Glu Ser Glu Asp Ile Arg Gly Phe Ser Ala Ala Gly 810 815 820	2563
atc cca cca tca atc agc cag gac caa gca gac ctg tct gct gtt ggt Ile Pro Pro Ser Ile Ser Gln Asp Gln Ala Asp Leu Ser Ala Val Gly 825 830 835	2611
gcc att gcc aac act gac gac tcc acc gaa acc ggc gga tcc gac gaa Ala Ile Ala Asn Thr Asp Asp Ser Thr Glu Thr Gly Gly Ser Asp Glu 840 845 850	2659
tca tcc gga caa tcc acc ggc aac acc ggc ggt gtc cga ggc tcc gaa Ser Ser Gly Gln Ser Thr Gly Asn Thr Gly Gly Val Arg Gly Ser Glu 855 860 865	2707
ggc atc aac ggc tcc aac gcc cgc ctg cca ttc aac ctg gac tac acc Gly Ile Asn Gly Ser Asn Ala Arg Leu Pro Phe Asn Leu Asp Tyr Thr 870 875 880 885	2755
caa gtt cca gtc gtc ggc tcc tgg tcc gct ggc acc caa aac cca gca Gln Val Pro Val Val Gly Ser Trp Ser Ala Gly Thr Gln Asn Pro Ala 890 895 900	2803
aac atc acc acc gac tgg tac gaa atc cca gaa gcc acc gaa gaa gca Asn Ile Thr Thr Asp Trp Tyr Glu Ile Pro Glu Ala Thr Glu Glu Ala 905 910 915	2851
ccc atc atc gtg gta tct gca gca ggt cgc atc gaa cac tac gac atc Pro Ile Ile Val Val Ser Ala Ala Gly Arg Ile Glu His Tyr Asp Ile 920 925 930	2899
aac ggc gtc cgc caa tcc gga caa tcc gtc atg ctc gaa tac ggt cgc Asn Gly Val Arg Gln Ser Gly Gln Ser Val Met Leu Glu Tyr Gly Arg 935 940 945	2947
ctt cgc gat aac ggc gac gtt gaa gac ctc ggc gaa gcc atg atg tac Leu Arg Asp Asn Gly Asp Val Glu Asp Leu Gly Glu Ala Met Met Tyr 950 955 960 965	2995
gac atc ggc ccc gag cca tcc tgg cgc aac ctc cgc tac cca ctt gac Asp Ile Gly Pro Glu Pro Ser Trp Arg Asn Leu Arg Tyr Pro Leu Asp 970 975 980	3043
caa ctc cca gaa gaa gcg gac gtc gtg cgc atc gtc gcc acc gac gtc Gln Leu Pro Glu Glu Ala Asp Val Val Arg Ile Val Ala Thr Asp Val 985 990 995	3091

aac ctc gac gaa gac caa tgg gta gca ctg acg cca cca cgc gta cct 3139
 Asn Leu Asp Glu Asp Gln Trp Val Ala Leu Thr Pro Pro Arg Val Pro
 1000 1005 1010

aac cta gat tct ctg aac aac gtc atc gga tcc gaa acc cca gga ctc 3187
 Asn Leu Asp Ser Leu Asn Asn Val Ile Gly Ser Glu Thr Pro Gly Leu
 1015 1020 1025

ctc gac tgg gca gtt ggc ctg caa ttc cca tgc caa cgc acc ttc gac 3235
 Leu Asp Trp Ala Val Gly Leu Gln Phe Pro Cys Gln Arg Thr Phe Asp
 1030 1035 1040 1045

cac tac gcc gga gtc acc gag att cct gaa tac cga atc tcc cca gac 3283
 His Tyr Ala Gly Val Thr Glu Ile Pro Glu Tyr Arg Ile Ser Pro Asp
 1050 1055 1060

cac ggc gga aaa tcc acc ctc tcc cca ttc caa gac tgg gca ggc ggc 3331
 His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln Asp Trp Ala Gly Gly
 1065 1070 1075

gga tcc atg ggc acg gcc gaa gca gta aac aac gcc tac gaa atc ccg 3379
 Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn Ala Tyr Glu Ile Pro
 1080 1085 1090

tcc tac ctc cgc aac gac tgg ggc cgc gac tgg ggt tcc atc gaa cgc 3427
 Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp Gly Ser Ile Glu Arg
 1095 1100 1105

tac tcg ctg cgc acc aac tcc aac ggc gat gca cct aag gtt gca gac 3475
 Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala Pro Lys Val Ala Asp
 1110 1115 1120 1125

atc aac ctt gaa acc atc caa cgt tcc gga ctc tgg aat cca ggg cat 3523
 Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu Trp Asn Pro Gly His
 1130 1135 1140

atg aag gta gat gaa taagaccttc agtactggaa gtt 3561
 Met Lys Val Asp Glu
 1145

<210> 476

<211> 1146

<212> PRT

<213> Corynebacterium glutamicum

<400> 476

Met Arg Gln Val Gly Gly Asn Gly Gly His Gln Leu Asp Ser Ile Asn
 1 5 10 15

Val Ser Asp Val Val Glu Ser Lys Lys Leu Lys Gly Ser Ala Gln Glu
 20 25 30

Pro Pro Gln Val Ala Pro Gly Trp Leu Lys Lys Leu Ala Ile Ser Ser
 35 40 45

Gly Leu Leu Gly Leu Leu Met Phe Val Leu Leu Pro Phe Leu Pro Val
 50 55 60

Asn Gln Val Gln Ser Ser Leu Ser Trp Pro Gln Asn Gly Glu Leu Ser
 65 70 75 80

Ser Val Asn Ala Pro Leu Ile Ser Tyr Ala Pro Gln Ser Met Asp Ala
 85 90 95
 Ser Ile Pro Val Ser Ala Leu Asp Ser Leu Asn Asp Asn Gln Ser Leu
 100 105 110
 Val Met Gly Thr Leu Pro Leu Asp Ser Thr Asp Ala Thr Asn Arg Gly
 115 120 125
 Leu Phe Val Arg Thr Ile Asp Gly Asn Leu Asp Val Ile Val Arg Gly
 130 135 140
 Glu Val Leu Leu Asp Leu Ser Pro Thr Glu Val Asn Arg Leu Pro Asp
 145 150 155 160
 Asp Ala Ile Leu Glu Ile Ser Ser Thr Glu Glu Thr Thr Ser Ala Glu
 165 170 175
 Ile Thr Gly Thr Ala Phe Ser Gly Glu Thr Glu Gly Asp Glu Arg Pro
 180 185 190
 Gln Val Thr Gly Val Tyr Thr Glu Leu Val Asp Asp Pro Ser Thr Ala
 195 200 205
 Ser Ala Leu Ala Ser Ala Gly Leu Asn Val Asp Ile Glu Ile Asn Ser
 210 215 220
 Arg Phe Thr Ser Ser Pro Ser Leu Leu Lys Tyr Ala Ala Ile Phe Ile
 225 230 235 240
 Gly Leu Ala Ser Val Leu Val Ser Leu Trp Thr Leu His Arg Met Asp
 245 250 255
 Ile Leu Asp Gly Arg Lys Ala His Arg Phe Leu Pro Ala Asn Trp Tyr
 260 265 270
 Lys Leu Lys Pro Leu Asp Gly Val Val Val Ala Ile Leu Val Phe Trp
 275 280 285
 His Phe Leu Gly Ala Asn Thr Ser Asp Asp Gly Phe Ile Met Thr Met
 290 295 300
 Ala Arg Val Ser Gln Asn Ala Asp Tyr Met Ala Asn Tyr Tyr Arg Trp
 305 310 315 320
 Phe Gly Val Pro Glu Ser Pro Phe Gly Ala Pro Tyr Tyr Asp Leu Leu
 325 330 335
 Ala Leu Met Ala Tyr Ile Ser Thr Ser Ser Ile Trp Leu Arg Leu Pro
 340 345 350
 Ala Leu Leu Ala Gly Leu Ile Met Trp Phe Val Ile Thr Arg Glu Val
 355 360 365
 Met Pro Arg Phe Gly Ser Leu Val Asn Gly Arg Arg Val Ala His Trp
 370 375 380
 Ser Ala Ala Met Val Phe Leu Ala Phe Trp Leu Pro Tyr Asn Asn Gly
 385 390 395 400

Thr Arg Pro Glu Pro Ile Ile Ala Met Gly Ala Leu Leu Ala Trp Val
 405 410 415
 Ser Phe Glu Arg Ala Ile Ala Thr Ser Arg Leu Leu Pro Ala Ala Ile
 420 425 430
 Gly Val Ile Ile Ala Thr Ile Ser Leu Ala Ser Gly Pro Thr Gly Leu
 435 440 445
 Met Ala Val Ala Ala Leu Leu Val Ser Leu Ser Ala Leu Ile Arg Ile
 450 455 460
 Leu Tyr Arg Arg Leu Pro Leu Ile Gly Ala Ser Arg Gly Ala Ser Lys
 465 470 475 480
 Ser Lys Val Phe Gly Ala Ser Met Ala Met Leu Ala Pro Phe Leu Ala
 485 490 495
 Ser Gly Thr Ala Ile Leu Ile Ala Val Phe Gly Asp Gln Thr Leu Ser
 500 505 510
 Thr Val Met Glu Ser Ile Ser Val Arg Ser Ala Lys Gly Pro Ala Leu
 515 520 525
 Thr Trp Tyr His Glu Tyr Val Arg Tyr Gln Thr Val Met Glu Gln Thr
 530 535 540
 Val Asp Gly Ser Phe Thr Arg Arg Phe Ala Val Leu Met Leu Met Ala
 545 550 555 560
 Cys Leu Ala Ile Val Val Ile Ala Ile Leu Arg Tyr Gly Arg Ile Pro
 565 570 575
 Gly Ala Ala Lys Gly Pro Ser Leu Arg Leu Met Met Val Ile Phe Gly
 580 585 590
 Thr Met Phe Phe Met Met Phe Thr Pro Thr Lys Trp Thr His His Phe
 595 600 605
 Gly Val Tyr Ala Gly Leu Ala Gly Ala Leu Ala Gly Leu Ala Ala Val
 610 615 620
 Gly Leu Ser Tyr Val Ala Val Lys Ser Pro Arg Met Arg Thr Ile Ser
 625 630 635 640
 Ile Gly Ala Phe Leu Phe Leu Leu Ala Leu Ala Leu Ala Gly Val Asn
 645 650 655
 Gly Phe Trp Tyr Thr Ser Ser Tyr Ala Val Pro Trp Trp Asp Lys Thr
 660 665 670
 Ile Gln Ile Lys Gly Ile Glu Ala Ser Thr Val Val Leu Val Ile Ala
 675 680 685
 Val Ile Val Leu Ile Ile Gly Val Ile Gln Ser Phe Val His Asp Val
 690 695 700
 Lys Thr Ala Gln Ala Glu Thr Asn His Ser Met Gly Glu Leu Val Ala
 705 710 715 720
 Glu Asp Glu Ala Lys Arg Glu Arg Ala Ser Arg Phe Thr Gly Leu Ala

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Arg Ile Ser Pro Asp His Gly Gly Lys Ser Thr Leu Ser Pro Phe Gln
 1060 1065 1070

Asp Trp Ala Gly Gly Gly Ser Met Gly Thr Ala Glu Ala Val Asn Asn
 1075 1080 1085

Ala Tyr Glu Ile Pro Ser Tyr Leu Arg Asn Asp Trp Gly Arg Asp Trp
 1090 1095 1100

Gly Ser Ile Glu Arg Tyr Ser Leu Arg Thr Asn Ser Asn Gly Asp Ala
 1105 1110 1115 1120

Pro Lys Val Ala Asp Ile Asn Leu Glu Thr Ile Gln Arg Ser Gly Leu
 1125 1130 1135

Trp Asn Pro Gly His Met Lys Val Asp Glu
 1140 1145

<210> 477
 <211> 1509
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1486)
 <223> RXN01175

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 Val Ser Trp Thr Val
 1 5

gat atc cct aaa gaa gtt ctc cct gat ttg cca cca ttg cca gaa ggc 163
 Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro Pro Leu Pro Glu Gly
 10 15 20

atg cag cag cag ttc gag gac acc att tcc cgt gac gct aag cag caa 211
 Met Gln Gln Gln Phe Glu Asp Thr Ile Ser Arg Asp Ala Lys Gln Gln
 25 30 35

cct acg tgg gat cgt gca cag gca gaa aac gtg cgc aag atc ctt gag 259
 Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val Arg Lys Ile Leu Glu
 40 45 50

tcg gtt cct cca atc gtt gtt gcc cct gag gta ctt gag ctg aag cag 307
 Ser Val Pro Pro Ile Val Val Ala Pro Glu Val Leu Glu Leu Lys Gln
 55 60 65

aag ctt gct gat gtt gcc aac ggt aag gcc ttc ctc ttg cag ggt ggt 355
 Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe Leu Leu Gln Gly Gly
 70 75 80 85

gac tgt gcg gaa act ttc gag tca aac act gag ccg cac att cgc gcc 403
 Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu Pro His Ile Arg Ala
 90 95 100

aac gta aag act ctg ctg cag atg gca gtt gtt ttg acc tac ggt gca	451
Asn Val Lys Thr Leu Leu Gln Met Ala Val Val Leu Thr Tyr Gly Ala	
105 110 115	
tcc act cct gtg atc aag atg gct cgt att gct ggt cag tac gca aag	499
Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala Gly Gln Tyr Ala Lys	
120 125 130	
cct cgc tct tct gat ctg gat gga aat ggt ctg cca aac tac cgt ggc	547
Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu Pro Asn Tyr Arg Gly	
135 140 145	
gat atc gtc aac ggt gtg gag gca acc cca gag gct cgt cgc cac gat	595
Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu Ala Arg Arg His Asp	
150 155 160 165	
cct gcc cgc atg atc cgt gct tac gct aac gct tct gct gcg atg aac	643
Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala Ser Ala Ala Met Asn	
170 175 180	
ttg gtg cgc gcg ctc acc agc tct ggc acc gct gat ctt tac cgt ctc	691
Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala Asp Leu Tyr Arg Leu	
185 190 195	
agc gag tgg aac cgc gag ttc gtt gcg aac tcc cca gct ggt gca cgc	739
Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser Pro Ala Gly Ala Arg	
200 205 210	
tac gag gct ctt gct cgt gag atc gac tcc ggt ctg cgc ttc atg gaa	787
Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly Leu Arg Phe Met Glu	
215 220 225	
gca tgt ggc gtg tcc gat gag tcc ctg cgt gct gca gat atc tac tgc	835
Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala Ala Asp Ile Tyr Cys	
230 235 240 245	
tcc cac gag gct ttg ctg gtg gat tac gag cgt tcc atg ctg cgt ctt	883
Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg Ser Met Leu Arg Leu	
250 255 260	
gca acc gat gag gaa ggc aac gag gaa ctt tac gat ctt tca gct cac	931
Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr Asp Leu Ser Ala His	
265 270 275	
cag ctg tgg atc ggc gag cgc acc cgt ggc atg gat gat ttc cat gtg	979
Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met Asp Asp Phe His Val	
280 285 290	
aac ttc gca tcc atg atc tct aac cca atc ggc atc aag att ggt cct	1027
Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly Ile Lys Ile Gly Pro	
295 300 305	
ggt atc acc cct gaa gag gct gtt gca tac gct gac aag ctc gat ccg	1075
Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala Asp Lys Leu Asp Pro	
310 315 320 325	
aac ttc gag cct ggc cgt ttg acc atc gtt gct cgc atg ggc cac gac	1123
Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala Arg Met Gly His Asp	
330 335 340	
aag gtt cgc tcc gta ctt cct ggt gtt atc cag gct gtt gag gca tcc	1171

Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln Ala Val Glu Ala Ser
 345 350 355
 gga cac aag gtt att tgg cag tcc gat ccg atg cac ggc aac act ttc 1219
 Gly His Lys Val Ile Trp Gln Ser Asp Pro Met His Gly Asn Thr Phe
 360 365 370
 acc gca tcc aat ggc tac aag acc cgt cac ttc gac aag gtt atc gat 1267
 Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe Asp Lys Val Ile Asp
 375 380 385
 gag gtc cag ggc ttc ttc gag gtc cac cgc gca ttg ggc acc cac cca 1315
 Glu Val Gln Gly Phe Phe Glu Val His Arg Ala Leu Gly Thr His Pro
 390 395 400 405
 ggc gga atc cac att gag ttc act ggt gaa gat gtc acc gag tgc ctc 1363
 Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp Val Thr Glu Cys Leu
 410 415 420
 ggt ggc gct gaa gac atc acc gat gtt gat ctg cca ggc cgc tac gag 1411
 Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu Pro Gly Arg Tyr Glu
 425 430 435
 tcc gca tgc gat cct cgc ctg aac act cag cag tct ttg gag ttg gct 1459
 Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln Ser Leu Glu Leu Ala
 440 445 450
 ttc ctc gtt gca gaa atg ctg cgt aac taagctttta gaccaactct 1506
 Phe Leu Val Ala Glu Met Leu Arg Asn
 455 460
 aaa 1509

<210> 478

<211> 462

<212> PRT

<213> Corynebacterium glutamicum

<400> 478

Val Ser Trp Thr Val Asp Ile Pro Lys Glu Val Leu Pro Asp Leu Pro
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 20 25 30
 Asp Ala Lys Gln Gln Pro Thr Trp Asp Arg Ala Gln Ala Glu Asn Val
 35 40 45
 Arg Lys Ile Leu Glu Ser Val Pro Pro Ile Val Val Ala Pro Glu Val
 50 55 60
 Leu Glu Leu Lys Gln Lys Leu Ala Asp Val Ala Asn Gly Lys Ala Phe
 65 70 75 80
 Leu Leu Gln Gly Gly Asp Cys Ala Glu Thr Phe Glu Ser Asn Thr Glu
 85 90 95
 Pro His Ile Arg Ala Asn Val Lys Thr Leu Leu Gln Met Ala Val Val
 100 105 110

Leu Thr Tyr Gly Ala Ser Thr Pro Val Ile Lys Met Ala Arg Ile Ala
 115 120 125
 Gly Gln Tyr Ala Lys Pro Arg Ser Ser Asp Leu Asp Gly Asn Gly Leu
 130 135 140
 Pro Asn Tyr Arg Gly Asp Ile Val Asn Gly Val Glu Ala Thr Pro Glu
 145 150 155 160
 Ala Arg Arg His Asp Pro Ala Arg Met Ile Arg Ala Tyr Ala Asn Ala
 165 170 175
 Ser Ala Ala Met Asn Leu Val Arg Ala Leu Thr Ser Ser Gly Thr Ala
 180 185 190
 Asp Leu Tyr Arg Leu Ser Glu Trp Asn Arg Glu Phe Val Ala Asn Ser
 195 200 205
 Pro Ala Gly Ala Arg Tyr Glu Ala Leu Ala Arg Glu Ile Asp Ser Gly
 210 215 220
 Leu Arg Phe Met Glu Ala Cys Gly Val Ser Asp Glu Ser Leu Arg Ala
 225 230 235 240
 Ala Asp Ile Tyr Cys Ser His Glu Ala Leu Leu Val Asp Tyr Glu Arg
 245 250 255
 Ser Met Leu Arg Leu Ala Thr Asp Glu Glu Gly Asn Glu Glu Leu Tyr
 260 265 270
 Asp Leu Ser Ala His Gln Leu Trp Ile Gly Glu Arg Thr Arg Gly Met
 275 280 285
 Asp Asp Phe His Val Asn Phe Ala Ser Met Ile Ser Asn Pro Ile Gly
 290 295 300
 Ile Lys Ile Gly Pro Gly Ile Thr Pro Glu Glu Ala Val Ala Tyr Ala
 305 310 315 320
 Asp Lys Leu Asp Pro Asn Phe Glu Pro Gly Arg Leu Thr Ile Val Ala
 325 330 335
 Arg Met Gly His Asp Lys Val Arg Ser Val Leu Pro Gly Val Ile Gln
 340 345 350
 Ala Val Glu Ala Ser Gly His Lys Val Ile Trp Gln Ser Asp Pro Met
 355 360 365
 His Gly Asn Thr Phe Thr Ala Ser Asn Gly Tyr Lys Thr Arg His Phe
 370 375 380
 Asp Lys Val Ile Asp Glu Val Gln Gly Phe Phe Glu Val His Arg Ala
 385 390 395 400
 Leu Gly Thr His Pro Gly Gly Ile His Ile Glu Phe Thr Gly Glu Asp
 405 410 415
 Val Thr Glu Cys Leu Gly Gly Ala Glu Asp Ile Thr Asp Val Asp Leu
 420 425 430
 Pro Gly Arg Tyr Glu Ser Ala Cys Asp Pro Arg Leu Asn Thr Gln Gln

435		440		445
Ser Leu Glu Leu Ala Phe	Leu Val Ala Glu Met	Leu Arg Asn		
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 <211> 984
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(961)
 <223> RXN01376

<400> 479
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 Val Thr Tyr Ser Pro
 1 5
 ggt aaa tac ttg gcg tcg ttc ctg gat tct ttg cct ggt gcg act tca 163
 Gly Lys Tyr Leu Ala Ser Phe Leu Asp Ser Leu Pro Gly Ala Thr Ser
 10 15 20
 cga gac acc cac gtt gtg atg gca gac aat ggt tct gtg gac ggt gtt 211
 Arg Asp Thr His Val Val Met Ala Asp Asn Gly Ser Val Asp Gly Val
 25 30 35
 cct gag cag gca gca gcc tca cgc agc aac gtg gag ttc ctc tca act 259
 Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val Glu Phe Leu Ser Thr
 40 45 50
 ggc ggc aac tta ggc tac gga acg gct att aat att gcc gcc cga tcg 307
 Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn Ile Ala Ala Arg Ser
 55 60 65
 ttg cgt gcg cgc cgg gag gca gga gag atc gat ggg gag ttc ttc ctc 355
 Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp Gly Glu Phe Phe Leu
 70 75 80 85
 gtc tca aac cct gat gtt gtt ttt gac gaa gac tct att gat caa ttg 403
 Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp Ser Ile Asp Gln Leu
 90 95 100
 ctt gaa tgt gcg aaa cgt cac cct gaa gca gga gcg gtt ggc ccg ttg 451
 Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly Ala Val Gly Pro Leu
 105 110 115
 atc cgt gag gcg gac ggt tcg gcg tat ccg tcg gct cgg gcg gta ccc 499
 Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser Ala Arg Ala Val Pro
 120 125 130
 act ttg gcg aat ggc att ggt cac gct ttg ttg ggt gct gtg tgg aaa 547
 Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu Gly Ala Val Trp Lys
 135 140 145
 tcc aat ccg tgg tcg gcg gct tac cgt gac gat gaa gat atg gac act 595
 Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp Glu Asp Met Asp Thr

150	155	160	165	
gag cgc act gct ggc tgg ctg tcg gga tgc tgc ctg tta tta agg tgg				643
Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys Leu Leu Leu Arg Trp				
170		175	180	
gat gcg ttt gat cga gtt ggt ggt ttt gat gag cgc tac ttc atg tac				691
Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu Arg Tyr Phe Met Tyr				
185		190	195	
atg gaa gac gtt gac ctg gga gat cgg ctg gtt cgc gcc ggt ttc acc				739
Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val Arg Ala Gly Phe Thr				
200		205	210	
aac gtc ttt tgc cca agt gcg cag atc atc cac gcg aaa ggt cat gtt				787
Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His Ala Lys Gly His Val				
215		220	225	
gcg ggt aaa aac cca gag aac atg ttg ccc gca cac cac gag agc gcg				835
Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala His His Glu Ser Ala				
230		235	240	245
tat cgc ttc cag gct gat cgc ctg gcg aag ccg tgg caa gcc cca att				883
Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro Trp Gln Ala Pro Ile				
250		255	260	
cgg ttg gct ctg cga att ggt ttg aaa tta cga gcc gga gtc gcg gtt				931
Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg Ala Gly Val Ala Val				
265		270	275	
ggt gtc tct aag atg aga acg aaa gcc tct tagaccgtcg acgaccaccg				981
Gly Val Ser Lys Met Arg Thr Lys Ala Ser				
280		285		
gac				984

<210> 480
 <211> 287
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 480
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 Pro Gly Ala Thr Ser Arg Asp Thr His Val Val Met Ala Asp Asn Gly
 20 25 30
 Ser Val Asp Gly Val Pro Glu Gln Ala Ala Ala Ser Arg Ser Asn Val
 35 40 45
 Glu Phe Leu Ser Thr Gly Gly Asn Leu Gly Tyr Gly Thr Ala Ile Asn
 50 55 60
 Ile Ala Ala Arg Ser Leu Arg Ala Arg Arg Glu Ala Gly Glu Ile Asp
 65 70 75 80
 Gly Glu Phe Phe Leu Val Ser Asn Pro Asp Val Val Phe Asp Glu Asp
 85 90 95

Ser Ile Asp Gln Leu Leu Glu Cys Ala Lys Arg His Pro Glu Ala Gly
 100 105 110
 Ala Val Gly Pro Leu Ile Arg Glu Ala Asp Gly Ser Ala Tyr Pro Ser
 115 120 125
 Ala Arg Ala Val Pro Thr Leu Ala Asn Gly Ile Gly His Ala Leu Leu
 130 135 140
 Gly Ala Val Trp Lys Ser Asn Pro Trp Ser Ala Ala Tyr Arg Asp Asp
 145 150 155 160
 Glu Asp Met Asp Thr Glu Arg Thr Ala Gly Trp Leu Ser Gly Ser Cys
 165 170 175
 Leu Leu Leu Arg Trp Asp Ala Phe Asp Arg Val Gly Gly Phe Asp Glu
 180 185 190
 Arg Tyr Phe Met Tyr Met Glu Asp Val Asp Leu Gly Asp Arg Leu Val
 195 200 205
 Arg Ala Gly Phe Thr Asn Val Phe Cys Pro Ser Ala Gln Ile Ile His
 210 215 220
 Ala Lys Gly His Val Ala Gly Lys Asn Pro Glu Asn Met Leu Pro Ala
 225 230 235 240
 His His Glu Ser Ala Tyr Arg Phe Gln Ala Asp Arg Leu Ala Lys Pro
 245 250 255
 Trp Gln Ala Pro Ile Arg Leu Ala Leu Arg Ile Gly Leu Lys Leu Arg
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 Ala Gly Val Ala Val Gly Val Ser Lys Met Arg Thr Lys Ala Ser
 275 280 285

<210> 481
 <211> 1002
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(979)
 <223> RXN01631

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 caaccagggc atttccgtaa acatctaaga ggagcactcc atg aaa cca caa ctt 115
 Met Lys Pro Gln Leu
 1 5
 att gca tct tgc tgg acc agc gcg gga gac gcc gca ccc gat cgt gac 163
 Ile Ala Ser Cys Trp Thr Ser Ala Gly Asp Ala Ala Pro Asp Arg Asp
 10 15 20
 gat ctc agc agc cca gta gca atc gat gag cgc atc gct cta gtc gct 211
 Asp Leu Ser Ser Pro Val Ala Ile Asp Glu Arg Ile Ala Leu Val Ala
 25 30 35

gaa acc ggt tgg gca ggc att ggg ctt gtt cac gcc gat ctc atc aaa	259
Glu Thr Gly Trp Ala Gly Ile Gly Leu Val His Ala Asp Leu Ile Lys	
40 45 50	
gca cgc gac acc att ggc tac gag gaa ttg cgc cga cgc atc cac gct	307
Ala Arg Asp Thr Ile Gly Tyr Glu Glu Leu Arg Arg Arg Ile His Ala	
55 60 65	
gca gga att gaa atc att gag gtg gag ttc ctc aat ggt tgg tgg gcg	355
Ala Gly Ile Glu Ile Ile Glu Val Glu Phe Leu Asn Gly Trp Trp Ala	
70 75 80 85	
act ggt gcg gaa cgc caa gag tcc gat gcc gtt cgt gcg gat ctg ttt	403
Thr Gly Ala Glu Arg Gln Glu Ser Asp Ala Val Arg Ala Asp Leu Phe	
90 95 100	
gct gcg gcg caa gct ctt ggt tcc cca cac att aag gtc gga gca gga	451
Ala Ala Ala Gln Ala Leu Gly Ser Pro His Ile Lys Val Gly Ala Gly	
105 110 115	
gag ggc acc aat ggt gtg gtt ccc att gct cac atg gcc agt gcg ttt	499
Glu Gly Thr Asn Gly Val Val Pro Ile Ala His Met Ala Ser Ala Phe	
120 125 130	
act gat ctc gct gcg gaa gct gaa gct cat ggc gtc aag ctc gcg ttg	547
Thr Asp Leu Ala Ala Glu Ala Glu Ala His Gly Val Lys Leu Ala Leu	
135 140 145	
gaa gca act ccg ttt tct cac ctg aag acc atc tac gac gcg ctg gaa	595
Glu Ala Thr Pro Phe Ser His Leu Lys Thr Ile Tyr Asp Ala Leu Glu	
150 155 160 165	
gtt gtc agc cat tcc gat agc cca tcg gct gga ctc atg gtt gat atc	643
Val Val Ser His Ser Asp Ser Pro Ser Ala Gly Leu Met Val Asp Ile	
170 175 180	
tgg cac acc gcg aaa atc gga atc ccc aac gat gaa ctg tgg cgc aac	691
Trp His Thr Ala Lys Ile Gly Ile Pro Asn Asp Glu Leu Trp Arg Asn	
185 190 195	
att cca ctg tcc aag gtc aac gca gtg gag gtt gat gat ggt ttc att	739
Ile Pro Leu Ser Lys Val Asn Ala Val Glu Val Asp Asp Gly Phe Ile	
200 205 210	
gac acc cca att gat ctt ttc gat gac tcc acc aac cgt cgc gcg tac	787
Asp Thr Pro Ile Asp Leu Phe Asp Asp Ser Thr Asn Arg Arg Ala Tyr	
215 220 225	
tgc ggt gaa ggc gaa ttt gat ccc gca agc ttc atc cgt ggc gcc atc	835
Cys Gly Glu Gly Glu Phe Asp Pro Ala Ser Phe Ile Arg Gly Ala Ile	
230 235 240 245	
gac gcc ggt tgg acg ggc gca tat ggt gtg gaa att att tcc gca gag	883
Asp Ala Gly Trp Thr Gly Ala Tyr Gly Val Glu Ile Ile Ser Ala Glu	
250 255 260	
cac cga agc ctc ccg gtg aaa gaa ggg ctg caa cgt gct ttc gac acc	931
His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln Arg Ala Phe Asp Thr	
265 270 275	

979

1002

<400> 482																
Met	Lys	Pro	Gln	Leu	Ile	Ala	Ser	Cys	Trp	Thr	Ser	Ala	Gly	Asp	Ala	
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Ala	Pro	Asp	Arg	Asp	Asp	Leu	Ser	Ser	Pro	Val	Ala	Ile	Asp	Glu	Arg	
			20					25					30			
Ile	Ala	Leu	Val	Ala	Glu	Thr	Gly	Trp	Ala	Gly	Ile	Gly	Leu	Val	His	
		35					40					45				
Ala	Asp	Leu	Ile	Lys	Ala	Arg	Asp	Thr	Ile	Gly	Tyr	Glu	Glu	Leu	Arg	
	50					55					60					
Arg	Arg	Ile	His	Ala	Ala	Gly	Ile	Glu	Ile	Ile	Glu	Val	Glu	Phe	Leu	
65					70					75					80	
Asn	Gly	Trp	Trp	Ala	Thr	Gly	Ala	Glu	Arg	Gln	Glu	Ser	Asp	Ala	Val	
				85					90					95		
Arg	Ala	Asp	Leu	Phe	Ala	Ala	Ala	Gln	Ala	Leu	Gly	Ser	Pro	His	Ile	
			100					105					110			
Lys	Val	Gly	Ala	Gly	Glu	Gly	Thr	Asn	Gly	Val	Val	Pro	Ile	Ala	His	
		115					120					125				
Met	Ala	Ser	Ala	Phe	Thr	Asp	Leu	Ala	Ala	Glu	Ala	Glu	Ala	His	Gly	
	130					135						140				
Val	Lys	Leu	Ala	Leu	Glu	Ala	Thr	Pro	Phe	Ser	His	Leu	Lys	Thr	Ile	
145					150					155					160	
Tyr	Asp	Ala	Leu	Glu	Val	Val	Ser	His	Ser	Asp	Ser	Pro	Ser	Ala	Gly	
				165					170					175		
Leu	Met	Val	Asp	Ile	Trp	His	Thr	Ala	Lys	Ile	Gly	Ile	Pro	Asn	Asp	
			180					185					190			
Glu	Leu	Trp	Arg	Asn	Ile	Pro	Leu	Ser	Lys	Val	Asn	Ala	Val	Glu	Val	
		195					200					205				
Asp	Asp	Gly	Phe	Ile	Asp	Thr	Pro	Ile	Asp	Leu	Phe	Asp	Asp	Ser	Thr	
	210					215					220					
Asn	Arg	Arg	Ala	Tyr	Cys	Gly	Glu	Gly	Glu	Phe	Asp	Pro	Ala	Ser	Phe	
225					230					235					240	
Ile	Arg	Gly	Ala	Ile	Asp	Ala	Gly	Trp	Thr	Gly	Ala	Tyr	Gly	Val	Glu	
				245					250					255		

Ile Ile Ser Ala Glu His Arg Ser Leu Pro Val Lys Glu Gly Leu Gln
260 265 270

Arg Ala Phe Asp Thr Thr Ile Ala Ala Phe Glu Gln Ala Ala Arg Leu
275 280 285

Ala Pro Ser Thr Asn
290

<210> 483

<211> 990

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(967)

<223> RXN01593

<400> 483

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gcacgtagtt tctgcgctct ctggcgccgg cctaccgctc atg tat gtc acc aat 115
Met Tyr Val Thr Asn
1 5

aat gcc tcc cgt gct ccg gag gtg gtg gct gcg caa ctc cgt gag att 163
Asn Ala Ser Arg Ala Pro Glu Val Val Ala Ala Gln Leu Arg Glu Ile
10 15 20

ggc ctt gcc gac acc act gcg gac aat gtg atg aca tct gct caa gct 211
Gly Leu Ala Asp Thr Thr Ala Asp Asn Val Met Thr Ser Ala Gln Ala
25 30 35

gcc tgc aag atg gcg gcg gag aag att ccc gct gga tcc aag gtg tat 259
Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala Gly Ser Lys Val Tyr
40 45 50

gtt ttg ggt tca gaa tcc ttc cgc gag cta gct act gaa gct ggt ttt 307
Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala Thr Glu Ala Gly Phe
55 60 65

gtg gtg gtt gat tcg gct gat gat aaa cct gtg gct gtg ctt cac ggc 355
Val Val Val Asp Ser Ala Asp Asp Lys Pro Val Ala Val Leu His Gly
70 75 80 85

cac aac cct gag acc ggt tgg gct cag ttg agc gag gct gcg ctg tca 403
His Asn Pro Glu Thr Gly Trp Ala Gln Leu Ser Glu Ala Ala Leu Ser
90 95 100

att aat gct ggc gcg cag tat ttt gca tca aat ttg gat tcc acc ctt 451
Ile Asn Ala Gly Ala Gln Tyr Phe Ala Ser Asn Leu Asp Ser Thr Leu
105 110 115

ccc atg gaa cgc ggt cgt cac att ggc aac ggt tcc atg gtg gct gcc 499
Pro Met Glu Arg Gly Arg His Ile Gly Asn Gly Ser Met Val Ala Ala
120 125 130

gtg gtc aac gcg act ggc gta aag cct ctt tcc gca ggt aag cca ggc 547
Val Val Asn Ala Thr Gly Val Lys Pro Leu Ser Ala Gly Lys Pro Gly

135	140	145	
ccc gcg atg ttc tat gcg ggg gct gaa act ctt aat tct tca aag cct			595
Pro Ala Met Phe Tyr Ala Gly Ala Glu Thr Leu Asn Ser Ser Lys Pro			
150	155	160	165
ttg gct gtc ggc gat cgt ctc gat acc gat atc gcc ggc gga aac gct			643
Leu Ala Val Gly Asp Arg Leu Asp Thr Asp Ile Ala Gly Gly Asn Ala			
	170	175	180
gca ggc atg gac aca ttc cag gtc ctg acc ggc gtc agc ggc tac tac			691
Ala Gly Met Asp Thr Phe Gln Val Leu Thr Gly Val Ser Gly Tyr Tyr			
	185	190	195
gat ttg gtg cgc gcc att ccc aga gca gcg ccc cac cta tat cgc cac			739
Asp Leu Val Arg Ala Ile Pro Arg Ala Ala Pro His Leu Tyr Arg His			
	200	205	210
ctc gat gca gga tct cta cag cga tcc ggg cga gct caa gcc agg tgc			787
Leu Asp Ala Gly Ser Leu Gln Arg Ser Gly Arg Ala Gln Ala Arg Cys			
	215	220	225
cca ggg cgg ttt ttc agc gct tat cga cgg cga cac cct ggt cat ttc			835
Pro Gly Arg Phe Phe Ser Ala Tyr Arg Arg Arg His Pro Gly His Phe			
	230	235	240
cgg cgg cga tgc cgg cgc aac tcc ggt tgc agc act ccg cac tgc gtt			883
Arg Arg Arg Cys Arg Arg Asn Ser Gly Cys Ser Thr Pro His Cys Val			
	250	255	260
gga tgt ggc ctg ggc ggc cac aga gca gtc acc gag gta cgc gct gat			931
Gly Cys Gly Leu Gly Gly His Arg Ala Val Thr Glu Val Arg Ala Asp			
	265	270	275
tca gag gta gct gct act gca ttg cag agc tgg tgg taaacggtga			977
Ser Glu Val Ala Ala Thr Ala Leu Gln Ser Trp Trp			
	280	285	
attcaccaaa gcc			990

<210> 484

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 484

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20 25 30

Thr Ser Ala Gln Ala Ala Cys Lys Met Ala Ala Glu Lys Ile Pro Ala
35 40 45

Gly Ser Lys Val Tyr Val Leu Gly Ser Glu Ser Phe Arg Glu Leu Ala
50 55 60

Thr Glu Ala Gly Phe Val Val Val Asp Ser Ala Asp Asp Lys Pro Val
65 70 75 80

Ala	Val	Leu	His	Gly 85	His	Asn	Pro	Glu	Thr 90	Gly	Trp	Ala	Gln	Leu 95	Ser
Glu	Ala	Ala	Leu 100	Ser	Ile	Asn	Ala	Gly 105	Ala	Gln	Tyr	Phe	Ala 110	Ser	Asn
Leu	Asp	Ser 115	Thr	Leu	Pro	Met	Glu 120	Arg	Gly	Arg	His	Ile 125	Gly	Asn	Gly
Ser	Met 130	Val	Ala	Ala	Val	Val 135	Asn	Ala	Thr	Gly	Val 140	Lys	Pro	Leu	Ser
Ala 145	Gly	Lys	Pro	Gly	Pro 150	Ala	Met	Phe	Tyr	Ala 155	Gly	Ala	Glu	Thr	Leu 160
Asn	Ser	Ser	Lys 165	Pro	Leu	Ala	Val	Gly 170	Asp	Arg	Leu	Asp	Thr 175	Asp	Ile
Ala	Gly	Gly	Asn 180	Ala	Ala	Gly	Met	Asp 185	Thr	Phe	Gln	Val	Leu 190	Thr	Gly
Val	Ser 195	Gly	Tyr	Tyr	Asp	Leu 200	Val	Arg	Ala	Ile	Pro 205	Arg	Ala	Ala	Pro
His 210	Leu	Tyr	Arg	His	Leu	Asp 215	Ala	Gly	Ser	Leu	Gln 220	Arg	Ser	Gly	Arg
Ala 225	Gln	Ala	Arg	Cys	Pro 230	Gly	Arg	Phe	Phe	Ser 235	Ala	Tyr	Arg	Arg	Arg 240
His	Pro	Gly	His 245	Phe	Arg	Arg	Arg	Cys 250	Arg	Arg	Asn	Ser	Gly	Cys 255	Ser
Thr	Pro	His	Cys 260	Val	Gly	Cys	Gly	Leu 265	Gly	Gly	His	Arg	Ala 270	Val	Thr
Glu	Val 275	Arg	Ala	Asp	Ser	Glu 280	Val	Ala	Ala	Thr	Ala 285	Leu	Gln	Ser	Trp

Trp

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<210> 485
<211> 1173
<212> DNA
<213> Corynebacterium glutamicum
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<221> CDS
<222> (101)..(1150)
<223> RXN00337
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attgccggac tgcggetgcc gtcaataaag aaccgcgacg atg ttg tta acg tat 115
Met Leu Leu Thr Tyr
1 5

gcg ttt gtg gat gtg gag gga ggc gtc gaa aag cat tct tta agc act	163
Ala Phe Val Asp Val Glu Gly Gly Val Glu Lys His Ser Leu Ser Thr	
10 15 20	
gcg gac att gca gct cgc gca cac gcc cat atg aaa tcc cat gat gtt	211
Ala Asp Ile Ala Ala Arg Ala His Ala His Met Lys Ser His Asp Val	
25 30 35	
ttg ggg cgg cag act acg ccg cct cag ccg gag ggc ggc gtt gct gcc	259
Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu Gly Gly Val Ala Ala	
40 45 50	
cgg ttg ggc ggg att gcg tgg aca atg atc cat aag caa atg ctt tcg	307
Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His Lys Gln Met Leu Ser	
55 60 65	
cgt gac aca aaa ggc ctg gat atc acc gtg ttg agc acc att cct gag	355
Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu Ser Thr Ile Pro Glu	
70 75 80 85	
ggg gtg ggg ctg ggt gaa aat tcc gcc atg gat gtg gcg ctc gca ttg	403
Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp Val Ala Leu Ala Leu	
90 95 100	
gcg ctg tat cgg gaa aat att gag gaa gcc ccc acg aag gcg cgc att	451
Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro Thr Lys Ala Arg Ile	
105 110 115	
gcg gag att tgt tcg cag tcc gca ttc atg ttc agt gag act tca gtg	499
Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe Ser Glu Thr Ser Val	
120 125 130	
ttg cgt gcg cgg cac acc gtg gcg ttg ccg ggt gaa act gga cag att	547
Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly Glu Thr Gly Gln Ile	
135 140 145	
tcg gtg gtt gat tac gcc gat ggt tcg gtc act cag gcg cca cat ccg	595
Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr Gln Ala Pro His Pro	
150 155 160 165	
gtg agt cgt tcc gct ggt ttg tcg gca ttt gtt gtt gct gcg caa act	643
Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val Val Ala Ala Gln Thr	
170 175 180	
gaa act gat ccg agc att tac cgc gag atc tat gct cga cat gcg ttt	691
Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr Ala Arg His Ala Phe	
185 190 195	
atc gat gaa gct gcg cgc gct ttc agt gtg gaa tct ttg ccg ttg ctt	739
Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu Ser Leu Arg Leu Leu	
200 205 210	
ccc gac gct tcc act cgt gtt gtg gat tgg ttg cag gcc gtg att gag	787
Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu Gln Ala Val Ile Glu	
215 220 225	
gtg act ggt cga gag gat ctg ccc tcg att gaa caa gcc cag cgc tgg	835
Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu Gln Ala Gln Arg Trp	
230 235 240 245	
ttg aat ctg tgg gaa aac gaa acc ccg cgc gct cag agg aca gcc aat	883

Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala Gln Arg Thr Ala Asn
 250 255 260
 gcc ctg cgt tcg aga agg ctg agt gag ttt tct gag ctg ctg atg gaa 931
 Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser Glu Leu Leu Met Glu
 265 270 275
 tcc caa gat gat ttg agc gac acc ttc gat ttc ccc cct gct gat ttg 979
 Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe Pro Pro Ala Asp Leu
 280 285 290
 gcg ctt gct cgt ttg tgc gtc gag cgg ggt gcc aca gct gct cgg tcc 1027
 Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala Thr Ala Ala Arg Ser
 295 300 305
 acg tca gcg cgc ggt gtg att gcg ttg gtt gat gcc cat cat gcg cac 1075
 Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp Ala His His Ala His
 310 315 320 325
 aat ttt gct gcg gat ctc agc gag gat ggc ttg ttg gtg gtt cct ctc 1123
 Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu Leu Val Val Pro Leu
 330 335 340
 ggg cac ggg gac gtc gcg gaa cag ggc tagcacgcct acttaaccag 1170
 Gly His Gly Asp Val Ala Glu Gln Gly
 345 350
 cct 1173

<210> 486
 <211> 350
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 486
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 20 25 30
 Lys Ser His Asp Val Leu Gly Arg Gln Thr Thr Pro Pro Gln Pro Glu
 35 40 45
 Gly Gly Val Ala Ala Arg Leu Gly Gly Ile Ala Trp Thr Met Ile His
 50 55 60
 Lys Gln Met Leu Ser Arg Asp Thr Lys Gly Leu Asp Ile Thr Val Leu
 65 70 75 80
 Ser Thr Ile Pro Glu Gly Val Gly Leu Gly Glu Asn Ser Ala Met Asp
 85 90 95
 Val Ala Leu Ala Leu Ala Leu Tyr Arg Glu Asn Ile Glu Glu Ala Pro
 100 105 110
 Thr Lys Ala Arg Ile Ala Glu Ile Cys Ser Gln Ser Ala Phe Met Phe
 115 120 125
 Ser Glu Thr Ser Val Leu Arg Ala Arg His Thr Val Ala Leu Arg Gly

130	135	140
Glu Thr Gly Gln Ile Ser Val Val Asp Tyr Ala Asp Gly Ser Val Thr 145 150 155 160		
Gln Ala Pro His Pro Val Ser Arg Ser Ala Gly Leu Ser Ala Phe Val 165 170 175		
Val Ala Ala Gln Thr Glu Thr Asp Pro Ser Ile Tyr Arg Glu Ile Tyr 180 185 190		
Ala Arg His Ala Phe Ile Asp Glu Ala Ala Arg Ala Phe Ser Val Glu 195 200 205		
Ser Leu Arg Leu Leu Pro Asp Ala Ser Thr Arg Val Val Asp Trp Leu 210 215 220		
Gln Ala Val Ile Glu Val Thr Gly Arg Glu Asp Leu Pro Ser Ile Glu 225 230 235 240		
Gln Ala Gln Arg Trp Leu Asn Leu Trp Glu Asn Glu Thr Arg Arg Ala 245 250 255		
Gln Arg Thr Ala Asn Ala Leu Arg Ser Arg Arg Leu Ser Glu Phe Ser 260 265 270		
Glu Leu Leu Met Glu Ser Gln Asp Asp Leu Ser Asp Thr Phe Asp Phe 275 280 285		
Pro Pro Ala Asp Leu Ala Leu Ala Arg Leu Cys Val Glu Arg Gly Ala 290 295 300		
Thr Ala Ala Arg Ser Thr Ser Ala Arg Gly Val Ile Ala Leu Val Asp 305 310 315 320		
Ala His His Ala His Asn Phe Ala Ala Asp Leu Ser Glu Asp Gly Leu 325 330 335		
Leu Val Val Pro Leu Gly His Gly Asp Val Ala Glu Gln Gly 340 345 350		

<210> 487

<211> 1248

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1225)

<223> RXS00584

<400> 487

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Met His Ser Pro Glu	
1 5	

agg caa gaa aaa atg agt tct cca gtc tca ctc gaa aac gcg gcg tca	163
Arg Gln Glu Lys Met Ser Ser Pro Val Ser Leu Glu Asn Ala Ala Ser	

10								15				20				
acc	agc	aac	aag	cgc	gtc	gtg	gct	ttc	cac	gag	ctg	cct	agc	cct	aca	211
Thr	Ser	Asn	Lys	Arg	Val	Val	Ala	Phe	His	Glu	Leu	Pro	Ser	Pro	Thr	
25				30				35								
gat	ctc	atc	gcc	gca	aac	cca	ctg	aca	cca	aag	cag	gct	tcc	aag	gtg	259
Asp	Leu	Ile	Ala	Ala	Asn	Pro	Leu	Thr	Pro	Lys	Gln	Ala	Ser	Lys	Val	
40				45				50								
gag	cag	gat	cgc	cag	gac	atc	gct	gat	atc	ttc	gct	ggc	gac	gat	gac	307
Glu	Gln	Asp	Arg	Gln	Asp	Ile	Ala	Asp	Ile	Phe	Ala	Gly	Asp	Asp	Asp	
55				60				65								
cgc	ctc	gtt	gtc	gtt	gtg	gga	cct	tgc	tca	gtt	cac	gat	cct	gaa	gca	355
Arg	Leu	Val	Val	Val	Val	Gly	Pro	Cys	Ser	Val	His	Asp	Pro	Glu	Ala	
70				75				80				85				
gcc	atc	gat	tac	gca	aac	cgc	ctg	gct	ccg	ctg	gca	aag	cgc	ctt	gat	403
Ala	Ile	Asp	Tyr	Ala	Asn	Arg	Leu	Ala	Pro	Leu	Ala	Lys	Arg	Leu	Asp	
90				95				100								
cag	gac	ctc	aag	att	gtc	atg	cgc	gtg	tac	ttc	gag	aag	cct	cgc	acc	451
Gln	Asp	Leu	Lys	Ile	Val	Met	Arg	Val	Tyr	Phe	Glu	Lys	Pro	Arg	Thr	
105				110				115								
atc	gtc	gga	tgg	aag	gga	ttg	atc	aat	gat	cct	cac	ctc	aac	gaa	acc	499
Ile	Val	Gly	Trp	Lys	Gly	Leu	Ile	Asn	Asp	Pro	His	Leu	Asn	Glu	Thr	
120				125				130								
tac	gac	atc	cca	gag	ggc	ttg	cgc	att	gcg	cgc	aaa	gtg	ctt	atc	gac	547
Tyr	Asp	Ile	Pro	Glu	Gly	Leu	Arg	Ile	Ala	Arg	Lys	Val	Leu	Ile	Asp	
135				140				145								
gtt	gtg	aac	ctt	gat	ctc	cca	gtc	ggc	tgc	gaa	ttc	ctc	gaa	cca	aac	595
Val	Val	Asn	Leu	Asp	Leu	Pro	Val	Gly	Cys	Glu	Phe	Leu	Glu	Pro	Asn	
150				155				160				165				
agc	cct	cag	tac	tac	gcc	gac	act	gtc	gca	tgg	gga	gca	atc	ggc	gct	643
Ser	Pro	Gln	Tyr	Tyr	Ala	Asp	Thr	Val	Ala	Trp	Gly	Ala	Ile	Gly	Ala	
170				175				180								
cgt	acc	acc	gaa	tct	cag	gtg	cac	cgc	cag	ctg	gct	tct	ggg	atg	tct	691
Arg	Thr	Thr	Glu	Ser	Gln	Val	His	Arg	Gln	Leu	Ala	Ser	Gly	Met	Ser	
185				190				195								
atg	cca	att	ggc	ttc	aag	aac	gga	act	gac	gga	aac	atc	cag	gtt	gca	739
Met	Pro	Ile	Gly	Phe	Lys	Asn	Gly	Thr	Asp	Gly	Asn	Ile	Gln	Val	Ala	
200				205				210								
gtc	gac	gcg	gta	cag	gct	gcc	cag	aac	cca	cac	ttc	ttc	ttc	gga	acc	787
Val	Asp	Ala	Val	Gln	Ala	Ala	Gln	Asn	Pro	His	Phe	Phe	Phe	Gly	Thr	
215				220				225								
tcc	gac	gac	ggc	gcg	ctg	agc	gtc	gtg	gag	acc	gca	ggc	aac	agc	aac	835
Ser	Asp	Asp	Gly	Ala	Leu	Ser	Val	Val	Glu	Thr	Ala	Gly	Asn	Ser	Asn	
230				235				240				245				
tcc	cac	atc	att	ttg	cgc	ggc	gg									

gct tgc gtg gag gcc gtc gtc gag aag ctt ggt gaa aac gct cgt ctc 931
 Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly Glu Asn Ala Arg Leu
 265 270 275
 atg atc gat gct tcc cat gct aac tcc ggc aag gat cat atc cga cag 979
 Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys Asp His Ile Arg Gln
 280 285 290
 gtt gag gtt gtt cgt gaa atc gca gag cag att tct ggc ggt tct gaa 1027
 Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile Ser Gly Gly Ser Glu
 295 300 305
 gct gtg gct gga atc atg att gag tcc ttc ctc gtt ggt ggc gca cag 1075
 Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu Val Gly Gly Ala Gln
 310 315 320 325
 aac ctt gat cct gcg aaa ttg cgc atc aat ggc ggt gaa ggc ctg gtg 1123
 Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly Gly Glu Gly Leu Val
 330 335 340
 tac gga cag tct gtg acc gat aag tgc atc gat att gac acc acc atc 1171
 Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp Ile Asp Thr Thr Ile
 345 350 355
 gat ttg ctc gct gag ctg gcc gca gca gta agg gaa cgc cga gca gca 1219
 Asp Leu Leu Ala Glu Leu Ala Ala Val Arg Glu Arg Arg Ala Ala
 360 365 370
 gcc aag taattaaggg cgctagactg tta 1248
 Ala Lys
 375

<210> 488

<211> 375

<212> PRT

<213> Corynebacterium glutamicum

<400> 488

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 Leu Pro Ser Pro Thr Asp Leu Ile Ala Ala Asn Pro Leu Thr Pro Lys
 35 40 45
 Gln Ala Ser Lys Val Glu Gln Asp Arg Gln Asp Ile Ala Asp Ile Phe
 50 55 60
 Ala Gly Asp Asp Asp Arg Leu Val Val Val Val Gly Pro Cys Ser Val
 65 70 75 80
 His Asp Pro Glu Ala Ala Ile Asp Tyr Ala Asn Arg Leu Ala Pro Leu
 85 90 95
 Ala Lys Arg Leu Asp Gln Asp Leu Lys Ile Val Met Arg Val Tyr Phe
 100 105 110

Glu Lys Pro Arg Thr Ile Val Gly Trp Lys Gly Leu Ile Asn Asp Pro
 115 120 125
 His Leu Asn Glu Thr Tyr Asp Ile Pro Glu Gly Leu Arg Ile Ala Arg
 130 135 140
 Lys Val Leu Ile Asp Val Val Asn Leu Asp Leu Pro Val Gly Cys Glu
 145 150 155 160
 Phe Leu Glu Pro Asn Ser Pro Gln Tyr Tyr Ala Asp Thr Val Ala Trp
 165 170 175
 Gly Ala Ile Gly Ala Arg Thr Thr Glu Ser Gln Val His Arg Gln Leu
 180 185 190
 Ala Ser Gly Met Ser Met Pro Ile Gly Phe Lys Asn Gly Thr Asp Gly
 195 200 205
 Asn Ile Gln Val Ala Val Asp Ala Val Gln Ala Ala Gln Asn Pro His
 210 215 220
 Phe Phe Phe Gly Thr Ser Asp Asp Gly Ala Leu Ser Val Val Glu Thr
 225 230 235 240
 Ala Gly Asn Ser Asn Ser His Ile Ile Leu Arg Gly Gly Thr Ser Gly
 245 250 255
 Pro Asn His Asp Ala Ala Ser Val Glu Ala Val Val Glu Lys Leu Gly
 260 265 270
 Glu Asn Ala Arg Leu Met Ile Asp Ala Ser His Ala Asn Ser Gly Lys
 275 280 285
 Asp His Ile Arg Gln Val Glu Val Val Arg Glu Ile Ala Glu Gln Ile
 290 295 300
 Ser Gly Gly Ser Glu Ala Val Ala Gly Ile Met Ile Glu Ser Phe Leu
 305 310 315 320
 Val Gly Gly Ala Gln Asn Leu Asp Pro Ala Lys Leu Arg Ile Asn Gly
 325 330 335
 Gly Glu Gly Leu Val Tyr Gly Gln Ser Val Thr Asp Lys Cys Ile Asp
 340 345 350
 Ile Asp Thr Thr Ile Asp Leu Leu Ala Glu Leu Ala Ala Ala Val Arg
 355 360 365
 Glu Arg Arg Ala Ala Ala Lys
 370 375

<210> 489
 <211> 1131
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1108)
 <223> RXS02574

<400> 489

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 Leu Ala Arg Ala Gln
 1 5
 atc cct gaa cag caa cgc gac caa gtc gcg tcg ctg atg atg gtt gga 163
 Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser Leu Met Met Val Gly
 10 15 20
 gtt gcg aat tat gat cag gca ttg gat gcg ctc aat cag ggg gtg ggt 211
 Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu Asn Gln Gly Val Gly
 25 30 35
 ggc atc ttt att ggt tcc tgg aca gat gaa aat ctg ctc acg gaa cct 259
 Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn Leu Leu Thr Glu Pro
 40 45 50
 ggc cgt aat att gag gcg ctc cgc gaa gcc gtc ggc agg gat ttc tcc 307
 Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val Gly Arg Asp Phe Ser
 55 60 65
 gtc agc atc gac ttc gaa ggc ggc cgc gtc cag cgt gcc acc aat att 355
 Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln Arg Ala Thr Asn Ile
 70 75 80 85
 ctt ggt gat ttc ccc tca ccg cgc gtg atg gcg caa acc atg acg ccg 403
 Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala Gln Thr Met Thr Pro
 90 95 100
 gaa caa gta gaa gat ctc gca gaa atc cta ggc act ggt tta gct gca 451
 Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly Thr Gly Leu Ala Ala
 105 110 115
 cat ggt gtg aca gtt aac ttt gca cct gtt gta gat gta gat gct tgg 499
 His Gly Val Thr Val Asn Phe Ala Pro Val Val Asp Val Asp Ala Trp
 120 125 130
 ggt ctc ccc gtc gtt ggc gat cgt tcc ttt tcc aac gac cca gcc gta 547
 Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser Asn Asp Pro Ala Val
 135 140 145
 gca gct act tat gcc aca gct ttt gca aag ggc tta agc aaa gta gga 595
 Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly Leu Ser Lys Val Gly
 150 155 160 165
 att acc cca gta ttc aaa cat ttc cca ggt cac ggt cgt gca agt ggc 643
 Ile Thr Pro Val Phe Lys His Phe Pro Gly His Gly Arg Ala Ser Gly
 170 175 180
 gat tcg cac acc caa gat gtg gtg acc ccc gca ctt gat gag ctt aaa 691
 Asp Ser His Thr Gln Asp Val Val Thr Pro Ala Leu Asp Glu Leu Lys
 185 190 195
 act tac gac ctc atc cct tat ggt caa gca ctt tct gaa act gac gga 739
 Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu Ser Glu Thr Asp Gly
 200 205 210
 gcc gtc atg gtg ggc cac atg att gtt cca ggt ctt ggc acc gac gga 787

Ala Val Met Val Gly His Met Ile Val Pro Gly Leu Gly Thr Asp Gly
 215 220 225

gtt cca tcc tct atc gac ccc gcc acc tat caa ctg ctc cgc agt ggc 835
 Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln Leu Leu Arg Ser Gly
 230 235 240 245

gat tac cca ggt ggc gtg cct ttc gat ggc gtg atc tac acc gac gat 883
 Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val Ile Tyr Thr Asp Asp
 250 255 260

ctc tct gga atg agt gcc att tcc gcc acc cat tca ccc gca gaa gca 931
 Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His Ser Pro Ala Glu Ala
 265 270 275

gtg ctt gcc tcc ctc aaa gca ggc gca gac caa gca cta tgg atc gac 979
 Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln Ala Leu Trp Ile Asp
 280 285 290

tat ggg tcc ttg ggc tcc gcg att gat cgc gtt gat gct gcc gtt agc 1027
 Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val Asp Ala Ala Val Ser
 295 300 305

agc ggt gaa tac cct caa gaa caa atg ctg gca tct gcg tta aga gtc 1075
 Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala Ser Ala Leu Arg Val
 310 315 320 325

caa ttg ctc tac atc aca cgt ctc gaa caa aag tgaagttacc agtccgtaac 1128
 Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 330 335

ccc 1131

<210> 490

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 490

Leu Ala Arg Ala Gln Ile Pro Glu Gln Gln Arg Asp Gln Val Ala Ser
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Leu Met Met Val Gly Val Ala Asn Tyr Asp Gln Ala Leu Asp Ala Leu
 20 25 30

Asn Gln Gly Val Gly Gly Ile Phe Ile Gly Ser Trp Thr Asp Glu Asn
 35 40 45

Leu Leu Thr Glu Pro Gly Arg Asn Ile Glu Ala Leu Arg Glu Ala Val
 50 55 60

Gly Arg Asp Phe Ser Val Ser Ile Asp Phe Glu Gly Gly Arg Val Gln
 65 70 75 80

Arg Ala Thr Asn Ile Leu Gly Asp Phe Pro Ser Pro Arg Val Met Ala
 85 90 95

Gln Thr Met Thr Pro Glu Gln Val Glu Asp Leu Ala Glu Ile Leu Gly
 100 105 110

Thr Gly Leu Ala Ala His Gly Val Thr Val Asn Phe Ala Pro Val Val
 115 120 125
 Asp Val Asp Ala Trp Gly Leu Pro Val Val Gly Asp Arg Ser Phe Ser
 130 135 140
 Asn Asp Pro Ala Val Ala Ala Thr Tyr Ala Thr Ala Phe Ala Lys Gly
 145 150 155 160
 Leu Ser Lys Val Gly Ile Thr Pro Val Phe Lys His Phe Pro Gly His
 165 170 175
 Gly Arg Ala Ser Gly Asp Ser His Thr Gln Asp Val Val Thr Pro Ala
 180 185 190
 Leu Asp Glu Leu Lys Thr Tyr Asp Leu Ile Pro Tyr Gly Gln Ala Leu
 195 200 205
 Ser Glu Thr Asp Gly Ala Val Met Val Gly His Met Ile Val Pro Gly
 210 215 220
 Leu Gly Thr Asp Gly Val Pro Ser Ser Ile Asp Pro Ala Thr Tyr Gln
 225 230 235 240
 Leu Leu Arg Ser Gly Asp Tyr Pro Gly Gly Val Pro Phe Asp Gly Val
 245 250 255
 Ile Tyr Thr Asp Asp Leu Ser Gly Met Ser Ala Ile Ser Ala Thr His
 260 265 270
 Ser Pro Ala Glu Ala Val Leu Ala Ser Leu Lys Ala Gly Ala Asp Gln
 275 280 285
 Ala Leu Trp Ile Asp Tyr Gly Ser Leu Gly Ser Ala Ile Asp Arg Val
 290 295 300
 Asp Ala Ala Val Ser Ser Gly Glu Tyr Pro Gln Glu Gln Met Leu Ala
 305 310 315 320
 Ser Ala Leu Arg Val Gln Leu Leu Tyr Ile Thr Arg Leu Glu Gln Lys
 325 330 335

<210> 491
 <211> 1038
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1008)
 <223> RXS03215

<400> 491
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gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca	96
Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro	
20 25 30	
ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc	144
Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly	
35 40 45	
cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc	192
Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg	
50 55 60	
cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu	
195 200 205	
gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc	672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly	
210 215 220	
gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa	720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu	
225 230 235 240	
gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc	768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg	
245 250 255	
ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa	816

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc 864
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta 912
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt 960
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
 Gly Glu Thr Val Ala Val Pro Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335
 tagaaactat tcagaaagca tcaccatgaa 1038

<210> 492
 <211> 336
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 492
 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
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 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60
 Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80
 Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95
 Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110
 Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125
 Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140
 Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160
 Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175

Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190
 Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205
 Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220
 Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240
 Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255
 Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270
 Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285
 Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300
 His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 493
 <211> 1031
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1008)
 <223> FRXA01915

<400> 493
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 Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
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 gtg gaa gca ctt ctg gca tcc ggc aag cat gtg ctg tgc gag aag cca 96
 Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30
 ctg tca gac acc atc gaa gat gca gaa gcc atg att gag gca gcc ggc 144
 Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45
 cgt gca gca aca aat ggc acc atc gcc cgc atc gga ctg acc tac cgc 192
 Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60

cgt tcc cca ggc gtg gca cac atc cgt gat ctc gtg cag tcc ggc gag	240
Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu	
65 70 75 80	
ctt ggc aag gtt cta cac gtc acc ggc cac tac tgg acc gac tac gga	288
Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly	
85 90 95	
tcc aat gca cag gca cca atc agc tgg cgt tac aag ggg cca aac ggc	336
Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly	
100 105 110	
tcc ggc gca ctg gca gat gtg gga agc cac ctc acc tac ctg gca gaa	384
Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu	
115 120 125	
ttc gtt gca gga tct gac ttc gcc gcc gtc cgt ggt ggc cag ttg tcc	432
Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser	
130 135 140	
acc gtg atc acc gag cgc ccc aag cca ctc ggc gcg att gtc ggc cac	480
Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His	
145 150 155 160	
gaa ggc ggc gca gtt tcc gat gaa tac gaa gca gtg gaa aat gat gac	528
Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp	
165 170 175	
att gca tca ttc tcc gga tcc ttc atc ggt ggc gga acc gca acc ctc	576
Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu	
180 185 190	
cag gtc agc cgc att tcc cag gga cac cca aac acc cta ggt ttt gaa	624
Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu	
195 200 205	
gtg ttc tgt gaa aag ggc tcc gtg ctc ttt gat ttc cgc aac tca ggc	672
Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly	
210 215 220	
gaa ttc aaa atc ttc acc cca gca acc tcc ggt gac atc agc caa gaa	720
Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu	
225 230 235 240	
gcc ggc tac cgc acc atc acc atc gga cca aag cac cca tac tgg cgc	768
Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg	
245 250 255	
ggc ggc ctt gca atg gat gca cca ggc gtg gga att ggc caa aac gaa	816
Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu	
260 265 270	
ggc ttc gtt ttc cag gcg cgc gca ttc ctc gaa gaa atc gca gga atc	864
Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile	
275 280 285	
tcc gaa gct gaa agc ctg cca cgc tgc gca act ttg gaa gaa ggg cta	912
Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu	
290 295 300	
cac aat atg cag ctc att gat gct gta tca cag tca gct gca gca ggt	960

His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320

ggc gaa acc gtt gcg gtc cca gcg gct gct ctg atc cct gca aac aac 1008
 Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

tagaaactat tcagaaagca tca 1031

<210> 494

<211> 336

<212> PRT

<213> Corynebacterium glutamicum

<400> 494

Ile Asp Val Val Ser Val Val Val Ala Asn Phe Leu His Arg Glu Ile
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Val Glu Ala Leu Leu Ala Ser Gly Lys His Val Leu Cys Glu Lys Pro
 20 25 30

Leu Ser Asp Thr Ile Glu Asp Ala Glu Ala Met Ile Glu Ala Ala Gly
 35 40 45

Arg Ala Ala Thr Asn Gly Thr Ile Ala Arg Ile Gly Leu Thr Tyr Arg
 50 55 60

Arg Ser Pro Gly Val Ala His Ile Arg Asp Leu Val Gln Ser Gly Glu
 65 70 75 80

Leu Gly Lys Val Leu His Val Thr Gly His Tyr Trp Thr Asp Tyr Gly
 85 90 95

Ser Asn Ala Gln Ala Pro Ile Ser Trp Arg Tyr Lys Gly Pro Asn Gly
 100 105 110

Ser Gly Ala Leu Ala Asp Val Gly Ser His Leu Thr Tyr Leu Ala Glu
 115 120 125

Phe Val Ala Gly Ser Asp Phe Ala Ala Val Arg Gly Gly Gln Leu Ser
 130 135 140

Thr Val Ile Thr Glu Arg Pro Lys Pro Leu Gly Ala Ile Val Gly His
 145 150 155 160

Glu Gly Gly Ala Val Ser Asp Glu Tyr Glu Ala Val Glu Asn Asp Asp
 165 170 175

Ile Ala Ser Phe Ser Gly Ser Phe Ile Gly Gly Gly Thr Ala Thr Leu
 180 185 190

Gln Val Ser Arg Ile Ser Gln Gly His Pro Asn Thr Leu Gly Phe Glu
 195 200 205

Val Phe Cys Glu Lys Gly Ser Val Leu Phe Asp Phe Arg Asn Ser Gly
 210 215 220

Glu Phe Lys Ile Phe Thr Pro Ala Thr Ser Gly Asp Ile Ser Gln Glu
 225 230 235 240

Ala Gly Tyr Arg Thr Ile Thr Ile Gly Pro Lys His Pro Tyr Trp Arg
 245 250 255

Gly Gly Leu Ala Met Asp Ala Pro Gly Val Gly Ile Gly Gln Asn Glu
 260 265 270

Gly Phe Val Phe Gln Ala Arg Ala Phe Leu Glu Glu Ile Ala Gly Ile
 275 280 285

Ser Glu Ala Glu Ser Leu Pro Arg Cys Ala Thr Leu Glu Glu Gly Leu
 290 295 300

His Asn Met Gln Leu Ile Asp Ala Val Ser Gln Ser Ala Ala Ala Gly
 305 310 315 320

Gly Glu Thr Val Ala Val Pro Ala Ala Ala Leu Ile Pro Ala Asn Asn
 325 330 335

<210> 495
 <211> 1288
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1258)
 <223> RXS03224

<400> 495
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tggaactcat tgaacgccgc gcccggtctaa ggtgggaggc atg agt ttt gct gaa 115
 Met Ser Phe Ala Glu
 1 5

cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
 His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
 10 15 20

atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
 Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
 25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg 259
 Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met
 40 45 50

ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat 307
 Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp
 55 60 65

ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg 355
 Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala
 70 75 80 85

ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc 403
 Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly

				90				95				100							
gtc	ttc	aat	cat	gtt	tcc	agt	tcc	tct	aaa	tat	ctc	gac	ctg	acc	acc	451			
Val	Phe	Asn	His	Val	Ser	Ser	Ser	Ser	Lys	Tyr	Leu	Asp	Leu	Thr	Thr				
105								110				115							
ggg	gcg	tca	ttt	gaa	ggc	cac	gac	atc	ctg	gcg	gaa	ctc	gac	cac	acg	499			
Gly	Ala	Ser	Phe	Glu	Gly	His	Asp	Ile	Leu	Ala	Glu	Leu	Asp	His	Thr				
120								125				130							
aat	ccc	gcc	gta	gtg	gat	ctg	gtt	gtc	gat	gtc	atg	aac	cac	tgg	ctc	547			
Asn	Pro	Ala	Val	Val	Asp	Leu	Val	Val	Asp	Val	Met	Asn	His	Trp	Leu				
135								140				145							
gac	cgc	gga	atc	gca	ggc	tgg	cga	ctc	gac	gct	gtc	tac	gcc	atc	gcc	595			
Asp	Arg	Gly	Ile	Ala	Gly	Trp	Arg	Leu	Asp	Ala	Val	Tyr	Ala	Ile	Ala				
150				155				160				165							
cct	gaa	ttt	tgg	gaa	aaa	gtc	ctg	cca	gaa	gtg	cga	cga	aaa	cac	cca	643			
Pro	Glu	Phe	Trp	Glu	Lys	Val	Leu	Pro	Glu	Val	Arg	Arg	Lys	His	Pro				
170								175				180							
cac	gca	tgg	atc	gtg	ggg	gag	atg	atc	cat	gga	gat	tac	tcc	gac	tac	691			
His	Ala	Trp	Ile	Val	Gly	Glu	Met	Ile	His	Gly	Asp	Tyr	Ser	Asp	Tyr				
185								190				195							
gtg	aaa	agc	tcc	ggc	att	gat	tcc	gtt	acc	gaa	tac	gaa	ctg	tgg	aaa	739			
Val	Lys	Ser	Ser	Gly	Ile	Asp	Ser	Val	Thr	Glu	Tyr	Glu	Leu	Trp	Lys				
200								205				210							
gcc	att	tgg	agc	agc	atc	aaa	gag	cgc	aat	ttc	ttt	gaa	ctc	gaa	tgg	787			
Ala	Ile	Trp	Ser	Ser	Ile	Lys	Glu	Arg	Asn	Phe	Phe	Glu	Leu	Glu	Trp				
215				220				225											
act	ttg	agt	cgc	cac	aat	gaa	ttc	ctc	gat	act	ttc	gta	ccg	cag	aca	835			
Thr	Leu	Ser	Arg	His	Asn	Glu	Phe	Leu	Asp	Thr	Phe	Val	Pro	Gln	Thr				
230				235				240				245							
ttc	att	ggt	aac	cat	gac	gtc	acc	cgc	att	gcc	acc	cga	atc	ggt	caa	883			
Phe	Ile	Gly	Asn	His	Asp	Val	Thr	Arg	Ile	Ala	Thr	Arg	Ile	Gly	Gln				
250								255				260							
tca	aat	gcg	atc	ctg	gcc	gca	gcg	atc	ctc	ttc	acg	gtc	gga	gga	acc	931			
Ser	Asn	Ala	Ile	Leu	Ala	Ala	Ala	Ile	Leu	Phe	Thr	Val	Gly	Gly	Thr				
265								270				275							
cca	agc	att	tac	tac	ggc	gat	gag	cag	ggc	ttt	acg	gga	ttg	aaa	gag	979			
Pro	Ser	Ile	Tyr	Tyr	Gly	Asp	Glu	Gln	Gly	Phe	Thr	Gly	Leu	Lys	Glu				
280								285				290							
gat	aac	gtt	ttc	ggt	gac	gat	gcc	att	agg	cca	cct	ctt	cct	gcc	gag	1027			
Asp	Asn	Val	Phe	Gly	Asp	Asp	Ala	Ile	Arg	Pro	Pro	Leu	Pro	Ala	Glu				
295				300				305											
ttt	tct	cca	ctg	ggc	acc	tgg	att	gaa	aac	att	tat	aag	gct	ctg	atc	1075			
Phe	Ser	Pro	Leu	Gly	Thr	Trp	Ile	Glu	Asn	Ile	Tyr	Lys	Ala	Leu	Ile				
310				315				320				325							
gcg	ctg	cgc	agg	caa	cac	cc													

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385

ttcaagggta ggggaacaaa 1288

<210> 496

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 496

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Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
 20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
 35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
 85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
 100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
 115 120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
 130 135 140

Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
 145 150 155 160

Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
 165 170 175

Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
 180 185 190

Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
 195 200 205

Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
 210 215 220
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
 225 230 235 240
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
 245 250 255
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
 260 265 270
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
 275 280 285
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
 290 295 300
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380
 Ser Ala
 385

<210> 497
 <211> 1281
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1258)
 <223> FRXA00038

<400> 497
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 Met Ser Phe Ala Glu
 1 5
 cat gcg atc atc tgg cac gtc tac ccc ctg ggc gct ttg ggt gct ccc 163
 His Ala Ile Ile Trp His Val Tyr Pro Leu Gly Ala Leu Gly Ala Pro
 10 15 20
 atc cgg cct gaa gcc ccc gca cct gtc aca cat cgg ctc ccc aat cta 211
 Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His Arg Leu Pro Asn Leu
 25 30 35

att ggg tgg ctg gat tat gtt gtc gaa cta ggc tgc aac gcc ctc atg Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly Cys Asn Ala Leu Met 40 45 50	259
ctg gga ccg gta ttc gag tcc gtc agc cac ggc tac gac acc ctc gat Leu Gly Pro Val Phe Glu Ser Val Ser His Gly Tyr Asp Thr Leu Asp 55 60 65	307
ttc tac cgc atc gac ccg cgc ctc ggc acc gag gaa gac atg gac gcg Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu Glu Asp Met Asp Ala 70 75 80 85	355
ctg ctg gag gct gcg aat cag cgg ggc att gga gtg ctt ttc gac ggc Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly Val Leu Phe Asp Gly 90 95 100	403
gtc ttc aat cat gtt tcc agt tcc tct aaa tat ctc gac ctg acc acc Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr Leu Asp Leu Thr Thr 105 110 115	451
ggg gcg tca ttt gaa ggc cac gac atc ctg gcg gaa ctc gac cac acg Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala Glu Leu Asp His Thr 120 125 130	499
aat ccc gcc gta gtg gat ctg gtt gtc gat gtc atg aac cac tgg ctc Asn Pro Ala Val Val Asp Leu Val Val Asp Val Met Asn His Trp Leu 135 140 145	547
gac cgc gga atc gca ggc tgg cga ctc gac gct gtc tac gcc atc gcc Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala Val Tyr Ala Ile Ala 150 155 160 165	595
cct gaa ttt tgg gaa aaa gtc ctg cca gaa gtg cga cga aaa cac cca Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val Arg Arg Lys His Pro 170 175 180	643
cac gca tgg atc gtg ggg gag atg atc cat gga gat tac tcc gac tac His Ala Trp Ile Val Gly Glu Met Ile His Gly Asp Tyr Ser Asp Tyr 185 190 195	691
gtg aaa agc tcc ggc att gat tcc gtt acc gaa tac gaa ctg tgg aaa Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu Tyr Glu Leu Trp Lys 200 205 210	739
gcc att tgg agc agc atc aaa gag cgc aat ttc ttt gaa ctc gaa tgg Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe Phe Glu Leu Glu Trp 215 220 225	787
act ttg agt cgc cac aat gaa ttc ctc gat act ttc gta ccg cag aca Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr Phe Val Pro Gln Thr 230 235 240 245	835
ttc att ggt aac cat gac gtc acc cgc att gcc acc cga atc ggt caa Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala Thr Arg Ile Gly Gln 250 255 260	883
tca aat gcg atc ctg gcc gca gcg atc ctc ttc acg gtc gga gga acc Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe Thr Val Gly Gly Thr 265 270 275	931

cca agc att tac tac ggc gat gag cag ggc ttt acg gga ttg aaa gag 979
 Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe Thr Gly Leu Lys Glu
 280 285 290

gat aac gtt ttc ggt gac gat gcc att agg cca cct ctt cct gcc gag 1027
 Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro Pro Leu Pro Ala Glu
 295 300 305

ttt tct cca ctg ggc acc tgg att gaa aac att tat aag gct ctg atc 1075
 Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile Tyr Lys Ala Leu Ile
 310 315 320 325

gcg ctg cgc agg caa cac ccg tgg ttg tat cag gcg cac acc gaa gtc 1123
 Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln Ala His Thr Glu Val
 330 335 340

ctt gag att gct aat gaa gcg atg acc tat aag tcc gtc ggt ctt gga 1171
 Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys Ser Val Gly Leu Gly
 345 350 355

ggt gaa gag ctg aca gtg cat ctt gat ttg gaa gag gtg tct gtt cgg 1219
 Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu Glu Val Ser Val Arg
 360 365 370

atc ctt gat ggc gag aag gtg ctg ttt cag tac agc gct tagttgtcgg 1268
 Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr Ser Ala
 375 380 385

ttcaagggta ggg 1281

<210> 498

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 498

Met Ser Phe Ala Glu His Ala Ile Ile Trp His Val Tyr Pro Leu Gly
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Ala Leu Gly Ala Pro Ile Arg Pro Glu Ala Pro Ala Pro Val Thr His
 20 25 30

Arg Leu Pro Asn Leu Ile Gly Trp Leu Asp Tyr Val Val Glu Leu Gly
 35 40 45

Cys Asn Ala Leu Met Leu Gly Pro Val Phe Glu Ser Val Ser His Gly
 50 55 60

Tyr Asp Thr Leu Asp Phe Tyr Arg Ile Asp Pro Arg Leu Gly Thr Glu
 65 70 75 80

Glu Asp Met Asp Ala Leu Leu Glu Ala Ala Asn Gln Arg Gly Ile Gly
 85 90 95

Val Leu Phe Asp Gly Val Phe Asn His Val Ser Ser Ser Ser Lys Tyr
 100 105 110

Leu Asp Leu Thr Thr Gly Ala Ser Phe Glu Gly His Asp Ile Leu Ala
 115 120 125

Glu Leu Asp His Thr Asn Pro Ala Val Val Asp Leu Val Val Asp Val
 130 135 140
 Met Asn His Trp Leu Asp Arg Gly Ile Ala Gly Trp Arg Leu Asp Ala
 145 150 155 160
 Val Tyr Ala Ile Ala Pro Glu Phe Trp Glu Lys Val Leu Pro Glu Val
 165 170 175
 Arg Arg Lys His Pro His Ala Trp Ile Val Gly Glu Met Ile His Gly
 180 185 190
 Asp Tyr Ser Asp Tyr Val Lys Ser Ser Gly Ile Asp Ser Val Thr Glu
 195 200 205
 Tyr Glu Leu Trp Lys Ala Ile Trp Ser Ser Ile Lys Glu Arg Asn Phe
 210 215 220
 Phe Glu Leu Glu Trp Thr Leu Ser Arg His Asn Glu Phe Leu Asp Thr
 225 230 235 240
 Phe Val Pro Gln Thr Phe Ile Gly Asn His Asp Val Thr Arg Ile Ala
 245 250 255
 Thr Arg Ile Gly Gln Ser Asn Ala Ile Leu Ala Ala Ala Ile Leu Phe
 260 265 270
 Thr Val Gly Gly Thr Pro Ser Ile Tyr Tyr Gly Asp Glu Gln Gly Phe
 275 280 285
 Thr Gly Leu Lys Glu Asp Asn Val Phe Gly Asp Asp Ala Ile Arg Pro
 290 295 300
 Pro Leu Pro Ala Glu Phe Ser Pro Leu Gly Thr Trp Ile Glu Asn Ile
 305 310 315 320
 Tyr Lys Ala Leu Ile Ala Leu Arg Arg Gln His Pro Trp Leu Tyr Gln
 325 330 335
 Ala His Thr Glu Val Leu Glu Ile Ala Asn Glu Ala Met Thr Tyr Lys
 340 345 350
 Ser Val Gly Leu Gly Gly Glu Glu Leu Thr Val His Leu Asp Leu Glu
 355 360 365
 Glu Val Ser Val Arg Ile Leu Asp Gly Glu Lys Val Leu Phe Gln Tyr
 370 375 380
 Ser Ala
 385

<210> 499
 <211> 517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(517)
 <223> RXC00233

<400> 500
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1 5 10 15
Arg Ala Pro Arg Gly Val Leu Asp Ile Ser Tyr Arg Ser Pro Asp Gly
20 25 30
Val Pro Gly Val Val Met Thr Ala Pro Lys Leu Asp Asp Gly Thr Pro
35 40 45
Phe Pro Thr Leu Tyr Tyr Leu Thr Asp Pro Arg Leu Thr Thr Glu Ala

50	55	60
Ser Arg Leu Glu Val Ala Leu Val Met Lys Trp Met Thr Asp Arg Leu		
65	70	75
Ser Thr Asp Glu Glu Leu Arg Ala Asp Tyr Gln Arg Ala His Glu His		
	85	90
Phe Leu Ala Lys Arg Asn Ala Ile Glu Asp Leu Gly Thr Asp Phe Ser		
	100	105
Gly Gly Gly Met Pro Asp Arg Val Lys Cys Leu His Val Leu Ile Asp		
	115	120
Tyr Ala Leu Ala Glu Gly Pro His His Phe Leu		
	130	135

<210> 501
 <211> 849
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(826)
 <223> RXC00236

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 agcaatggga tttggatgcg gttcgggtttt ggccgtcattc atg gtg atc tca ttt 115
 Met Val Ile Ser Phe
 1 5
 gtt gga tgg gcg ctc agc ttc atg gat gga acg gca cct att cgc caa 163
 Val Gly Trp Ala Leu Ser Phe Met Asp Gly Thr Ala Pro Ile Arg Gln
 10 15 20
 ctc cag caa atc cct gaa gat gtt ccg ccg gcg cgt ggt gta gaa gtt 211
 Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala Arg Gly Val Glu Val
 25 30 35
 ccg caa att gat aca gag gca gat gga cgc aca tcc aac cat ttg cgt 259
 Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr Ser Asn His Leu Arg
 40 45 50
 ttt tgg gcg gaa cca att gct caa gat act ggt gtg tcc gct caa gcg 307
 Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly Val Ser Ala Gln Ala
 55 60 65
 att gcg gct tat gga aac gca gag ctc atc gcg agt act gcg tgg cct 355
 Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala Ser Thr Ala Trp Pro
 70 75 80 85
 ggc tgc aat ctg ggg tgg aat acc ttg gca ggt atc ggc cag gtg gaa 403
 Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly Ile Gly Gln Val Glu
 90 95 100
 acc cgt cac ggt acc tac aac ggc aaa atg ttc ggg ggc agt tcc ctg 451
 Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe Gly Gly Ser Ser Leu

105										110					115					
gat	gaa	aat	gga	gtt	gca	acc	cct	cca	atc	atc	ggc	gtt	cca	ctt	gat	499				
Asp	Glu	Asn	Gly	Val	Ala	Thr	Pro	Pro	Ile	Ile	Gly	Val	Pro	Leu	Asp					
120							125					130								
ggt	tca	ccg	ggg	ttt	gcg	gaa	att	ccc	gac	act	gat	ggt	ggg	gaa	tta	547				
Gly	Ser	Pro	Gly	Phe	Ala	Glu	Ile	Pro	Asp	Thr	Asp	Gly	Gly	Glu	Leu					
135							140					145								
gat	ggc	gat	act	gaa	tat	gat	cgc	gcg	gta	ggt	ccc	atg	cag	ttc	att	595				
Asp	Gly	Asp	Thr	Glu	Tyr	Asp	Arg	Ala	Val	Gly	Pro	Met	Gln	Phe	Ile					
150							155					160			165					
ccg	gaa	acg	tgg	cga	ctt	atg	gga	ttg	gat	gca	aac	ggt	gat	ggg	gta	643				
Pro	Glu	Thr	Trp	Arg	Leu	Met	Gly	Leu	Asp	Ala	Asn	Gly	Asp	Gly	Val					
170							175					180								
gcg	gac	ccc	aac	caa	att	gat	gac	gca	gca	ttg	agt	gcc	gca	aac	ctg	691				
Ala	Asp	Pro	Asn	Gln	Ile	Asp	Asp	Ala	Ala	Leu	Ser	Ala	Ala	Asn	Leu					
185							190					195								
ttg	tgt	tcc	aac	gat	cgt	gac	ttg	tcc	act	cct	gaa	gga	tgg	acc	gca	739				
Leu	Cys	Ser	Asn	Asp	Arg	Asp	Leu	Ser	Thr	Pro	Glu	Gly	Trp	Thr	Ala					
200							205					210								
gct	gtt	cat	tct	tac	aac	atg	tct	aat	cag	tat	ttg	atg	gac	gtt	cga	787				
Ala	Val	His	Ser	Tyr	Asn	Met	Ser	Asn	Gln	Tyr	Leu	Met	Asp	Val	Arg					
215							220					225								
gat	gct	gcc	gcg	tcc	tac	gct	tta	cga	cag	ccg	gcg	atc	taaaacttaa			836				
Asp	Ala	Ala	Ala	Ser	Tyr	Ala	Leu	Arg	Gln	Pro	Ala	Ile								
230							235					240								
caagcgcaac ccc																849				

<210> 502
 <211> 242
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 502
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 1 5 10 15
 Ala Pro Ile Arg Gln Leu Gln Gln Ile Pro Glu Asp Val Pro Pro Ala
 20 25 30
 Arg Gly Val Glu Val Pro Gln Ile Asp Thr Glu Ala Asp Gly Arg Thr
 35 40 45
 Ser Asn His Leu Arg Phe Trp Ala Glu Pro Ile Ala Gln Asp Thr Gly
 50 55 60
 Val Ser Ala Gln Ala Ile Ala Ala Tyr Gly Asn Ala Glu Leu Ile Ala
 65 70 75 80
 Ser Thr Ala Trp Pro Gly Cys Asn Leu Gly Trp Asn Thr Leu Ala Gly
 85 90 95

Ile Gly Gln Val Glu Thr Arg His Gly Thr Tyr Asn Gly Lys Met Phe
 100 105 110
 Gly Gly Ser Ser Leu Asp Glu Asn Gly Val Ala Thr Pro Pro Ile Ile
 115 120 125
 Gly Val Pro Leu Asp Gly Ser Pro Gly Phe Ala Glu Ile Pro Asp Thr
 130 135 140
 Asp Gly Gly Glu Leu Asp Gly Asp Thr Glu Tyr Asp Arg Ala Val Gly
 145 150 155 160
 Pro Met Gln Phe Ile Pro Glu Thr Trp Arg Leu Met Gly Leu Asp Ala
 165 170 175
 Asn Gly Asp Gly Val Ala Asp Pro Asn Gln Ile Asp Asp Ala Ala Leu
 180 185 190
 Ser Ala Ala Asn Leu Leu Cys Ser Asn Asp Arg Asp Leu Ser Thr Pro
 195 200 205
 Glu Gly Trp Thr Ala Ala Val His Ser Tyr Asn Met Ser Asn Gln Tyr
 210 215 220
 Leu Met Asp Val Arg Asp Ala Ala Ala Ser Tyr Ala Leu Arg Gln Pro
 225 230 235 240
 Ala Ile

<210> 503
 <211> 1113
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1090)
 <223> RXC00271

<400> 503
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 tctgccccctt tttgaaaata acactttaag gagatgtgcc atg ttt tct tcc cgt 115
 Met Phe Ser Ser Arg
 1 5
 tcg aag gta ctc gca agc atc ttt act gtt ggc gcc ttg gcg ttg gct 163
 Ser Lys Val Leu Ala Ser Ile Phe Thr Val Gly Ala Leu Ala Leu Ala
 10 15 20
 tcg tgc tca agc gat tcc agt gac agc tcc acc tcc act gat gct gca 211
 Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr Ser Thr Asp Ala Ala
 25 30 35
 ggt ggc gac tct tac cga gtt ggc atc aac cag ctt gtt cag cac cct 259
 Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln Leu Val Gln His Pro
 40 45 50
 gca ctt gat gca gcg acc act ggt ttc aag gaa gct ttt gaa gag gca 307

Ala	Leu	Asp	Ala	Ala	Thr	Thr	Gly	Phe	Lys	Glu	Ala	Phe	Glu	Glu	Ala		
55						60					65						
ggc	gtt	gac	gtc	acc	ttt	gat	gag	caa	aac	gct	aac	ggc	gag	cag	ggc	355	
Gly	Val	Asp	Val	Thr	Phe	Asp	Glu	Gln	Asn	Ala	Asn	Gly	Glu	Gln	Gly	85	
70					75					80							
act	gca	ctg	act	att	tct	cag	cag	ttc	gct	tct	gac	aat	ttg	gat	ctc	403	
Thr	Ala	Leu	Thr	Ile	Ser	Gln	Gln	Phe	Ala	Ser	Asp	Asn	Leu	Asp	Leu	100	
				90					95								
gtg	ttg	gct	gtt	gca	act	cca	gca	gca	cag	gca	act	gcg	cag	aat	atc	451	
Val	Leu	Ala	Val	Ala	Thr	Pro	Ala	Ala	Gln	Ala	Thr	Ala	Gln	Asn	Ile	115	
			105				110						115				
act	gat	atc	cca	gtc	ctg	ttc	acc	gca	gtt	acc	gat	gca	gtg	tcg	gca	499	
Thr	Asp	Ile	Pro	Val	Leu	Phe	Thr	Ala	Val	Thr	Asp	Ala	Val	Ser	Ala	130	
		120					125										
gag	ctg	gtg	gat	tct	aat	gaa	gca	cct	ggc	gga	aac	gtc	acc	ggt	act	547	
Glu	Leu	Val	Asp	Ser	Asn	Glu	Ala	Pro	Gly	Gly	Asn	Val	Thr	Gly	Thr	145	
	135					140					145						
tct	gat	atc	gca	ccg	att	gag	cag	cag	ttg	gag	ctt	ttg	cag	cag	ctg	595	
Ser	Asp	Ile	Ala	Pro	Ile	Glu	Gln	Gln	Leu	Glu	Leu	Leu	Gln	Gln	Leu	165	
150					155					160							
gtt	cct	gac	gca	aag	tcc	atc	ggc	atc	gtc	tac	gcg	tct	ggt	gag	gtc	643	
Val	Pro	Asp	Ala	Lys	Ser	Ile	Gly	Ile	Val	Tyr	Ala	Ser	Gly	Glu	Val	180	
				170					175								
aac	tct	cag	gtg	cag	gtc	gat	gag	gtc	acc	aag	gct	gct	gag	cca	ctg	691	
Asn	Ser	Gln	Val	Gln	Val	Asp	Glu	Val	Thr	Lys	Ala	Ala	Glu	Pro	Leu	195	
			185				190						195				
ggg	ctg	tcc	gtt	aat	act	cag	act	gtc	act	acc	gtg	aac	gag	att	cag	739	
Gly	Leu	Ser	Val	Asn	Thr	Gln	Thr	Val	Thr	Thr	Val	Asn	Glu	Ile	Gln	210	
	200					205						210					
cag	gct	gtt	gaa	gct	ctc	ggc	gat	gtt	gat	gtc	atc	tac	gtt	cca	act	787	
Gln	Ala	Val	Glu	Ala	Leu	Gly	Asp	Val	Asp	Val	Ile	Tyr	Val	Pro	Thr	225	
	215					220					225						
gac	aac	atg	gtt	gtt	tcc	ggt	att	tct	tct	ctg	gtt	cag	gtt	gct	gag	835	
Asp	Asn	Met	Val	Val	Ser	Gly	Ile	Ser	Ser	Leu	Val	Gln	Val	Ala	Glu	245	
230					235					240							
cag	aag	cag	atc	cct	gtg	atc	ggc	gct	gag	tcc	ggc	act	gtt	gag	ggt	883	
Gln	Lys	Gln	Ile	Pro	Val	Ile	Gly	Ala	Glu	Ser	Gly	Thr	Val	Glu	Gly	260	
				250					255								
ggc	gca	ctg	gca	acc	ctg	ggt	atc	gat	tac	acc	gag	ctt	ggc	cgc	cag	931	
Gly	Ala	Leu	Ala	Thr	Leu	Gly	Ile	Asp	Tyr	Thr	Glu	Leu	Gly	Arg	Gln	275	
			265				270						275				
act	ggt	gag	atg	gct	ctg	cgt	att	ctg	cag	gac	ggc	gaa	gac	cca	gca	979	
Thr	Gly	Glu	Met	Ala	Leu	Arg	Ile	Leu	Gln	Asp	Gly	Glu	Asp	Pro	Ala	290	
		280					285					290					
acc	atg	cct	gtg	gag	act	gca	act	gag	ttc	acc	tac	gtg	atc	aac	gaa	1027	
Thr	Met	Pro	Val	Glu	Thr	Ala	Thr	Glu	Phe	Thr	Tyr	Val	Ile	Asn	Glu		

295 300 305
 gat gca gca gag cgc cag ggc gtg gag atc cct caa gag att ttg gat 1075
 Asp Ala Ala Glu Arg Gln Gly Val Glu Ile Pro Gln Glu Ile Leu Asp
 310 315 320 325

aag gcc gaa cgc gta tgatcggcgc ttttgagttc gga 1113
 Lys Ala Glu Arg Val
 330

<210> 504
 <211> 330
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 504
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 1 5 10 15
 Ala Leu Ala Leu Ala Ser Cys Ser Ser Asp Ser Ser Asp Ser Ser Thr
 20 25 30
 Ser Thr Asp Ala Ala Gly Gly Asp Ser Tyr Arg Val Gly Ile Asn Gln
 35 40 45
 Leu Val Gln His Pro Ala Leu Asp Ala Ala Thr Thr Gly Phe Lys Glu
 50 55 60
 Ala Phe Glu Glu Ala Gly Val Asp Val Thr Phe Asp Glu Gln Asn Ala
 65 70 75 80
 Asn Gly Glu Gln Gly Thr Ala Leu Thr Ile Ser Gln Gln Phe Ala Ser
 85 90 95
 Asp Asn Leu Asp Leu Val Leu Ala Val Ala Thr Pro Ala Ala Gln Ala
 100 105 110
 Thr Ala Gln Asn Ile Thr Asp Ile Pro Val Leu Phe Thr Ala Val Thr
 115 120 125
 Asp Ala Val Ser Ala Glu Leu Val Asp Ser Asn Glu Ala Pro Gly Gly
 130 135 140
 Asn Val Thr Gly Thr Ser Asp Ile Ala Pro Ile Glu Gln Gln Leu Glu
 145 150 155 160
 Leu Leu Gln Gln Leu Val Pro Asp Ala Lys Ser Ile Gly Ile Val Tyr
 165 170 175
 Ala Ser Gly Glu Val Asn Ser Gln Val Gln Val Asp Glu Val Thr Lys
 180 185 190
 Ala Ala Glu Pro Leu Gly Leu Ser Val Asn Thr Gln Thr Val Thr Thr
 195 200 205
 Val Asn Glu Ile Gln Gln Ala Val Glu Ala Leu Gly Asp Val Asp Val
 210 215 220
 Ile Tyr Val Pro Thr Asp Asn Met Val Val Ser Gly Ile Ser Ser Leu
 225 230 235 240

<400> 505																
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tgggaaacga acatgcggta ccaaccaggg gagttaatgc <div> gtc agt gat gta acc Val Ser Asp Val Thr 1 5 </div>																115
gtt ggc gat att cgc cgc att ttg gat gag gct tat ccg ccg gcg ttg <div> Val Gly Asp Ile Arg Arg Ile Leu Asp Glu Ala Tyr Pro Pro Ala Leu 10 15 20 </div>																163
gcg gaa agc tgg gac aaa gtg ggg ctg atc tgc ggt gat cca aca gag <div> Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys Gly Asp Pro Thr Glu 25 30 35 </div>																211
tcg gtg aag cgt gtc ggt tta gca ctc gat tgc acc cag gca gtg gcc <div> Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys Thr Gln Ala Val Ala 40 45 50 </div>																259
gac aag gct gtg gac atg ggt ttg gac atg ctg atc att cac cac cca <div> Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu Ile Ile His His Pro 55 60 65 </div>																307
ttg ctg ctg cgt ggg gtg acg tct gtt gct gcg gat gag cca aaa ggc <div> Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala Asp Glu Pro Lys Gly 70 75 80 85 </div>																355
aag gtc att cac acc cta att cgc ggc ggg gtg gca ctg ttt tcc gcg <div> Lys Val Ile His Thr Leu Ile Arg Gly Gly Val Ala Leu Phe Ser Ala 90 95 100 </div>																403

cac act aat gcg gat tcc gcg cgc cca ggt gtc aac gat aaa ctc gcc	451
His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val Asn Asp Lys Leu Ala	
105 110 115	
gag ctc gtc ggc atc acg gcc ggg cga ccc atc gcg aca cgg ctt tta	499
Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile Ala Thr Arg Leu Leu	
120 125 130	
ggc ggc atg gac aaa tgg ggc gtg cac gtt ctg ccc aag gat gca gcg	547
Gly Gly Met Asp Lys Trp Gly Val His Val Leu Pro Lys Asp Ala Ala	
135 140 145	
tac cta aag aag atg ctt ttc gac gca ggt gcc ggt gcg atc ggc gac	595
Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala Gly Ala Ile Gly Asp	
150 155 160 165	
tac cga gag tgt gcc ttt gag atc gaa gga acc ggg cag ttt agg ccc	643
Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr Gly Gln Phe Arg Pro	
170 175 180	
gtg gag ggg gcg aat ccg gca gag ggg gac gtc gat aag ctt ttt aaa	691
Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val Asp Lys Leu Phe Lys	
185 190 195	
tcc ctt gag ctg cgc atc gag ttt gtt gca ccg cgc aac ctg cgc gcc	739
Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro Arg Asn Leu Arg Ala	
200 205 210	
cgg ctc acg tcg gtg ctg ccg gag gct cat ccg tat gag gag cct gcc	787
Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro Tyr Glu Glu Pro Ala	
215 220 225	
ttc gat att gtt gaa atg cac agc gct gag agt tta gaa aat gcg acc	835
Phe Asp Ile Val Glu Met His Ser Ala Glu Ser Leu Glu Asn Ala Thr	
230 235 240 245	
gga ttg ggt cgt gtg ggt gaa ttg ccg gag ccg atg cgc ctc gcg gat	883
Gly Leu Gly Arg Val Gly Glu Leu Pro Glu Pro Met Arg Leu Ala Asp	
250 255 260	
ttc gtg caa caa gtg gcc aac aac ctg cct gtc acc gaa tgg ggc gtg	931
Phe Val Gln Gln Val Ala Asn Asn Leu Pro Val Thr Glu Trp Gly Val	
265 270 275	
cgc gct acc ggc gat cct gaa caa atg gtg tcc cgt gtg gcg gtt tca	979
Arg Ala Thr Gly Asp Pro Glu Gln Met Val Ser Arg Val Ala Val Ser	
280 285 290	
tca ggg tcg ggt gac agt ttc tta aac gat gtg att aag ctc gga gtg	1027
Ser Gly Ser Gly Asp Ser Phe Leu Asn Asp Val Ile Lys Leu Gly Val	
295 300 305	
gac gtt tat gtc act tct gat ctg cgc cac cat cca gtt gat gaa tat	1075
Asp Val Tyr Val Thr Ser Asp Leu Arg His His Pro Val Asp Glu Tyr	
310 315 320 325	
ctc cga gaa ggt ggc cct gca gta atc gat act gca cac tgg gcc agc	1123
Leu Arg Glu Gly Gly Pro Ala Val Ile Asp Thr Ala His Trp Ala Ser	
330 335 340	
gaa ttt cca tgg act tcc caa gcc caa gaa att ttg cag gac aaa gcc	1171

Glu Phe Pro Trp Thr Ser Gln Ala Gln Glu Ile Leu Gln Asp Lys Ala
 345 350 355

cca cag gtt gaa gtt gat gtg att tcg atc cgc aca gac ccc tgg acc 1219
 Pro Gln Val Glu Val Asp Val Ile Ser Ile Arg Thr Asp Pro Trp Thr
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atg tct gcg cga gca gtg aac taaattcttg agaactaaaa aag 1263
 Met Ser Ala Arg Ala Val Asn
 375 380

<210> 506

<211> 380

<212> PRT

<213> Corynebacterium glutamicum

<400> 506

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Tyr Pro Pro Ala Leu Ala Glu Ser Trp Asp Lys Val Gly Leu Ile Cys
 20 25 30

Gly Asp Pro Thr Glu Ser Val Lys Arg Val Gly Leu Ala Leu Asp Cys
 35 40 45

Thr Gln Ala Val Ala Asp Lys Ala Val Asp Met Gly Leu Asp Met Leu
 50 55 60

Ile Ile His His Pro Leu Leu Leu Arg Gly Val Thr Ser Val Ala Ala
 65 70 75 80

Asp Glu Pro Lys Gly Lys Val Ile His Thr Leu Ile Arg Gly Gly Val
 85 90 95

Ala Leu Phe Ser Ala His Thr Asn Ala Asp Ser Ala Arg Pro Gly Val
 100 105 110

Asn Asp Lys Leu Ala Glu Leu Val Gly Ile Thr Ala Gly Arg Pro Ile
 115 120 125

Ala Thr Arg Leu Leu Gly Gly Met Asp Lys Trp Gly Val His Val Leu
 130 135 140

Pro Lys Asp Ala Ala Tyr Leu Lys Lys Met Leu Phe Asp Ala Gly Ala
 145 150 155 160

Gly Ala Ile Gly Asp Tyr Arg Glu Cys Ala Phe Glu Ile Glu Gly Thr
 165 170 175

Gly Gln Phe Arg Pro Val Glu Gly Ala Asn Pro Ala Glu Gly Asp Val
 180 185 190

Asp Lys Leu Phe Lys Ser Leu Glu Leu Arg Ile Glu Phe Val Ala Pro
 195 200 205

Arg Asn Leu Arg Ala Arg Leu Thr Ser Val Leu Arg Glu Ala His Pro
 210 215 220

Tyr Glu Glu Pro Ala Phe Asp Ile Val Glu Met His Ser Ala Glu Ser

225					230					235					240				
Leu	Glu	Asn	Ala	Thr	Gly	Leu	Gly	Arg	Val	Gly	Glu	Leu	Pro	Glu	Pro				
				245					250					255					
Met	Arg	Leu	Ala	Asp	Phe	Val	Gln	Gln	Val	Ala	Asn	Asn	Leu	Pro	Val				
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Thr	Glu	Trp	Gly	Val	Arg	Ala	Thr	Gly	Asp	Pro	Glu	Gln	Met	Val	Ser				
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Arg	Val	Ala	Val	Ser	Ser	Gly	Ser	Gly	Asp	Ser	Phe	Leu	Asn	Asp	Val				
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Ile	Lys	Leu	Gly	Val	Asp	Val	Tyr	Val	Thr	Ser	Asp	Leu	Arg	His	His				
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Pro	Val	Asp	Glu	Tyr	Leu	Arg	Glu	Gly	Gly	Pro	Ala	Val	Ile	Asp	Thr				
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Ala	His	Trp	Ala	Ser	Glu	Phe	Pro	Trp	Thr	Ser	Gln	Ala	Gln	Glu	Ile				
				340					345					350					
Leu	Gln	Asp	Lys	Ala	Pro	Gln	Val	Glu	Val	Asp	Val	Ile	Ser	Ile	Arg				
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Thr	Asp	Pro	Trp	Thr	Met	Ser	Ala	Arg	Ala	Val	Asn								
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<213> Corynebacterium glutamicum
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<223> RXC00362
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											Met	Gly	Ile	Ile	Ala		
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ctg ctc gtt ttt atc gca att gcc gtg ata ttg aat gtg ttt ttg aaa															163		
Leu	Leu	Val	Phe	Ile	Ala	Ile	Ala	Val	Ile	Leu	Asn	Val	Phe	Leu	Lys		
				10					15					20			
cga gat att tca gaa gca ttg cta gtt gga tta gta gga act gcg ctt															211		
Arg	Asp	Ile	Ser	Glu	Ala	Leu	Leu	Val	Gly	Leu	Val	Gly	Thr	Ala	Leu		
			25					30					35				
gtc ggc ggt gta aat gca ccg aca tta ctg att gat gct gta gtg gat															259		
Val	Gly	Gly	Val	Asn	Ala	Pro	Thr	Leu	Leu	Ile	Asp	Ala	Val	Val	Asp		
		40					45					50					
gct gct cag tcg gaa gtt act ttc gca ggt atg gcc ttt gtt ttc atg															307		
Ala	Ala	Gln	Ser	Glu	Val	Thr	Phe	Ala	Gly	Met	Ala	Phe	Val	Phe	Met		

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ctt aac tcg att ttt ggt cgg ctt cga ggt ggc gca ggt tat gtt tcc Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly Ala Gly Tyr Val Ser 90 95 100			403
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aac tcc gcg acg gtt ggc tca gtg acg atc cct tgg atg aaa aag acg Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro Trp Met Lys Lys Thr 120 125 130			499
gga tgg act gct gaa agg tcc gca acg tta gtc gcg ggc aac tct ggc Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val Ala Gly Asn Ser Gly 135 140 145			547
ctt ggt gtt gcg ttg cct ccc aat tca aca atg ttc atc att ttg gca Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met Phe Ile Ile Leu Ala 150 155 160 165			595
ttg cca gct gca gca gct tct tcg gcc tct cag gtg tac att gct ttg Leu Pro Ala Ala Ala Ser Ser Ala Ser Gln Val Tyr Ile Ala Leu 170 175 180			643
gct tgt ggt ggt gcg tat gca gtg ctc tac cgc tta gcg gtc gtc ttt Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg Leu Ala Val Val Phe 185 190 195			691
tac tgg aca cgt aaa gat aaa att cct gcc acc cct gat gat caa cgg Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr Pro Asp Asp Gln Arg 200 205 210			739
gtg tca ttc ggt gag gca atg aag act gga tgg cgt tca ccg ttg atc Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp Arg Ser Pro Leu Ile 215 220 225			787
ttc ctt gga att ttg atc ccc gta atc ctc aca atc ggc cca ttg tct Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr Thr Ile Gly Pro Leu Ser 230 235 240 245			835
gaa tgg tta aag aca cat gga gtt ggg gag tct ggt gtt aaa tcg atg Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser Gly Val Lys Ser Met 250 255 260			883
tcg atc atc gtg tgg gtg cca att ctg att acg gca att gct ctg att Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr Ala Ile Ala Leu Ile 265 270 275			931
gaa ggg cgt aaa cga att gct aac aac atg gca cac ttt agg gtt cag Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala His Phe Arg Val Gln 280 285 290			979
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 Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu Leu Gly Val Gly Pro
 310 315 320 325

cag ttg tct aac tgg ctt gat tcc atg gac cta cct aag tct gtc atg 1123
 Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu Pro Lys Ser Val Met
 330 335 340

gtg atc att gtc tgc atc atg tgc att gtg gtg gca acg cca ctg tcg 1171
 Val Ile Ile Val Cys Ile Met Cys Ile Val Val Ala Thr Pro Leu Ser
 345 350 355

tca aca gca acc gcg gct gcg att ggt gct ccc gct gtc gct gcg ttg 1219
 Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro Ala Val Ala Ala Leu
 360 365 370

gct gcg gta ggt att gat cca act gtg gcg atc gta gtg atc ttg ctg 1267
 Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile Val Val Ile Leu Leu
 375 380 385

tgc act tcc act gaa ggt gca tcc ccg ccg gtg ggc gcg ccg att tac 1315
 Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val Gly Ala Pro Ile Tyr
 390 395 400 405

ctt tct gct gcg atc gcc gat gca aac cca acg aaa atg ttc gta cca 1363
 Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr Lys Met Phe Val Pro
 410 415 420

ctg att acg tac ttt gtt gtc ccc atg att ctg ctt gct tgg cta gtt 1411
 Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu Leu Ala Trp Leu Val
 425 430 435

gga atg gga ttc tta cca gtg att gtt cct acg ggt taaaggggta 1457
 Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr Gly
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aaaatgaact caa 1470

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<211> 449

<212> PRT

<213> Corynebacterium glutamicum

<400> 508

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Val Gly Thr Ala Leu Val Gly Gly Val Asn Ala Pro Thr Leu Leu Ile
 35 40 45

Asp Ala Val Val Asp Ala Ala Gln Ser Glu Val Thr Phe Ala Gly Met
 50 55 60

Ala Phe Val Phe Met Gly Ile Val Val Gln Ser Thr Gly Leu Ile Asp
 65 70 75 80

Arg Leu Ile Ala Ile Leu Asn Ser Ile Phe Gly Arg Leu Arg Gly Gly
 85 90 95
 Ala Gly Tyr Val Ser Thr Leu Gly Ser Ala Leu Ile Gly Leu Ile Ala
 100 105 110
 Gly Ser Thr Ala Gly Asn Ser Ala Thr Val Gly Ser Val Thr Ile Pro
 115 120 125
 Trp Met Lys Lys Thr Gly Trp Thr Ala Glu Arg Ser Ala Thr Leu Val
 130 135 140
 Ala Gly Asn Ser Gly Leu Gly Val Ala Leu Pro Pro Asn Ser Thr Met
 145 150 155 160
 Phe Ile Ile Leu Ala Leu Pro Ala Ala Ala Ala Ser Ser Ala Ser Gln
 165 170 175
 Val Tyr Ile Ala Leu Ala Cys Gly Gly Ala Tyr Ala Val Leu Tyr Arg
 180 185 190
 Leu Ala Val Val Phe Tyr Trp Thr Arg Lys Asp Lys Ile Pro Ala Thr
 195 200 205
 Pro Asp Asp Gln Arg Val Ser Phe Gly Glu Ala Met Lys Thr Gly Trp
 210 215 220
 Arg Ser Pro Leu Ile Phe Leu Gly Ile Leu Ile Pro Val Ile Leu Thr
 225 230 235 240
 Ile Gly Pro Leu Ser Glu Trp Leu Lys Thr His Gly Val Gly Glu Ser
 245 250 255
 Gly Val Lys Ser Met Ser Ile Ile Val Trp Val Pro Ile Leu Ile Thr
 260 265 270
 Ala Ile Ala Leu Ile Glu Gly Arg Lys Arg Ile Ala Asn Asn Met Ala
 275 280 285
 His Phe Arg Val Gln Ile Ser Lys Asp Leu Pro Gln Phe Ala Thr Val
 290 295 300
 Gly Ile Ser Leu Phe Ser Ala Leu Ala Ala Ala Asn Ile Met Glu Glu
 305 310 315 320
 Leu Gly Val Gly Pro Gln Leu Ser Asn Trp Leu Asp Ser Met Asp Leu
 325 330 335
 Pro Lys Ser Val Met Val Ile Ile Val Cys Ile Met Cys Ile Val Val
 340 345 350
 Ala Thr Pro Leu Ser Ser Thr Ala Thr Ala Ala Ala Ile Gly Ala Pro
 355 360 365
 Ala Val Ala Ala Leu Ala Ala Val Gly Ile Asp Pro Thr Val Ala Ile
 370 375 380
 Val Val Ile Leu Leu Cys Thr Ser Thr Glu Gly Ala Ser Pro Pro Val
 385 390 395 400
 Gly Ala Pro Ile Tyr Leu Ser Ala Ala Ile Ala Asp Ala Asn Pro Thr

	405		410		415
Lys Met Phe Val Pro Leu Ile Thr Tyr Phe Val Val Pro Met Ile Leu					
	420		425		430
Leu Ala Trp Leu Val Gly Met Gly Phe Leu Pro Val Ile Val Pro Thr					
	435		440		445

Gly

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 <212> DNA
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<220>
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 <222> (101)..(1180)
 <223> RXC00412

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 cttttgtccc ccgacttttg tacgaatcga ggacaccgtc gtg tca cac acc gcg 115
 Val Ser His Thr Ala 5
 1
 tcc aca ccg acg cca gag gaa tac tcc gcg cag caa ccc agc acc cag 163
 Ser Thr Pro Thr Pro Glu Glu Tyr Ser Ala Gln Gln Pro Ser Thr Gln 20
 10 15
 ggc act cgc gtt gag ttc cgc ggc ata acc aaa gtc ttt agc aac aat 211
 Gly Thr Arg Val Glu Phe Arg Gly Ile Thr Lys Val Phe Ser Asn Asn 35
 25 30
 aaa tct gct aaa acc acc gcg ctt gat aat gtc act ctc acc gta gaa 259
 Lys Ser Ala Lys Thr Thr Ala Leu Asp Asn Val Thr Leu Thr Val Glu 50
 40 45
 ccc ggt gag gta atc ggc atc atc ggt tac tct ggc gcc ggc aag tcc 307
 Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser Gly Ala Gly Lys Ser 65
 55 60
 act ctt gtc cgc ctc atc aat ggc ctt gac tcc ccc acg agc ggt tcg 355
 Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser Pro Thr Ser Gly Ser 85
 70 75 80
 ttg ctg ctc aac ggc acc gac atc gtc gga atg ccc gag tct aag ctg 403
 Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met Pro Glu Ser Lys Leu 100
 90 95
 cgt aaa ctg cgc agt aat atc ggc atg att ttc cag cag ttc aac ctg 451
 Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe Gln Gln Phe Asn Leu 115
 105 110
 ttc cag tcg cgt act gcg gct gga aat gtg gag tac ccg ctg gaa gtt 499
 Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu Tyr Pro Leu Glu Val 130
 120 125

gcc aag atg gac aag gca gct cgt aaa gct cgc gtg caa gaa atg ctc Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg Val Gln Glu Met Leu 135 140 145	547
gag ttc gtc ggc ctg ggc gac aaa ggc aaa aac tac ccc gag cag ctg Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn Tyr Pro Glu Gln Leu 150 155 160 165	595
tcg ggc ggc cag aag cag cgc gtc ggc att gcc cgt gca ctg gcc acc Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala Arg Ala Leu Ala Thr 170 175 180	643
aat cca acg ctt ttg ctt gcc gac gaa gcc acc tcc gct ttg gac cca Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr Ser Ala Leu Asp Pro 185 190 195	691
gaa acc acc cat gaa gtt ctg gag ctg ctg cgc aag gta aac cgc gaa Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg Lys Val Asn Arg Glu 200 205 210	739
ctg ggc atc acc atc gtt gtg atc acc cac gaa atg gaa gtt gtg cgt Leu Gly Ile Thr Ile Val Val Ile Thr His Glu Met Glu Val Val Arg 215 220 225	787
tcc atc gca gac aag gtt gct gtg atg gaa tcc ggc aaa gtt gtg gaa Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser Gly Lys Val Val Glu 230 235 240 245	835
tac ggc agc gtc tac gag gtg ttc tcc aat cca caa aca cag gtt gct Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro Gln Thr Gln Val Ala 250 255 260	883
caa aag ttc gtg gcc acc gcg ctg cgt aac acc cca gac caa gtg gaa Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr Pro Asp Gln Val Glu 265 270 275	931
tcg gaa gat ctg ctt agc cat gag gga cgt ctg ttc acc att gat ctg Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu Phe Thr Ile Asp Leu 280 285 290	979
act gaa acg tcc ggc ttc ttt gca gca acc gct cgt gct gcc gaa caa Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala Arg Ala Ala Glu Gln 295 300 305	1027
ggg gct ttt gtc aac atc gtt cac ggt ggc gtg acc acc ttg caa cgc Gly Ala Phe Val Asn Ile Val His Gly Gly Val Thr Thr Leu Gln Arg 310 315 320 325	1075
caa tca ttt ggc aaa atg act gtt cga ctc acc ggc aac acc gct gcg Gln Ser Phe Gly Lys Met Thr Val Arg Leu Thr Gly Asn Thr Ala Ala 330 335 340	1123
att gaa gag ttc tat caa acc ttg acc aag acc acg acc atc aag gag Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr Thr Thr Ile Lys Glu 345 350 355	1171
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 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Thr Leu Thr Val Glu Pro Gly Glu Val Ile Gly Ile Ile Gly Tyr Ser
 50 55 60
 Gly Ala Gly Lys Ser Thr Leu Val Arg Leu Ile Asn Gly Leu Asp Ser
 65 70 75 80
 Pro Thr Ser Gly Ser Leu Leu Leu Asn Gly Thr Asp Ile Val Gly Met
 85 90 95
 Pro Glu Ser Lys Leu Arg Lys Leu Arg Ser Asn Ile Gly Met Ile Phe
 100 105 110
 Gln Gln Phe Asn Leu Phe Gln Ser Arg Thr Ala Ala Gly Asn Val Glu
 115 120 125
 Tyr Pro Leu Glu Val Ala Lys Met Asp Lys Ala Ala Arg Lys Ala Arg
 130 135 140
 Val Gln Glu Met Leu Glu Phe Val Gly Leu Gly Asp Lys Gly Lys Asn
 145 150 155 160
 Tyr Pro Glu Gln Leu Ser Gly Gly Gln Lys Gln Arg Val Gly Ile Ala
 165 170 175
 Arg Ala Leu Ala Thr Asn Pro Thr Leu Leu Leu Ala Asp Glu Ala Thr
 180 185 190
 Ser Ala Leu Asp Pro Glu Thr Thr His Glu Val Leu Glu Leu Leu Arg
 195 200 205
 Lys Val Asn Arg Glu Leu Gly Ile Thr Ile Val Val Ile Thr His Glu
 210 215 220
 Met Glu Val Val Arg Ser Ile Ala Asp Lys Val Ala Val Met Glu Ser
 225 230 235 240
 Gly Lys, Val Val Glu Tyr Gly Ser Val Tyr Glu Val Phe Ser Asn Pro
 245 250 255
 Gln Thr Gln Val Ala Gln Lys Phe Val Ala Thr Ala Leu Arg Asn Thr
 260 265 270
 Pro Asp Gln Val Glu Ser Glu Asp Leu Leu Ser His Glu Gly Arg Leu
 275 280 285
 Phe Thr Ile Asp Leu Thr Glu Thr Ser Gly Phe Phe Ala Ala Thr Ala

290	295	300
Arg Ala Ala Glu Gln Gly	Ala Phe Val Asn Ile	Val His Gly Gly Val
305	310	315
Thr Thr Leu Gln Arg Gln Ser Phe Gly	Lys Met Thr Val Arg Leu Thr	
	325	330
Gly Asn Thr Ala Ala Ile Glu Glu Phe Tyr Gln Thr Leu Thr Lys Thr		
	340	345
Thr Thr Ile Lys Glu Ile Thr Arg		
	355	360

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(790)
 <223> RXC00526

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 Met Ser Leu Ile Glu
 1 5
 atg cga aat att gtc aag acc tac aac att gga tct gaa ggt gaa ctc 163
 Met Arg Asn Ile Val Lys Thr Tyr Asn Ile Gly Ser Glu Gly Glu Leu
 10 15 20
 acc gtg ttg cac ggt gtg gat ttc cat gtg gac cgt ggc gaa ttc gtg 211
 Thr Val Leu His Gly Val Asp Phe His Val Asp Arg Gly Glu Phe Val
 25 30 35
 tcg gtt gtg ggt acg tcc ggc tca ggt aaa tca acg atg atg aac atc 259
 Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser Thr Met Met Asn Ile
 40 45 50
 att ggg ttg ttg gat aag cca act gat ggc acg tac acc ttg gat ggc 307
 Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr Tyr Thr Leu Asp Gly
 55 60 65
 gtg gat gtg ttg gat atc agc gat gat gct ttg gcg agc cac cgc gct 355
 Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu Ala Ser His Arg Ala
 70 75 80 85
 aaa tcg att ggt ttt gtg ttt cag aac ttc aat ctg att ggc cgc atc 403
 Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn Leu Ile Gly Arg Ile
 90 95 100
 gat gcg ttg aag aat gtg gaa atg ccc atg atg tat gcg ggc att ccg 451
 Asp Ala Leu Lys Asn Val Glu Met Pro Met Met Tyr Ala Gly Ile Pro
 105 110 115
 gct aag cag cgg aga agt cgt gcg gtt gaa tta ttg gaa atg gtc ggg 499

Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu Leu Glu Met Val Gly
 120 125 130

atg ggt gag cgt ctc aac cat gag ccc aat gag ctt tcg ggt ggt cag 547
 Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu Leu Ser Gly Gly Gln
 135 140 145

aag cag cgc gtg gcc att gct cgc gcg ttg gcg aac gat cct gag atc 595
 Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala Asn Asp Pro Glu Ile
 150 155 160 165

att ctt gct gat gaa cca act ggt gcg ttg gat tct gca acg ggc cgg 643
 Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp Ser Ala Thr Gly Arg
 170 175 - 180

atg gtg atg gat att ttc cac cag ctc aac aag gag cag ggc aaa acc 691
 Met Val Met Asp Ile Phe His Gln Leu Asn Lys Glu Gln Gly Lys Thr
 185 190 195

atc gtg ttt att act cac aac cct gag ctt gct gat gaa tct gat cgg 739
 Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala Asp Glu Ser Asp Arg
 200 205 210

gtg gtc acc atg gtt gac ggg cgc atc att ggg tct gag gtg aaa cac 787
 Val Val Thr Met Val Asp Gly Arg Ile Ile Gly Ser Glu Val Lys His
 215 220 225

tca tgagccttgc agaatacaatt ctt 813
 Ser
 230

<210> 512
 <211> 230
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 512
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Ser Glu Gly Glu Leu Thr Val Leu His Gly Val Asp Phe His Val Asp
 20 25 30

Arg Gly Glu Phe Val Ser Val Val Gly Thr Ser Gly Ser Gly Lys Ser
 35 40 45

Thr Met Met Asn Ile Ile Gly Leu Leu Asp Lys Pro Thr Asp Gly Thr
 50 55 60

Tyr Thr Leu Asp Gly Val Asp Val Leu Asp Ile Ser Asp Asp Ala Leu
 65 70 75 80

Ala Ser His Arg Ala Lys Ser Ile Gly Phe Val Phe Gln Asn Phe Asn
 85 90 95

Leu Ile Gly Arg Ile Asp Ala Leu Lys Asn Val Glu Met Pro Met Met
 100 105 110

Tyr Ala Gly Ile Pro Ala Lys Gln Arg Arg Ser Arg Ala Val Glu Leu
 115 120 125

Leu Glu Met Val Gly Met Gly Glu Arg Leu Asn His Glu Pro Asn Glu
 130 135 140
 Leu Ser Gly Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ala
 145 150 155 160
 Asn Asp Pro Glu Ile Ile Leu Ala Asp Glu Pro Thr Gly Ala Leu Asp
 165 170 175
 Ser Ala Thr Gly Arg Met Val Met Asp Ile Phe His Gln Leu Asn Lys
 180 185 190
 Glu Gln Gly Lys Thr Ile Val Phe Ile Thr His Asn Pro Glu Leu Ala
 195 200 205
 Asp Glu Ser Asp Arg Val Val Thr Met Val Asp Gly Arg Ile Ile Gly
 210 215 220
 Ser Glu Val Lys His Ser
 225 230

<210> 513
 <211> 1185
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1162)
 <223> RXC01004

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 Val Ser Ile Trp Ala
 1 5
 act gtc ctt cta att atc gtc ctt ctt tcc gcc aac gcc ttc ttc gtg 163
 Thr Val Leu Leu Ile Ile Val Leu Leu Ser Ala Asn Ala Phe Phe Val
 10 15 20
 gcc gcg gag ttc gca ctg att tcc tcg cgc cgg gac cgc ctg gat tcc 211
 Ala Ala Glu Phe Ala Leu Ile Ser Ser Arg Arg Asp Arg Leu Asp Ser
 25 30 35
 ctg gta tcc cag ggt aaa aag gga gct gaa aag gtt ctc tac gca acc 259
 Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys Val Leu Tyr Ala Thr
 40 45 50
 gag cac ctc tcc atc atg ttg gcg ggc gct cag ttc ggt att acg gtc 307
 Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln Phe Gly Ile Thr Val
 55 60 65
 tgt tct ctg att ctg ggt aaa gtc gca gaa cct gcg atc gcc cac ttc 355
 Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro Ala Ile Ala His Phe
 70 75 80 85
 att gag gtg cct ttc acc tcc tgg ggt gtt cca aat gat ttg atc cac 403

Ile	Glu	Val	Pro	Phe	Thr	Ser	Trp	Gly	Val	Pro	Asn	Asp	Leu	Ile	His		
				90					95					100			
cca	att	tcc	ttc	gtc	atc	gca	ctg	gcg	atc	atc	acc	tgg	ttg	cac	att	451	
Pro	Ile	Ser	Phe	Val	Ile	Ala	Leu	Ala	Ile	Ile	Thr	Trp	Leu	His	Ile		
			105					110					115				
ctc	ttt	ggc	gaa	atg	gtg	cca	aag	aac	atc	gct	att	gct	ggc	cct	gaa	499	
Leu	Phe	Gly	Glu	Met	Val	Pro	Lys	Asn	Ile	Ala	Ile	Ala	Gly	Pro	Glu		
		120					125					130					
acc	tta	ggc	atg	tgg	ctt	gct	cca	gtg	ctc	att	gcg	ttt	gtg	aag	att	547	
Thr	Leu	Gly	Met	Trp	Leu	Ala	Pro	Val	Leu	Ile	Ala	Phe	Val	Lys	Ile		
	135					140					145						
acc	cgc	ccg	ttg	atc	gag	ttc	atg	aac	tgg	atc	gcc	cgt	ctg	acc	ctt	595	
Thr	Arg	Pro	Leu	Ile	Glu	Phe	Met	Asn	Trp	Ile	Ala	Arg	Leu	Thr	Leu		
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cgc	gcc	ttt	ggc	gtg	gag	caa	aaa	aac	gag	ctg	gat	tcc	acc	gtg	gac	643	
Arg	Ala	Phe	Gly	Val	Glu	Gln	Lys	Asn	Glu	Leu	Asp	Ser	Thr	Val	Asp		
			170						175					180			
cca	gag	cag	ctg	gca	tca	atg	att	tcc	gag	tcc	cgt	tcc	gaa	ggc	ctc	691	
Pro	Glu	Gln	Leu	Ala	Ser	Met	Ile	Ser	Glu	Ser	Arg	Ser	Glu	Gly	Leu		
			185					190					195				
ctt	gat	gct	gaa	gag	cac	gcc	cgc	ctg	tcc	aag	gcg	ctg	cgc	tct	gag	739	
Leu	Asp	Ala	Glu	Glu	His	Ala	Arg	Leu	Ser	Lys	Ala	Leu	Arg	Ser	Glu		
		200					205					210					
cag	cgt	tcc	atc	aag	gaa	ctg	gtg	att	aag	gat	gag	gac	gtg	cgc	acg	787	
Gln	Arg	Ser	Ile	Lys	Glu	Leu	Val	Ile	Lys	Asp	Glu	Asp	Val	Arg	Thr		
	215					220				225							
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Leu	Ala	Phe	Gly	Lys	Ser	Gly	Pro	Thr	Leu	His	Gln	Leu	Glu	Glu	Ala		
230					235				240						245		
gtc	cgc	gag	acc	ggc	ttc	tcc	cgc	ttc	cct	gtc	acc	ggc	cgc	gat	gga	883	
Val	Arg	Glu	Thr	Gly	Phe	Ser	Arg	Phe	Pro	Val	Thr	Gly	Arg	Asp	Gly		
			250						255					260			
tcc	tac	ttg	ggc	tat	atc	cac	atc	aag	gat	att	ttg	cct	cgt	ctg	gct	931	
Ser	Tyr	Leu	Gly	Tyr	Ile	His	Ile	Lys	Asp	Ile	Leu	Pro	Arg	Leu	Ala		
		265						270					275				
gat	cct	gag	atg	gat	ccc	tcc	gag	acc	att	ccg	cgt	tct	gca	ctg	cgc	979	
Asp	Pro	Glu	Met	Asp	Pro	Ser	Glu	Thr	Ile	Pro	Arg	Ser	Ala	Leu	Arg		
		280					285					290					
cct	ttg	agc	aat	gtg	gat	gcc	gac	ggc	ctc	atg	gat	gac	gtc	ttg	gat	1027	
Pro	Leu	Ser	Asn	Val	Asp	Ala	Asp	Gly	Leu	Met	Asp	Asp	Val	Leu	Asp		
	295					300					305						
ttt	atg	cac	tac	cgc	tcc	gcg	cac	atg	gct	cag	gtt	cgc	ctc	aaa	ggc	1075	
Phe	Met	His	Tyr	Arg	Ser	Ala	His	Met	Ala	Gln	Val	Arg	Leu	Lys	Gly		
310					315				320						325		
gag	ctt	ctc	ggc	gtg	att	acg	ctg	gag	gat	ctc	atc	gaa	gaa	tac	gtg	1123	
Glu	Leu	Leu	Gly	Val	Ile	Thr	Leu	Glu	Asp	Leu	Ile	Glu	Glu	Tyr	Val		

330 335 340
 ggc acc gtc aac gat tgg act cac gaa agc tcc gac gac tagaaatagt 1172
 Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser Asp Asp
 345 350

aactgtgttg gac 1185

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 514
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Asp Arg Leu Asp Ser Leu Val Ser Gln Gly Lys Lys Gly Ala Glu Lys
 35 40 45

Val Leu Tyr Ala Thr Glu His Leu Ser Ile Met Leu Ala Gly Ala Gln
 50 55 60

Phe Gly Ile Thr Val Cys Ser Leu Ile Leu Gly Lys Val Ala Glu Pro
 65 70 75 80

Ala Ile Ala His Phe Ile Glu Val Pro Phe Thr Ser Trp Gly Val Pro
 85 90 95

Asn Asp Leu Ile His Pro Ile Ser Phe Val Ile Ala Leu Ala Ile Ile
 100 105 110

Thr Trp Leu His Ile Leu Phe Gly Glu Met Val Pro Lys Asn Ile Ala
 115 120 125

Ile Ala Gly Pro Glu Thr Leu Gly Met Trp Leu Ala Pro Val Leu Ile
 130 135 140

Ala Phe Val Lys Ile Thr Arg Pro Leu Ile Glu Phe Met Asn Trp Ile
 145 150 155 160

Ala Arg Leu Thr Leu Arg Ala Phe Gly Val Glu Gln Lys Asn Glu Leu
 165 170 175

Asp Ser Thr Val Asp Pro Glu Gln Leu Ala Ser Met Ile Ser Glu Ser
 180 185 190

Arg Ser Glu Gly Leu Leu Asp Ala Glu Glu His Ala Arg Leu Ser Lys
 195 200 205

Ala Leu Arg Ser Glu Gln Arg Ser Ile Lys Glu Leu Val Ile Lys Asp
 210 215 220

Glu Asp Val Arg Thr Leu Ala Phe Gly Lys Ser Gly Pro Thr Leu His
 225 230 235 240

Gln Leu Glu Glu Ala Val Arg Glu Thr Gly Phe Ser Arg Phe Pro Val

	245		250		255
Thr Gly Arg Asp Gly Ser Tyr Leu Gly Tyr Ile His Ile Lys Asp Ile	260	265	270		
Leu Pro Arg Leu Ala Asp Pro Glu Met Asp Pro Ser Glu Thr Ile Pro	275	280	285		
Arg Ser Ala Leu Arg Pro Leu Ser Asn Val Asp Ala Asp Gly Leu Met	290	295	300		
Asp Asp Val Leu Asp Phe Met His Tyr Arg Ser Ala His Met Ala Gln	305	310	315	320	
Val Arg Leu Lys Gly Glu Leu Leu Gly Val Ile Thr Leu Glu Asp Leu	325	330	335		
Ile Glu Glu Tyr Val Gly Thr Val Asn Asp Trp Thr His Glu Ser Ser	340	345	350		
Asp Asp					

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXC01017

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 Met Ala Gln Lys Val
 1 5
 acc ttc tgg ttc gat acc acc tgc cca ttc tgc tgg gtc acc tcc cgc 163
 Thr Phe Trp Phe Asp Thr Thr Cys Pro Phe Cys Trp Val Thr Ser Arg
 10 15 20
 tgg att aag gaa gtc gaa caa gtc cgc gat att gaa atc cag tgg gtt 211
 Trp Ile Lys Glu Val Glu Gln Val Arg Asp Ile Glu Ile Gln Trp Val
 25 30 35
 cca atg agc ctc gct gtc cta aac gaa ggc cgt gat ctc cca gag gat 259
 Pro Met Ser Leu Ala Val Leu Asn Glu Gly Arg Asp Leu Pro Glu Asp
 40 45 50
 tac aag gag cgc atg aag gct gca tgg gga cca gca cgc gtt ttc gca 307
 Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro Ala Arg Val Phe Ala
 55 60 65
 gct gtc gcc acc gac cat gct gac aag ctc ggc gac ctg tac acc gca 355
 Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly Asp Leu Tyr Thr Ala
 70 75 80 85

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 Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly Pro Ile Glu Gly Ser
 90 95 100
 ttc aat gat gtc atc gca gag gca ctt gaa gag gtc ggc cta gac gct 451
 Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu Val Gly Leu Asp Ala
 105 110 115
 gca ctt ggt gaa gtt gca gac acc acc gaa tgg gac gac gca ctt cgc 499
 Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp Asp Asp Ala Leu Arg
 120 125 130
 gca ttc cac cag acc gca atg gac gag gtc ggc aac gat gtc gga acc 547
 Ala Phe His Gln Thr Ala Met Asp Glu Val Gly Asn Asp Val Gly Thr
 135 140 145
 cca gtg gtc aag ctc ggc gac acc gct ttc ttc ggc cca gtg ctc acc 595
 Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe Gly Pro Val Leu Thr
 150 155 160 165
 cgc atc cca cgc ggc gag gaa gca gga gag atc ttc gac gct tcc ttc 643
 Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile Phe Asp Ala Ser Phe
 170 175 180
 aag ctc gca agc tat ccc cac ttc ttt gaa atc aag cgc agc cgc act 691
 Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile Lys Arg Ser Arg Thr
 185 190 195
 gag aac cca cag ttc gac taattaacgc tgtctctgct tat 732
 Glu Asn Pro Gln Phe Asp
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<210> 516

<211> 203

<212> PRT

<213> Corynebacterium glutamicum

<400> 516

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 35 40 45
 Asp Leu Pro Glu Asp Tyr Lys Glu Arg Met Lys Ala Ala Trp Gly Pro
 50 55 60
 Ala Arg Val Phe Ala Ala Val Ala Thr Asp His Ala Asp Lys Leu Gly
 65 70 75 80
 Asp Leu Tyr Thr Ala Met Gly Thr Arg Ile His Asn Asp Gly Arg Gly
 85 90 95
 Pro Ile Glu Gly Ser Phe Asn Asp Val Ile Ala Glu Ala Leu Glu Glu
 100 105 110
 Val Gly Leu Asp Ala Ala Leu Gly Glu Val Ala Asp Thr Thr Glu Trp

115	120	125
Asp Asp Ala Leu Arg Ala Phe His Gln Thr Ala Met Asp Glu Val Gly		
130	135	140
Asn Asp Val Gly Thr Pro Val Val Lys Leu Gly Asp Thr Ala Phe Phe		
145	150	155
Gly Pro Val Leu Thr Arg Ile Pro Arg Gly Glu Glu Ala Gly Glu Ile		
	165	170
		175
Phe Asp Ala Ser Phe Lys Leu Ala Ser Tyr Pro His Phe Phe Glu Ile		
180	185	190
Lys Arg Ser Arg Thr Glu Asn Pro Gln Phe Asp		
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 <223> RXC01021

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 Met Ser Ser Ser Glu 5
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 agc tcg cgt tcc gaa ggc tcg cag cca gca ccg tct gta cag cct gaa 163
 Ser Ser Arg Ser Glu Gly Ser Gln Pro Ala Pro Ser Val Gln Pro Glu 20
 10 15
 cgc cgt gct gat tca acg ggg gct cct gcg gca gct tcc aag gaa gct 211
 Arg Arg Ala Asp Ser Thr Gly Ala Pro Ala Ala Ala Ser Lys Glu Ala 35
 25 30
 tcc caa caa atg gac gct gcc gga gtt ctt gag tgg gcc agg acc gct 259
 Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu Trp Ala Arg Thr Ala 50
 40 45
 gtc gag cag ctt tct gaa cgt cgt gca gag atc aat gca ctg aat gtc 307
 Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile Asn Ala Leu Asn Val 65
 55 60
 ttt cct gtt cca gat gca gac act gga tca aac atg acc tac acc atg 355
 Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn Met Thr Tyr Thr Met 85
 70 75 80
 aca gct gcg ttg gat gaa gcg ctg aaa ctg ggg gag ttg ggt gat gtc 403
 Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly Glu Leu Gly Asp Val 100
 90 95
 gca agg att act gag gct ttg gct gtt ggt tct gtg cgt gga gcc cga 451
 Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser Val Arg Gly Ala Arg

105	110	115	
gga aat tct gga gta gtc ctt agt cag gtc ctt cgc gct att gct cag			499
Gly Asn Ser Gly Val Val Leu Ser Ser Gln Val Leu Arg Ala Ile Ala Gln			
120	125	130	
gca gct gct gac ggg gtt att gat ggc cac aca atc caa gaa gcg cta			547
Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr Ile Gln Glu Ala Leu			
135	140	145	
tcc att gct cgc tcc cta gtt gat cgc gca att aca gat cct gtg gag			595
Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile Thr Asp Pro Val Glu			
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ggc act gtt gtc act gtg ttg cgt tct			622
Gly Thr Val Val Thr Val Leu Arg Ser			
170			

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 <213> Corynebacterium glutamicum

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Ala Ser Lys Glu Ala Ser Gln Gln Met Asp Ala Ala Gly Val Leu Glu
35 40 45
Trp Ala Arg Thr Ala Val Glu Gln Leu Ser Glu Arg Arg Ala Glu Ile
50 55 60
Asn Ala Leu Asn Val Phe Pro Val Pro Asp Ala Asp Thr Gly Ser Asn
65 70 75 80
Met Thr Tyr Thr Met Thr Ala Ala Leu Asp Glu Ala Leu Lys Leu Gly
85 90 95
Glu Leu Gly Asp Val Ala Arg Ile Thr Glu Ala Leu Ala Val Gly Ser
100 105 110
Val Arg Gly Ala Arg Gly Asn Ser Gly Val Val Leu Ser Gln Val Leu
115 120 125
Arg Ala Ile Ala Gln Ala Ala Ala Asp Gly Val Ile Asp Gly His Thr
130 135 140
Ile Gln Glu Ala Leu Ser Ile Ala Arg Ser Leu Val Asp Arg Ala Ile
145 150 155 160
Thr Asp Pro Val Glu Gly Thr Val Val Thr Val Leu Arg Ser
165 170

<210> 519
 <211> 1047

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1024)

<223> RXC01212

<400> 519

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                                         1 5

aca cca gca atc gac gta aca gac ctc gtg aga acc tac ggc gac tac 163
Thr Pro Ala Ile Asp Val Thr Asp Leu Val Arg Thr Tyr Gly Asp Tyr
                        10 15 20

acc gca gtc aag ggc ctg aat ttc cat gta cag cgc ggt gaa gta ttt 211
Thr Ala Val Lys Gly Leu Asn Phe His Val Gln Arg Gly Glu Val Phe
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Gly Leu Leu Gly Thr Asn Gly Ala Gly Lys Thr Ser Thr Leu Glu Val
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atc gaa gga ctt tcc gca ccc agc tcc ggc acc gtg cgc atc tcc ggg 307
Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr Val Arg Ile Ser Gly
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ctt gac ccc gtt gcc gac cgc gcg atc ctg cgc ccc gag ctc ggc atc 355
Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg Pro Glu Leu Gly Ile
                        70 75 80 85

atg ctg caa tca ggc ggc ctg cca tca cag ctc acc gtc gcc gaa acc 403
Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu Thr Val Ala Glu Thr
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atg gac atg tgg cac ggc acc tgc acg tat ccg cgc gcc att aaa gat 451
Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro Arg Ala Ile Lys Asp
                        105 110 115

gtg ctt gcc gac gtc gac ctc cta cac cgc gaa aac gtc aag gtc ggc 499
Val Leu Ala Asp Val Asp Leu Leu His Arg Glu Asn Val Lys Val Gly
                        120 125 130

gcg ctt tcc gga ggc gaa caa cga cgc ctt gat ttg gcc tgc gca ctg 547
Ala Leu Ser Gly Gly Glu Gln Arg Arg Leu Asp Leu Ala Cys Ala Leu
                        135 140 145

ctt ggc gac ccc tca att ttg ttc ctc gac gaa ccc acc acc ggc ctc 595
Leu Gly Asp Pro Ser Ile Leu Phe Leu Asp Glu Pro Thr Thr Gly Leu
                        150 155 160 165

gac cca gaa tct agg cgc cac acc tgg caa ctc ctg ctg gac ctg aaa 643
Asp Pro Glu Ser Arg Arg His Thr Trp Gln Leu Leu Leu Asp Leu Lys
                        170 175 180

cag cgc ggc gtc acc atg atg ctg acc acc cac tac ctg gag gaa gcc 691
Gln Arg Gly Val Thr Met Met Leu Thr Thr His Tyr Leu Glu Glu Ala

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Glu Phe Leu Cys Asp Arg Ile Ala Ile Met Asn Ala Gly Glu Ile Ala															
200													210		
gtg gaa ggc acc ttg gat gaa ctg gtg gcc cgc gag aag tcg atc atc														787	
Val Glu Gly Thr Leu Asp Glu Leu Val Ala Arg Glu Lys Ser Ile Ile															
215													225		
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Ser Phe Val Leu Arg Gly Gly Gln Val Glu Leu Pro Val Leu Ser Gly															
230													245		
gct gaa atc atc cgc gac aac aac cac gtc cgc atc gcc acc acc acc														883	
Ala Glu Ile Ile Arg Asp Asn Asn His Val Arg Ile Ala Thr Thr Thr															
250													260		
ctg cag cag cac acc tta gaa ata ctt acc tgg gct gca gag acc ggg														931	
Leu Gln Gln His Thr Leu Glu Ile Leu Thr Trp Ala Ala Glu Thr Gly															
265													275		
atc gcg ctg gaa ggc ttc gct gca aaa ccc gcc acc ttg gaa tcc gta														979	
Ile Ala Leu Glu Gly Phe Ala Ala Lys Pro Ala Thr Leu Glu Ser Val															
280													290		
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Phe Met Asp Ile Ala Ser Leu Glu Asn Thr Ser Leu Gln Thr Ala															
295													305		

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 <213> Corynebacterium glutamicum

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 35 40 45
 Ser Thr Leu Glu Val Ile Glu Gly Leu Ser Ala Pro Ser Ser Gly Thr
 50 55 60
 Val Arg Ile Ser Gly Leu Asp Pro Val Ala Asp Arg Ala Ile Leu Arg
 65 70 75 80
 Pro Glu Leu Gly Ile Met Leu Gln Ser Gly Gly Leu Pro Ser Gln Leu
 85 90 95
 Thr Val Ala Glu Thr Met Asp Met Trp His Gly Thr Cys Thr Tyr Pro
 100 105 110
 Arg Ala Ile Lys Asp Val Leu Ala Asp Val Asp Leu Leu His Arg Glu

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Met Thr Glu Trp Tyr																
1 5																
gtc gtt tta ccc gcc act att cta ctc atc gcg ctg tct gcg ttt ttc															163	
Val	Val	Leu	Pro	Ala	Thr	Ile	Leu	Leu	Ile	Ala	Leu	Ser	Ala	Phe	Phe	
10 15 20																
gtc atc att gag ttc gct ttg ctt gca gct agg cgg aac cgg tta gag															211	

Val	Ile	Ile	Glu	Phe	Ala	Leu	Leu	Ala	Ala	Arg	Arg	Asn	Arg	Leu	Glu		
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Glu	Thr	Val	Glu	Thr	Ser	Arg	Ser	Ser	Arg	Ala	Ala	Leu	Arg	Ser	Leu		
		40					45					50					
aat	gaa	ctt	act	ctc	atg	ctc	gcg	ggc	gcg	cag	ttg	gga	atc	acc	atg	307	
Asn	Glu	Leu	Thr	Leu	Met		Leu	Ala	Gly	Ala	Gln	Leu	Gly	Ile	Thr	Met	
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gtg	act	ttc	gcg	ttg	ggt	gct	atc	acg	aag	cgc	tgg	gtt	cat	tat	gct	355	
Val	Thr	Phe	Ala	Leu	Gly	Ala	Ile	Thr	Lys	Pro	Trp	Val	His	Tyr	Ala		
	70				75				80						85		
ttg	atg	ccg	ctc	ttc	gaa	tgg	gcg	cgt	ata	ccg	ctg	gtt	atg	gca	gat	403	
Leu	Met	Pro	Leu	Phe	Glu	Trp	Ala	Arg	Ile	Pro	Leu	Val	Met	Ala	Asp		
				90				95						100			
gtc	att	gcg	ttt	att	ttg	tcg	ctg	ttt	atc	gta	acg	ttt	ctg	cac	ttg	451	
Val	Ile	Ala	Phe	Ile	Leu	Ser	Leu	Phe	Ile	Val	Thr	Phe	Leu	His	Leu		
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gtc	atc	ggc	gaa	atg	gct	ccg	aaa	tcc	tgg	gca	atc	gcg	cat	ccg	gag	499	
Val	Ile	Gly	Glu	Met	Ala	Pro	Lys	Ser	Trp	Ala	Ile	Ala	His	Pro	Glu		
		120					125					130					
acg	gca	ctt	cga	act	atc	gcg	att	ccc	gca	cgg	ggc	ttc	att	aac	ctg	547	
Thr	Ala	Leu	Arg	Thr	Ile	Ala	Ile	Pro	Ala	Arg	Gly	Phe	Ile	Asn	Leu		
	135					140					145						
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Phe	Arg	Pro	Leu	Leu	Gln	Trp	Ile	Asn	Lys	Met	Ala	Asn	Asp	Leu	Val		
	150				155				160						165		
cgc	aaa	gtt	ggt	gaa	act	ccc	gtt	gat	cga	gct	gca	gct	ggt	ggc	tat	643	
Arg	Lys	Val	Gly	Glu	Thr	Pro	Val	Asp	Arg	Ala	Ala	Ala	Gly	Gly	Tyr		
			170					175						180			
gac	acc	gat	acc	ctc	cat	gcc	ctc	att	gag	cat	tcc	cga	gaa	act	ggc	691	
Asp	Thr	Asp	Thr	Leu	His	Ala	Leu	Ile	Glu	His	Ser	Arg	Glu	Thr	Gly		
			185					190					195				
gct	ctg	gat	cag	caa	tcc	gcc	gcc	caa	atc	agc	gga	att	atc	aag	ctg	739	
Ala	Leu	Asp	Gln	Gln	Ser	Ala	Ala	Gln	Ile	Ser	Gly	Ile	Ile	Lys	Leu		
		200				205						210					
gat	aaa	atc	acg	gtc	ggt	caa	acc	ctg	acc	gca	tct	cca	ttt	acg	cac	787	
Asp	Lys	Ile	Thr	Val	Gly	Gln	Thr	Leu	Thr	Ala	Ser	Pro	Phe	Thr	His		
	215					220				225							
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Ser	Ala	Ser	Ala	Thr	Val	Ala	Glu	Val	Gln	Ala	Ala	Ala	Gln	Arg	Ser		
	230				235				240						245		
ggc	agc	ttg	cgt	gtg	ctt	atc	gac	gcc	ccc	tcc	cac	ctt	ttc	cca	cac	883	
Gly	Ser	Leu	Arg	Val	Leu	Ile	Asp	Ala	Pro	Ser	His	Leu	Phe	Pro	His		
			250					255						260			
gtc	att	cat	gtg	cga	gac	acc	ctt	ggt	gcc	tcg	cca	gac	gag	aag	gct	931	
Val	Ile	His	Val	Arg	Asp	Thr	Leu	Gly	Ala	Ser	Pro	Asp	Glu	Lys	Ala		

	265		270		275	
tcg aag tgg tct cgc cca atc ctc acc gtt gct gag acc gac acg tta						979
Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala Glu Thr Asp Thr Leu						
	280		285		290	
cac caa gcg ctg gaa tac atg cgg gag cat aac gag cag atc agt gcg						1027
His Gln Ala Leu Glu Tyr Met Arg Glu His Asn Glu Gln Ile Ser Ala						
	295		300		305	
gtg ctt tcc gct gat ggg aaa acg gtg ctt ggt gta ata act tgg gat						1075
Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly Val Ile Thr Trp Asp						
	310		315		320	325
cac atc ttg aaa tac ctg tgg cct gca tcg gtg tagctaattt gaggtgcgct						1128
His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val						
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gaa						1131

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 522
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 Leu Ser Ala Phe Phe Val Ile Ile Glu Phe Ala Leu Leu Ala Ala Arg
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 Arg Asn Arg Leu Glu Glu Thr Val Glu Thr Ser Arg Ser Ser Arg Ala
 35 40 45
 Ala Leu Arg Ser Leu Asn Glu Leu Thr Leu Met Leu Ala Gly Ala Gln
 50 55 60
 Leu Gly Ile Thr Met Val Thr Phe Ala Leu Gly Ala Ile Thr Lys Pro
 65 70 75 80
 Trp Val His Tyr Ala Leu Met Pro Leu Phe Glu Trp Ala Arg Ile Pro
 85 90 95
 Leu Val Met Ala Asp Val Ile Ala Phe Ile Leu Ser Leu Phe Ile Val
 100 105 110
 Thr Phe Leu His Leu Val Ile Gly Glu Met Ala Pro Lys Ser Trp Ala
 115 120 125
 Ile Ala His Pro Glu Thr Ala Leu Arg Thr Ile Ala Ile Pro Ala Arg
 130 135 140
 Gly Phe Ile Asn Leu Phe Arg Pro Leu Leu Gln Trp Ile Asn Lys Met
 145 150 155 160
 Ala Asn Asp Leu Val Arg Lys Val Gly Glu Thr Pro Val Asp Arg Ala
 165 170 175
 Ala Ala Gly Gly Tyr Asp Thr Asp Thr Leu His Ala Leu Ile Glu His

180	185	190
Ser Arg Glu Thr Gly Ala Leu Asp Gln Gln Ser Ala Ala Gln Ile Ser		
195	200	205
Gly Ile Ile Lys Leu Asp Lys Ile Thr Val Gly Gln Thr Leu Thr Ala		
210	215	220
Ser Pro Phe Thr His Ser Ala Ser Ala Thr Val Ala Glu Val Gln Ala		
225	230	235
Ala Ala Gln Arg Ser Gly Ser Leu Arg Val Leu Ile Asp Ala Pro Ser		
245	250	255
His Leu Phe Pro His Val Ile His Val Arg Asp Thr Leu Gly Ala Ser		
260	265	270
Pro Asp Glu Lys Ala Ser Lys Trp Ser Arg Pro Ile Leu Thr Val Ala		
275	280	285
Glu Thr Asp Thr Leu His Gln Ala Leu Glu Tyr Met Arg Glu His Asn		
290	295	300
Glu Gln Ile Ser Ala Val Leu Ser Ala Asp Gly Lys Thr Val Leu Gly		
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Val Ile Thr Trp Asp His Ile Leu Lys Tyr Leu Trp Pro Ala Ser Val		
325	330	335

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(490)
 <223> RXC01366

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 Val Ser Gln Phe Arg 5
 cgt tgt tcc cgc cct ggt tgt ggc aag cct gcc gtc gca acc ctc acc 163
 Arg Cys Ser Arg Pro Gly Cys Gly Lys Pro Ala Val Ala Thr Leu Thr 20
 10 15
 tac gca tat tgc gat tcc act gcg gtg gtt ggt cct ttg gcg cct gca 211
 Tyr Ala Tyr Ser Asp Ser Thr Ala Val Val Gly Pro Leu Ala Pro Ala 35
 25 30
 gca gag ccc cat agt tgg gat ctg tgt gag cat cat gcc gag cgt att 259
 Ala Glu Pro His Ser Trp Asp Leu Cys Glu His His Ala Glu Arg Ile 50
 40 45

act gcg ccc ctt ggt tgg gag atg ctg cgg gtg aac gac atc aaa gtc 307
 Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val Asn Asp Ile Lys Val
 55 60 65

gat gac gat gag gat ctg acg gct ctt gct cag gct gtt cgt gag gct 355
 Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln Ala Val Arg Glu Ala
 70 75 80 85

gga cgc act gtg agt ggt ctg gtt cct gaa gac gaa gtg ggc ggc aac 403
 Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp Glu Val Gly Gly Asn
 90 95 100

cat ccg gtg aac cgg agt gcg cgg atc gcg gaa cag aag gtt cac cgc 451
 His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu Gln Lys Val His Arg
 105 110 115

agg ggt cat ctc tat gtt gtg cct gat cag gac gaa tca taagggtttgc 500
 Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp Glu Ser
 120 125 130

tattcggatt gga 513

<210> 524
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 524
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Pro Leu Ala Pro Ala Ala Glu Pro His Ser Trp Asp Leu Cys Glu His
 35 40 45

His Ala Glu Arg Ile Thr Ala Pro Leu Gly Trp Glu Met Leu Arg Val
 50 55 60

Asn Asp Ile Lys Val Asp Asp Asp Glu Asp Leu Thr Ala Leu Ala Gln
 65 70 75 80

Ala Val Arg Glu Ala Gly Arg Thr Val Ser Gly Leu Val Pro Glu Asp
 85 90 95

Glu Val Gly Gly Asn His Pro Val Asn Arg Ser Ala Arg Ile Ala Glu
 100 105 110

Gln Lys Val His Arg Arg Gly His Leu Tyr Val Val Pro Asp Gln Asp
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Glu Ser
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 <212> DNA

<213> Corynebacterium glutamicum

<220>

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<223> RXC01372

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cct gcc cgc atc gtg gcg tcg ata agc act ctt tta gat ctt tta gaa	96
Pro Ala Arg Ile Val Ala Ser Ile Ser Thr Leu Leu Asp Leu Leu Glu	
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gca gac ccc agc att att tcc gac cgc ttg gaa cac ctc gcc gac tgc	144
Ala Asp Pro Ser Ile Ile Ser Asp Arg Leu Glu His Leu Ala Asp Cys	
35 40 45	
att gat gag gaa gtg gaa tcg cta tcg ccg gaa cgt gac gaa cta gtc	192
Ile Asp Glu Glu Val Glu Ser Leu Ser Pro Glu Arg Asp Glu Leu Val	
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aat ccc ggc cga aaa ctg cgc gca tac gta gat cac gca cgg atc gtg	240
Asn Pro Gly Arg Lys Leu Arg Ala Tyr Val Asp His Ala Arg Ile Val	
65 70 75 80	
cat acc ggc cga act gat gtg gga ctc gcg att gcc aac gtt atc gcc	288
His Thr Gly Arg Thr Asp Val Gly Leu Ala Ile Ala Asn Val Ile Ala	
85 90 95	
cca atc tgg acc cga cga ggc ctg gta tca gcc gtg ctg gat ttt ccc	336
Pro Ile Trp Thr Arg Arg Gly Leu Val Ser Ala Val Leu Asp Phe Pro	
100 105 110	
gag ctc atg gaa tca ttg ccg gaa ctc cgc gga ccc gag cca att acc	384
Glu Leu Met Glu Ser Leu Pro Glu Leu Arg Gly Pro Glu Pro Ile Thr	
115 120 125	
gac gat ata ttc cat gac cca ttc ata gat gac gaa ccc ggg gtg gta	432
Asp Asp Ile Phe His Asp Pro Phe Ile Asp Asp Glu Pro Gly Val Val	
130 135 140	
ccg ttt agg gct gtt gtc tgg gcc gaa gag gaa ccc gga atc ccc gat	480
Pro Phe Arg Ala Val Val Trp Ala Glu Glu Glu Pro Gly Ile Pro Asp	
145 150 155 160	
gcc atg gcg caa agc tgc gac gga cct agc aaa ggg gcg ctg aca caa	528
Ala Met Ala Gln Ser Cys Asp Gly Pro Ser Lys Gly Ala Leu Thr Gln	
165 170 175	
gca ctg cgt ttg ctg gtg cgc gga cag tca gcc acg acc tat tcc att	576
Ala Leu Arg Leu Leu Val Arg Gly Gln Ser Ala Thr Thr Tyr Ser Ile	
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Glu Glu Lys Asp Leu	
195	

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 Val Ala Gly Val Ala

	1	5	
cag cgt ttt gtc gac gag cgc att cac gtc ggt ttg gat tcc atg cca			163
Gln Arg Phe Val Asp Glu Arg Ile His Val Gly Leu Asp Ser Met Pro			
	10	20	
gaa gct gtg act gct gtg tgg atg gaa tct gat tgg gtg ttg gcg gaa			211
Glu Ala Val Thr Ala Val Trp Met Glu Ser Asp Trp Val Leu Ala Glu			
	25	35	
acc atc aag ggt tcc acg cct tcc gat tgg gaa gag att ttg cgg ccg			259
Thr Ile Lys Gly Ser Thr Pro Ser Asp Trp Glu Glu Ile Leu Arg Pro			
	40	50	
ttg gcg ctg ctc acg gac gcg tct ttc acg ttg cca cct cgt tcc acg			307
Leu Ala Leu Leu Thr Asp Ala Ser Phe Thr Leu Pro Pro Arg Ser Thr			
	55	65	
cgt gcg caa acc ttg gat ttg aag cat ttg gaa cca agc cgt ctg aag			355
Arg Ala Gln Thr Leu Asp Leu Lys His Leu Glu Pro Ser Arg Leu Lys			
	70	85	
ccg gag cag cca gaa aag cca gcg ttt act ccc aat gct tcg gaa gaa			403
Pro Glu Gln Pro Glu Lys Pro Ala Phe Thr Pro Asn Ala Ser Glu Glu			
	90	100	
gat ttg tct cag ccg ttg gtg atc cgc ccc gag gag ccg ttg cag atg			451
Asp Leu Ser Gln Pro Leu Val Ile Arg Pro Glu Glu Pro Leu Gln Met			
	105	115	
ccg gtt cgc ggt gtg cag gaa agc cgc gga gtg gtc gag cca cgg tca			499
Pro Val Arg Gly Val Gln Glu Ser Arg Gly Val Val Glu Pro Arg Ser			
	120	130	
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Leu Gly Ala Asp Asp Val Glu Ser Ile Ala Glu Gly Asp Pro Glu Arg			
	135	145	
ccg agc gat ctt tat ggc acg cgt gtg ctg cgt gat ctc aat ggt cag			595
Pro Ser Asp Leu Tyr Gly Thr Arg Val Leu Arg Asp Leu Asn Gly Gln			
	150	165	
tcc agt att ttc caa gat tcc acc gac gcg gat gag cca cca aaa aag			643
Ser Ser Ile Phe Gln Asp Ser Thr Asp Ala Asp Glu Pro Pro Lys Lys			
	170	180	
tggtagaaaaactg gtgttttttcg gcc			669
Trp			

<210> 528

<211> 182

<212> PRT

<213> Corynebacterium glutamicum

<400> 528

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Leu	Asp	Ser	Met	Pro	Glu	Ala	Val	Thr	Ala	Val	Trp	Met	Glu	Ser	Asp
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Trp	Val	Leu	Ala	Glu	Thr	Ile	Lys	Gly	Ser	Thr	Pro	Ser	Asp	Trp	Glu				
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Glu	Ile	Leu	Arg	Pro	Leu	Ala	Leu	Leu	Thr	Asp	Ala	Ser	Phe	Thr	Leu				
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Pro	Pro	Arg	Ser	Thr	Arg	Ala	Gln	Thr	Leu	Asp	Leu	Lys	His	Leu	Glu				
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Pro	Ser	Arg	Leu	Lys	Pro	Glu	Gln	Pro	Glu	Lys	Pro	Ala	Phe	Thr	Pro				
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Asn	Ala	Ser	Glu	Glu	Asp	Leu	Ser	Gln	Pro	Leu	Val	Ile	Arg	Pro	Glu				
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Glu	Pro	Leu	Gln	Met	Pro	Val	Arg	Gly	Val	Gln	Glu	Ser	Arg	Gly	Val				
		115					120					125							
Val	Glu	Pro	Arg	Ser	Leu	Gly	Ala	Asp	Asp	Val	Glu	Ser	Ile	Ala	Glu				
	130					135					140								
Gly	Asp	Pro	Glu	Arg	Pro	Ser	Asp	Leu	Tyr	Gly	Thr	Arg	Val	Leu	Arg				
	145				150				155						160				
Asp	Leu	Asn	Gly	Gln	Ser	Ser	Ile	Phe	Gln	Asp	Ser	Thr	Asp	Ala	Asp				
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Glu	Pro	Pro	Lys	Lys	Trp														
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 <211> 981
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(958)
 <223> RXC01663

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 Met Glu Ile Ser Val
 1 5
 ttg atc atc gcc gca ctg atc ttg gtg gca ggc atc gta ctg tgg cgc 163
 Leu Ile Ile Ala Ala Leu Ile Leu Val Ala Gly Ile Val Leu Trp Arg
 10 15 20
 gcg gac tcg tct aaa cag gca gct aaa aag gct gaa tca cct gtg ggc 211
 Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala Glu Ser Pro Val Gly
 25 30 35
 tca gtc gca cct gcg ccc gtg ctg gtt gaa gaa gag ccg gac cct gag 259
 Ser Val Ala Pro Ala Pro Val Leu Val Glu Glu Glu Pro Asp Pro Glu
 40 45 50

ttt gag cca gaa ctg gac cct gaa cca gaa gcg caa cca gaa cca gag	307
Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala Gln Pro Glu Pro Glu	
55 60 65	
ctg gaa gtt gcg cct aga ttt gcg cca gaa cca gtt caa gat ctt gag	355
Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro Val Gln Asp Leu Glu	
70 75 80 85	
ccg gat cag gct gag gac att tat ttt gat gat tcc cct gaa ctc gat	403
Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp Ser Pro Glu Leu Asp	
90 95 100	
gct gat gtt gaa aat gcc ttg gct gag ctt act gag gta gaa gac tac	451
Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr Glu Val Glu Asp Tyr	
105 110 115	
ccg gaa gag cca gtg cag tct gag caa cct caa gcc cct gcc acg gcg	499
Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln Ala Pro Ala Thr Ala	
120 125 130	
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Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val Asp Lys His Ser Phe	
135 140 145	
ttg agc tct ttg cct ggt tcg cag cgc cgg gag cgc cga aac tgg gcg	595
Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu Arg Arg Asn Trp Ala	
150 155 160 165	
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Ala Lys His His Phe Asp Phe Ile Lys Glu Asp Ala Phe Leu Thr Asp	
170 175 180	
gaa tgg tca agg ggt gcg gca tcg act ggt gcc gtt gca cgt gat gtg	691
Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala Val Ala Arg Asp Val	
185 190 195	
gtc agt ggc atg gct gaa gga tat gaa acg cat ctg gtg gat ttg gcg	739
Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His Leu Val Asp Leu Ala	
200 205 210	
ggc gtg ccc gtg atg gcg atg cgc cgt gga att acc tct gac gtg gtc	787
Gly Val Pro Val Met Ala Met Arg Arg Gly Ile Thr Ser Asp Val Val	
215 220 225	
att gat gcg cgc cgc ggt gag cag cct gcc gat cca gag cgt gaa gaa	835
Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp Pro Glu Arg Glu Glu	
230 235 240 245	
tct gat gat tta gtc gag att gat acc gtc tct gga ttc cgc ctg ctc	883
Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser Gly Phe Arg Leu Leu	
250 255 260	
agt acg tgg cgg ggg ttg cgc agc gtt ttg tcg acg agc gca ttc acg	931
Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser Thr Ser Ala Phe Thr	
265 270 275	
tcg gtt tgg att cca tgc cag aag ctg tgactgctgt gtggatggaa	978
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280 285	

tct

981

<210> 530

<211> 286

<212> PRT

<213> Corynebacterium glutamicum

<400> 530

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Ile Val Leu Trp Arg Ala Asp Ser Ser Lys Gln Ala Ala Lys Lys Ala
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 35 40 45

Glu Pro Asp Pro Glu Phe Glu Pro Glu Leu Asp Pro Glu Pro Glu Ala
 50 55 60

Gln Pro Glu Pro Glu Leu Glu Val Ala Pro Arg Phe Ala Pro Glu Pro
 65 70 75 80

Val Gln Asp Leu Glu Pro Asp Gln Ala Glu Asp Ile Tyr Phe Asp Asp
 85 90 95

Ser Pro Glu Leu Asp Ala Asp Val Glu Asn Ala Leu Ala Glu Leu Thr
 100 105 110

Glu Val Glu Asp Tyr Pro Glu Glu Pro Val Gln Ser Glu Gln Pro Gln
 115 120 125

Ala Pro Ala Thr Ala Glu Val Ala Ala Asp Glu Glu Gln Arg Gly Val
 130 135 140

Asp Lys His Ser Phe Leu Ser Ser Leu Pro Gly Ser Gln Arg Arg Glu
 145 150 155 160

Arg Arg Asn Trp Ala Ala Lys His His Phe Asp Phe Ile Lys Glu Asp
 165 170 175

Ala Phe Leu Thr Asp Glu Trp Ser Arg Gly Ala Ala Ser Thr Gly Ala
 180 185 190

Val Ala Arg Asp Val Val Ser Gly Met Ala Glu Gly Tyr Glu Thr His
 195 200 205

Leu Val Asp Leu Ala Gly Val Pro Val Met Ala Met Arg Arg Gly Ile
 210 215 220

Thr Ser Asp Val Val Ile Asp Ala Arg Arg Gly Glu Gln Pro Ala Asp
 225 230 235 240

Pro Glu Arg Glu Glu Ser Asp Asp Leu Val Glu Ile Asp Thr Val Ser
 245 250 255

Gly Phe Arg Leu Leu Ser Thr Trp Arg Gly Leu Arg Ser Val Leu Ser
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Thr Ser Ala Phe Thr Ser Val Trp Ile Pro Cys Gln Lys Leu


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275                                280                                285

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<223> RXC01693

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                                         Met Asn Thr Ala Pro
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ttc aaa ctc gaa gct gac ttc gca tca gcc ctg ccc acc atg gca gcc 163
Phe Lys Leu Glu Ala Asp Phe Ala Ser Ala Leu Pro Thr Met Ala Ala
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Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu Leu Val Ile Leu Asn
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gac gac ctc gcc tac agc ctc ggg ctt gat ccg aca tgg ctt cgc aca 259
Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro Thr Trp Leu Arg Thr
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cct gag ggc gtt caa ttt ctt ctc gga ctc aac ccc gag ccc tta aca 307
Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn Pro Glu Pro Leu Thr
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Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln Phe Gly Gln Phe Val
                        70                        75                        80                        85

gca agc ctt ggt gat ggc cga gcg ctt ctt ctc ggc gaa gcc cgc tca 403
Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu Gly Glu Ala Arg Ser
                        90                        95                        100

gct gac ggc gta ctg cat gat atc cac ctc aaa gga tct gga cga acc 451
Ala Asp Gly Val Leu His Asp Ile His Leu Lys Gly Ser Gly Arg Thr
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caa ttc tcc cga gga gcc gat gga cgc gcc gtc ctt ggc ccc gtc tta 499
Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val Leu Gly Pro Val Leu
                        120                        125                        130

cgc gaa tac atc atc tcc gaa gcg atg cat gca ctt ggt gtt ccc acc 547
Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala Leu Gly Val Pro Thr
                        135                        140                        145

acc agg tca ctt gca gta att agc acc ggt agg aaa atc caa cga gga 595
Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg Lys Ile Gln Arg Gly
                        150                        155                        160                        165

agc gta gcc cca ggc gca gtc ctt gtt cga gta gca acc agc ctc att 643

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cga	gtc	gga	tcc	ttc	caa	tac	tcc	aac	atc	tct	ggg	ggc	atc	gaa	cta	691	
Arg	Val	Gly	Ser	Phe	Gln	Tyr	Ser	Asn	Ile	Ser	Gly	Gly	Ile	Glu	Leu		
			185					190					195				
tct	caa	cac	ctg	gcg	aac	tat	acg	atc	acc	agg	cat	ttc	cct	tcg	ttg	739	
Ser	Gln	His	Leu	Ala	Asn	Tyr	Thr	Ile	Thr	Arg	His	Phe	Pro	Ser	Leu		
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Val	Ala	Glu	Leu	Ser	Ala	Pro	Thr	Pro	Ala	Thr	Tyr	Val	Ser	Leu	Phe		
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Lys	Ala	Ile	Leu	Gln	Arg	Gln	Ala	Asp	Thr	Val	Gly	Lys	Trp	Thr	Arg		
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Leu	Gly	Phe	Val	His	Gly	Ala	Leu	Asn	Thr	Asp	Asn	Thr	Leu	Ile	Ser		
				250				255						260			
gga	gaa	act	gtt	gac	tac	ggc	cca	tgc	gct	ttc	atg	gag	cgc	tac	cgt	931	
Gly	Glu	Thr	Val	Asp	Tyr	Gly	Pro	Cys	Ala	Phe	Met	Glu	Arg	Tyr	Arg		
			265					270					275				
ggc	gac	gcg	aaa	ttt	agc	tcc	atc	gac	act	tat	ggg	cgc	tac	aaa	ttt	979	
Gly	Asp	Ala	Lys	Phe	Ser	Ser	Ile	Asp	Thr	Tyr	Gly	Arg	Tyr	Lys	Phe		
		280					285					290					
gaa	aac	caa	cct	atg	atc	ctc	gga	tgg	aac	atg	gcc	cgc	ctc	gta	gaa	1027	
Glu	Asn	Gln	Pro	Met	Ile	Leu	Gly	Trp	Asn	Met	Ala	Arg	Leu	Val	Glu		
	295					300					305						
acc	ctc	ctc	cca	ctc	ctg	ggc	gcc	aca	cca	gac	gaa	ggc	atg	aca	gca	1075	
Thr	Leu	Leu	Pro	Leu	Leu	Gly	Ala	Thr	Pro	Asp	Glu	Gly	Met	Thr	Ala		
	310				315					320					325		
gcc	caa	gaa	gct	ctc	gta	gaa	ttc	gat	gac	ctc	tgc	gaa	caa	gca	atc	1123	
Ala	Gln	Glu	Ala	Leu	Val	Glu	Phe	Asp	Asp	Leu	Cys	Glu	Gln	Ala	Ile		
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cga	aaa	gaa	ttc	gcc	act	gca	ctg	ggc	ctt	gac	gag	tca	gac	acc	ggc	1171	
Arg	Lys	Glu	Phe	Ala	Thr	Ala	Leu	Gly	Leu	Asp	Glu	Ser	Asp	Thr	Gly		
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Thr	Val	Glu	Gln	Phe	Arg	Glu	Leu	Leu	Tyr	Leu	His	Asn	Pro	Asp	Ile		
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acc	acg	ctg	ctg	cgc	gca	ctc	acc	gac	aac	acc	gca	cca	ccg	agt	ggc	1267	
Thr	Thr	Leu	Leu	Arg	Ala	Leu	Thr	Asp	Asn	Thr	Ala	Pro	Pro	Ser	Gly		
		375				380					385						
ttt	gaa	gca	ttc	gtt	cac	gac	tgg	aaa	acc	caa	gac	cca	gat	atc	gaa	1315	
Phe	Glu	Ala	Phe	Val	His	Asp	Trp	Lys	Thr	Gln	Asp	Pro	Asp	Ile	Glu		
	390				395					400					405		
gca	atg	cga	gca	gta	aat	cca	ctt	ttc	att	cca	cgc	aat	cac	ctc	gtg	1363	
Ala	Met	Arg	Ala	Val	Asn	Pro	Leu	Phe	Ile	Pro	Arg	Asn	His	Leu	Val		

410	415	420	
gaa gct gct ctc gca gac gca gtt	gaa ggg aat cta gaa aag ttc cac		1411
Glu Ala Ala Leu Ala Asp Ala Val	Glu Gly Asn Leu Glu Lys Phe His		
425	430	435	
gaa ctc ctc gct gct gtc acc aat cct ttt gat cca act gcg ggc ccc			1459
Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp Pro Thr Ala Gly Pro			
440	445	450	
gat gaa cta cgc ctg cca agc gaa gaa gga ttt gaa gaa gac tac atg			1507
Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe Glu Glu Asp Tyr Met			
455	460	465	
acc ttc tgc ggt acc taggacagat ggtggggcag acg			1545
Thr Phe Cys Gly Thr			
470			

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<211> 474

<212> PRT

<213> Corynebacterium glutamicum

<400> 532

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Pro Thr Met Ala Ala Pro Trp Gln Gly Glu Glu Ala Pro Asn Pro Glu	
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Leu Val Ile Leu Asn Asp Asp Leu Ala Tyr Ser Leu Gly Leu Asp Pro	
35 40 45	
Thr Trp Leu Arg Thr Pro Glu Gly Val Gln Phe Leu Leu Gly Leu Asn	
50 55 60	
Pro Glu Pro Leu Thr Lys Ala Val Ala Gln Ala Tyr Ser Gly His Gln	
65 70 75 80	
Phe Gly Gln Phe Val Ala Ser Leu Gly Asp Gly Arg Ala Leu Leu Leu	
85 90 95	
Gly Glu Ala Arg Ser Ala Asp Gly Val Leu His Asp Ile His Leu Lys	
100 105 110	
Gly Ser Gly Arg Thr Gln Phe Ser Arg Gly Ala Asp Gly Arg Ala Val	
115 120 125	
Leu Gly Pro Val Leu Arg Glu Tyr Ile Ile Ser Glu Ala Met His Ala	
130 135 140	
Leu Gly Val Pro Thr Thr Arg Ser Leu Ala Val Ile Ser Thr Gly Arg	
145 150 155 160	
Lys Ile Gln Arg Gly Ser Val Ala Pro Gly Ala Val Leu Val Arg Val	
165 170 175	
Ala Thr Ser Leu Ile Arg Val Gly Ser Phe Gln Tyr Ser Asn Ile Ser	
180 185 190	

Gly Gly Ile Glu Leu Ser Gln His Leu Ala Asn Tyr Thr Ile Thr Arg
 195 200 205
 His Phe Pro Ser Leu Val Ala Glu Leu Ser Ala Pro Thr Pro Ala Thr
 210 215 220
 Tyr Val Ser Leu Phe Lys Ala Ile Leu Gln Arg Gln Ala Asp Thr Val
 225 230 235 240
 Gly Lys Trp Thr Arg Leu Gly Phe Val His Gly Ala Leu Asn Thr Asp
 245 250 255
 Asn Thr Leu Ile Ser Gly Glu Thr Val Asp Tyr Gly Pro Cys Ala Phe
 260 265 270
 Met Glu Arg Tyr Arg Gly Asp Ala Lys Phe Ser Ser Ile Asp Thr Tyr
 275 280 285
 Gly Arg Tyr Lys Phe Glu Asn Gln Pro Met Ile Leu Gly Trp Asn Met
 290 295 300
 Ala Arg Leu Val Glu Thr Leu Leu Pro Leu Leu Gly Ala Thr Pro Asp
 305 310 315 320
 Glu Gly Met Thr Ala Ala Gln Glu Ala Leu Val Glu Phe Asp Asp Leu
 325 330 335
 Cys Glu Gln Ala Ile Arg Lys Glu Phe Ala Thr Ala Leu Gly Leu Asp
 340 345 350
 Glu Ser Asp Thr Gly Thr Val Glu Gln Phe Arg Glu Leu Leu Tyr Leu
 355 360 365
 His Asn Pro Asp Ile Thr Thr Leu Leu Arg Ala Leu Thr Asp Asn Thr
 370 375 380
 Ala Pro Pro Ser Gly Phe Glu Ala Phe Val His Asp Trp Lys Thr Gln
 385 390 395 400
 Asp Pro Asp Ile Glu Ala Met Arg Ala Val Asn Pro Leu Phe Ile Pro
 405 410 415
 Arg Asn His Leu Val Glu Ala Ala Leu Ala Asp Ala Val Glu Gly Asn
 420 425 430
 Leu Glu Lys Phe His Glu Leu Leu Ala Ala Val Thr Asn Pro Phe Asp
 435 440 445
 Pro Thr Ala Gly Pro Asp Glu Leu Arg Leu Pro Ser Glu Glu Gly Phe
 450 455 460
 Glu Glu Asp Tyr Met Thr Phe Cys Gly Thr
 465 470

<210> 533

<211> 1236

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS
 <222> (101)..(1213)
 <223> RXC01703

<400> 533

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cgcgagggtt tggggctctgc ctcgaacaaa tcttggggttt  gtg gca tgg cca tcc  115
                                           Val Ala Trp Pro Ser
                                           1           5

aac gcc aaa gaa aaa ctg ttt atc cac tgg cac tac tgg tgg caa gcg  163
Asn Ala Lys Glu Lys Leu Phe Ile His Trp His Tyr Trp Trp Gln Ala
                10                15                20

cat tat cta gac tgc ctg gtg gat gct gct cgt cga cgc acc aca aag  211
His Tyr Leu Asp Cys Leu Val Asp Ala Ala Arg Arg Arg Thr Thr Lys
                25                30                35

gcc cgt cgc gac cgc atc agg gac acc atc cgc ggc att tcg gtg cgc  259
Ala Arg Arg Asp Arg Ile Arg Asp Thr Ile Arg Gly Ile Ser Val Arg
                40                45                50

aat gtg ggc aag ctg acc tcg aat cgt tat tac gac gac aaa gct tgg  307
Asn Val Gly Lys Leu Thr Ser Asn Arg Tyr Tyr Asp Asp Lys Ala Trp
                55                60                65

ctg gcc ctt gct ctt ggg cgt gcc gga aaa gtg cga aag gtg cgc aca  355
Leu Ala Leu Ala Leu Gly Arg Ala Gly Lys Val Arg Lys Val Arg Thr
                70                75                80                85

cca aaa tca ttg ccc tcg ttg gaa caa aac atc gtc gat ggc att gat  403
Pro Lys Ser Leu Pro Ser Leu Glu Gln Asn Ile Val Asp Gly Ile Asp
                90                95                100

tcc ctt act ggt gtg ctg ccg tgg cgt tcc ggc gaa acc ttc tac aac  451
Ser Leu Thr Gly Val Leu Pro Trp Arg Ser Gly Glu Thr Phe Tyr Asn
                105                110                115

gtt ccc tcc aac ggt cct gct gcg atc atg atg gcc cgc acc gac cgt  499
Val Pro Ser Asn Gly Pro Ala Ala Ile Met Met Ala Arg Thr Asp Arg
                120                125                130

ttg gac gag gct atg aaa atc acc gat tgg att ttt gac aac ctg atc  547
Leu Asp Glu Ala Met Lys Ile Thr Asp Trp Ile Phe Asp Asn Leu Ile
                135                140                145

gat ggc gac ggc ctt gtg atg gac gga ttg cgc atg cgc atg cac gga  595
Asp Gly Asp Gly Leu Val Met Asp Gly Leu Arg Met Arg Met His Gly
                150                155                160                165

cct gag ctt gtc cgt tcc atc cac ccg tat tgc caa ggt gtc gcc att  643
Pro Glu Leu Val Arg Ser Ile His Pro Tyr Cys Gln Gly Val Ala Ile
                170                175                180

ggg ggc tgt ttg gaa att gct ctc aaa ctg cgt gag cgc gca ggc ttg  691
Gly Ala Cys Leu Glu Ile Ala Leu Lys Leu Arg Glu Arg Ala Gly Leu
                185                190                195

acc act act gtg gtg gat cac tgg tcg gat gcc gat aag gca gaa gac  739
Thr Thr Thr Val Val Asp His Trp Ser Asp Ala Asp Lys Ala Glu Asp

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200	205	210	
tcc ctc aaa tac ttt gca cac atc cac gct gtg gtt cag gct gtg tcg Ser Leu Lys Tyr Phe Ala His Ile His Ala Val Val Gln Ala Val Ser 215 220 225			787
cgg aag atg acc aac ttc cac ggc gtt att gat tgg gac acc ggt gac Arg Lys Met Thr Asn Phe His Gly Val Ile Asp Trp Asp Thr Gly Asp 230 235 240 245			835
ggc gac ggc ggt ttg ttc aag ggc att ttg gtc cgc tat tta gct gat Gly Asp Gly Gly Leu Phe Lys Gly Ile Leu Val Arg Tyr Leu Ala Asp 250 255 260			883
gtg gcc atc cgc ctg cct gac gat tca cca acc aac cgg gaa acc aaa Val Ala Ile Arg Leu Pro Asp Asp Ser Pro Thr Asn Arg Glu Thr Lys 265 270 275			931
aag att gca gca cgc ctg gta ctg gaa tcg gcg gaa agc gta tgg aac Lys Ile Ala Ala Arg Leu Val Leu Glu Ser Ala Glu Ser Val Trp Asn 280 285 290			979
cac cga ttg gaa gtt gat ggc ctt ccg gta ttc gcc aca gac tgg aca His Arg Leu Glu Val Asp Gly Leu Pro Val Phe Ala Thr Asp Trp Thr 295 300 305			1027
acg gat gca cgc ctg cca caa aac ttt ggt ttg agt tcc tct agt ttg Thr Asp Ala Arg Leu Pro Gln Asn Phe Gly Leu Ser Ser Ser Ser Leu 310 315 320 325			1075
agc gat ctg gtg agt gtt gtg cgc gtg gat gaa cgt gat ctg tcc gtg Ser Asp Leu Val Ser Val Val Arg Val Asp Glu Arg Asp Leu Ser Val 330 335 340			1123
caa ttg tcc ggt tgg atg ctc atg gaa gca gca gcg aaa gtg gcc gaa Gln Leu Ser Gly Trp Met Leu Met Glu Ala Ala Ala Lys Val Ala Glu 345 350 355			1171
gaa ctg gaa aac aac ggc aat agt tac acc ggt cgc tcc cga Glu Leu Glu Asn Asn Gly Asn Ser Tyr Thr Gly Arg Ser Arg 360 365 370			1213
tagccccgat agtgtatgtg ctg			1236

<210> 534

<211> 371

<212> PRT

<213> Corynebacterium glutamicum

<400> 534

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Tyr	Trp	Trp	Gln	Ala	His	Tyr	Leu	Asp	Cys	Leu	Val	Asp	Ala	Ala	Arg
			20					25					30		

Arg	Arg	Thr	Thr	Lys	Ala	Arg	Arg	Asp	Arg	Ile	Arg	Asp	Thr	Ile	Arg
		35					40					45			

Gly	Ile	Ser	Val	Arg	Asn	Val	Gly	Lys	Leu	Thr	Ser	Asn	Arg	Tyr	Tyr
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50					55					60					
Asp	Asp	Lys	Ala	Trp	Leu	Ala	Leu	Ala	Leu	Gly	Arg	Ala	Gly	Lys	Val
65					70					75					80
Arg	Lys	Val	Arg	Thr	Pro	Lys	Ser	Leu	Pro	Ser	Leu	Glu	Gln	Asn	Ile
			85						90					95	
Val	Asp	Gly	Ile	Asp	Ser	Leu	Thr	Gly	Val	Leu	Pro	Trp	Arg	Ser	Gly
			100					105					110		
Glu	Thr	Phe	Tyr	Asn	Val	Pro	Ser	Asn	Gly	Pro	Ala	Ala	Ile	Met	Met
		115					120					125			
Ala	Arg	Thr	Asp	Arg	Leu	Asp	Glu	Ala	Met	Lys	Ile	Thr	Asp	Trp	Ile
		130				135					140				
Phe	Asp	Asn	Leu	Ile	Asp	Gly	Asp	Gly	Leu	Val	Met	Asp	Gly	Leu	Arg
145					150					155					160
Met	Arg	Met	His	Gly	Pro	Glu	Leu	Val	Arg	Ser	Ile	His	Pro	Tyr	Cys
			165						170					175	
Gln	Gly	Val	Ala	Ile	Gly	Ala	Cys	Leu	Glu	Ile	Ala	Leu	Lys	Leu	Arg
			180					185					190		
Glu	Arg	Ala	Gly	Leu	Thr	Thr	Thr	Val	Val	Asp	His	Trp	Ser	Asp	Ala
		195					200					205			
Asp	Lys	Ala	Glu	Asp	Ser	Leu	Lys	Tyr	Phe	Ala	His	Ile	His	Ala	Val
	210					215					220				
Val	Gln	Ala	Val	Ser	Arg	Lys	Met	Thr	Asn	Phe	His	Gly	Val	Ile	Asp
225					230					235					240
Trp	Asp	Thr	Gly	Asp	Gly	Asp	Gly	Gly	Leu	Phe	Lys	Gly	Ile	Leu	Val
			245						250					255	
Arg	Tyr	Leu	Ala	Asp	Val	Ala	Ile	Arg	Leu	Pro	Asp	Asp	Ser	Pro	Thr
		260						265					270		
Asn	Arg	Glu	Thr	Lys	Lys	Ile	Ala	Ala	Arg	Leu	Val	Leu	Glu	Ser	Ala
		275					280					285			
Glu	Ser	Val	Trp	Asn	His	Arg	Leu	Glu	Val	Asp	Gly	Leu	Pro	Val	Phe
	290					295					300				
Ala	Thr	Asp	Trp	Thr	Thr	Asp	Ala	Arg	Leu	Pro	Gln	Asn	Phe	Gly	Leu
305					310					315					320
Ser	Ser	Ser	Ser	Leu	Ser	Asp	Leu	Val	Ser	Val	Val	Arg	Val	Asp	Glu
				325					330					335	
Arg	Asp	Leu	Ser	Val	Gln	Leu	Ser	Gly	Trp	Met	Leu	Met	Glu	Ala	Ala
		340						345					350		
Ala	Lys	Val	Ala	Glu	Glu	Leu	Glu	Asn	Asn	Gly	Asn	Ser	Tyr	Thr	Gly
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Arg	Ser	Arg													
		370													

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 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(777)
 <223> RXC02254

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 cgc ttc ggt gga cat ggt gcg cta gct ggt cac gcc ttg gga aac ctc 96
 Arg Phe Gly Gly His Gly Ala Leu Ala Gly His Ala Leu Gly Asn Leu
 20 25 30
 gtg atc gcg gcg ttg acc gac att ttg ggc acc tcc cag cat gcg ctt 144
 Val Ile Ala Ala Leu Thr Asp Ile Leu Gly Thr Ser Gln His Ala Leu
 35 40 45
 gat caa atc gct caa ctc gct gga gcc aaa gga cgc atc atc ccg gta 192
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
 50 55 60
 tgt gct gaa cct ttg gat ctt gaa gcg gaa gta tca ggt cta gac tct 240
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65 70 75 80
 gat gct cga gtc atg cgt caa gtt cgt ggt caa gtg gcg gta gct gca 288
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
 85 90 95
 acc ccc ggg cag gtg cga cgc gtt cga atc att ccg gac aat cca gaa 336
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
 100 105 110
 ccg aac ccc gct gcc atc gag gcc att ctc gat gca gat ttg gtc acc 384
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
 115 120 125
 ctt ggc cca ggt tcc tgg ttc tcc tct gtg att cca cac att ttg gtc 432
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
 130 135 140
 cca ggg atc gtt gat gcc ttg gcg cag aca aaa gca acc aaa acc gtg 480
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
 145 150 155 160
 gtg tta aac ctg acg tcc gag cca ggg gag acc gcg gga ttc tct gca 528
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
 165 170 175
 gaa cga cac atc cat gtg ctc cgc cag cat gct cga aac ctt cag gtt 576
 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val
 180 185 190

gac caa gtc att gtc gat gcc aag aca ctg tcc tca caa acc gaa cgc 624
 Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg
 195 200 205
 aat cat gta gaa cga gct gct cgc acc ctt ggt gca gaa gtc tcc ttc 672
 Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe
 210 215 220
 cat gat gtc cag gct gaa gat ggc, cgt ggt cga ttc acc agt att cac 720
 His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His
 225 230 235 240
 gat cca gca aag ctg tgt gca gcg ttg ctg gca agt ttt gct gga gca 768
 Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala
 245 250 255
 cga aag cgt taaggagtag gcgtgtcact gac 800
 Arg Lys Arg

<210> 536
 <211> 259
 <212> PRT
 <213> *Corynebacterium glutamicum*

<400> 536
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 35 40 45
 Asp Gln Ile Ala Gln Leu Ala Gly Ala Lys Gly Arg Ile Ile Pro Val
 50 55 60
 Cys Ala Glu Pro Leu Asp Leu Glu Ala Glu Val Ser Gly Leu Asp Ser
 65 70 75 80
 Asp Ala Arg Val Met Arg Gln Val Arg Gly Gln Val Ala Val Ala Ala
 85 90 95
 Thr Pro Gly Gln Val Arg Arg Val Arg Ile Ile Pro Asp Asn Pro Glu
 100 105 110
 Pro Asn Pro Ala Ala Ile Glu Ala Ile Leu Asp Ala Asp Leu Val Thr
 115 120 125
 Leu Gly Pro Gly Ser Trp Phe Ser Ser Val Ile Pro His Ile Leu Val
 130 135 140
 Pro Gly Ile Val Asp Ala Leu Ala Gln Thr Lys Ala Thr Lys Thr Val
 145 150 155 160
 Val Leu Asn Leu Thr Ser Glu Pro Gly Glu Thr Ala Gly Phe Ser Ala
 165 170 175
 Glu Arg His Ile His Val Leu Arg Gln His Ala Arg Asn Leu Gln Val

180	185	190
Asp Gln Val Ile Val Asp Ala Lys Thr Leu Ser Ser Gln Thr Glu Arg		
195	200	205
Asn His Val Glu Arg Ala Ala Arg Thr Leu Gly Ala Glu Val Ser Phe		
210	215	220
His Asp Val Gln Ala Glu Asp Gly Arg Gly Arg Phe Thr Ser Ile His		
225	230	235
Asp Pro Ala Lys Leu Cys Ala Ala Leu Leu Ala Ser Phe Ala Gly Ala		
245	250	255

Arg Lys Arg

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1036)
 <223> RXC02255

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 Val Ala Lys Asn Ser 5
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 gtt cgt gct gcg gaa gtg tct gca att tta agg ttt gct ggt gag atg 163
 Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg Phe Ala Gly Glu Met 20
 10 15
 caa gct gtc ggc ggc aag ctg gtc atc gaa gca aat ttg gac agc atg 211
 Gln Ala Val Gly Gly Lys Leu Val Ile Glu Ala Asn Leu Asp Ser Met 35
 25 30
 caa gtc ggt atg agg ctt cag gag ttt atc caa ggt ttg tac aac tct 259
 Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln Gly Leu Tyr Asn Ser 50
 40 45
 cga gtc gat gtg cac acc gtg aac ccg act gtg agc agg aaa acg cca 307
 Arg Val Asp Val His Thr Val Asn Pro Thr Val Ser Arg Lys Thr Pro 65
 55 60
 cgg tat ttg gtg cgc atc att gac aat gcc gat gaa att gcg cga cgc 355
 Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp Glu Ile Ala Arg Arg 85
 70 75 80
 acc gga ctg gtc acc agg tct gga cat gtg gtt aaa ggt cta gcg cct 403
 Thr Gly Leu Val Thr Arg Ser Gly His Val Val Lys Gly Leu Ala Pro 100
 90 95
 tct gtg gtc agc gga aca atc agt gac gct gaa gct gca tgg cgc ggt 451
 Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu Ala Ala Trp Arg Gly

105					110					115						
gcg	ttt	cta	gcc	aat	gga	tct	tta	agt	gat	cca	ggt	cgt	tcc	tct	tcg	499
Ala	Phe	Leu	Ala	Asn	Gly	Ser	Leu	Ser	Asp	Pro	Gly	Arg	Ser	Ser	Ser	
		120					125					130				
ttg	gag	gtg	ttg	tgt	cct	ggt	caa	gaa	tca	gca	ttg	gca	ctg	gtt	gga	547
Leu	Glu	Val	Leu	Cys	Pro	Gly	Gln	Glu	Ser	Ala	Leu	Ala	Leu	Val	Gly	
		135				140					145					
tgt	gcg	cga	aga	att	ggg	atc	gcg	gcg	aaa	acg	aaa	gat	tct	cga	gga	595
Cys	Ala	Arg	Arg	Ile	Gly	Ile	Ala	Ala	Lys	Thr	Lys	Asp	Ser	Arg	Gly	
150					155				160						165	
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Phe	Asp	Arg	Val	Asn	Val	Arg	Asp	Ala	Glu	Ala	Ile	Gly	Ala	Leu	Leu	
				170				175						180		
act	cga	atg	ggt	gcc	cag	aaa	act	cgc	atg	ttg	tgg	gaa	gaa	aaa	cgc	691
Thr	Arg	Met	Gly	Ala	Gln	Lys	Thr	Arg	Met	Leu	Trp	Glu	Glu	Lys	Arg	
			185					190					195			
atc	aag	cgg	gaa	agt	cga	act	ccg	caa	acc	ggg	ttg	gcc	aac	ttc	gac	739
Ile	Lys	Arg	Glu	Ser	Arg	Thr	Pro	Gln	Thr	Gly	Leu	Ala	Asn	Phe	Asp	
		200					205					210				
gat	gcc	aat	ctg	cgc	agg	tca	gcc	cga	gca	gca	gtt	gcc	gct	gca	gcg	787
Asp	Ala	Asn	Leu	Arg	Arg	Ser	Ala	Arg	Ala	Ala	Val	Ala	Ala	Ala	Ala	
		215				220					225					
agg	gta	gaa	cgc	gcc	atg	aag	att	ctt	ggt	gat	gat	gtt	cct	gag	cat	835
Arg	Val	Glu	Arg	Ala	Met	Lys	Ile	Leu	Gly	Asp	Asp	Val	Pro	Glu	His	
230					235				240						245	
ttg	gct	gag	gct	gga	cag	ctg	cgt	gtg	cag	cac	cgt	cag	gca	tcg	ttg	883
Leu	Ala	Glu	Ala	Gly	Gln	Leu	Arg	Val	Gln	His	Arg	Gln	Ala	Ser	Leu	
				250				255						260		
gag	gag	ttg	ggc	cgg	ttg	gct	gat	cct	caa	atg	acc	aag	gat	gct	gtg	931
Glu	Glu	Leu	Gly	Arg	Leu	Ala	Asp	Pro	Gln	Met	Thr	Lys	Asp	Ala	Val	
			265				270					275				
gcc	ggt	cgt	att	cgt	cgt	ctt	ttg	acg	atg	gca	gat	aag	cgc	gcc	gaa	979
Ala	Gly	Arg	Ile	Arg	Arg	Leu	Leu	Thr	Met	Ala	Asp	Lys	Arg	Ala	Glu	
		280					285					290				
gat	ctg	aag	att	cct	gat	aca	aat	tct	gtt	gtg	acg	gaa	gat	ttg	ttg	1027
Asp	Leu	Lys	Ile	Pro	Asp	Thr	Asn	Ser	Val	Val	Thr	Glu	Asp	Leu	Leu	
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gaa	gaa	att	tagatgattg	aagcctaaaa	acg											1059
Glu	Glu	Ile														
310																

<210> 538

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 538

Val Ala Lys Asn Ser Val Arg Ala Ala Glu Val Ser Ala Ile Leu Arg
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 Asn Leu Asp Ser Met Gln Val Gly Met Arg Leu Gln Glu Phe Ile Gln
 35 40 45
 Gly Leu Tyr Asn Ser Arg Val Asp Val His Thr Val Asn Pro Thr Val
 50 55 60
 Ser Arg Lys Thr Pro Arg Tyr Leu Val Arg Ile Ile Asp Asn Ala Asp
 65 70 75 80
 Glu Ile Ala Arg Arg Thr Gly Leu Val Thr Arg Ser Gly His Val Val
 85 90 95
 Lys Gly Leu Ala Pro Ser Val Val Ser Gly Thr Ile Ser Asp Ala Glu
 100 105 110
 Ala Ala Trp Arg Gly Ala Phe Leu Ala Asn Gly Ser Leu Ser Asp Pro
 115 120 125
 Gly Arg Ser Ser Ser Leu Glu Val Leu Cys Pro Gly Gln Glu Ser Ala
 130 135 140
 Leu Ala Leu Val Gly Cys Ala Arg Arg Ile Gly Ile Ala Ala Lys Thr
 145 150 155 160
 Lys Asp Ser Arg Gly Phe Asp Arg Val Asn Val Arg Asp Ala Glu Ala
 165 170 175
 Ile Gly Ala Leu Leu Thr Arg Met Gly Ala Gln Lys Thr Arg Met Leu
 180 185 190
 Trp Glu Glu Lys Arg Ile Lys Arg Glu Ser Arg Thr Pro Gln Thr Gly
 195 200 205
 Leu Ala Asn Phe Asp Asp Ala Asn Leu Arg Arg Ser Ala Arg Ala Ala
 210 215 220
 Val Ala Ala Ala Ala Arg Val Glu Arg Ala Met Lys Ile Leu Gly Asp
 225 230 235 240
 Asp Val Pro Glu His Leu Ala Glu Ala Gly Gln Leu Arg Val Gln His
 245 250 255
 Arg Gln Ala Ser Leu Glu Glu Leu Gly Arg Leu Ala Asp Pro Gln Met
 260 265 270
 Thr Lys Asp Ala Val Ala Gly Arg Ile Arg Arg Leu Leu Thr Met Ala
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Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr Gln Arg Thr Arg Trp 165																
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 Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
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His Ile Gly Pro Gly His Met Leu Leu Asn Leu Val Leu Leu Trp Leu
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Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala Tyr Thr Leu Met Ser
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Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly Leu Ile Thr Gly Ala
135 140 145

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 Ala Leu Phe Thr Ala Met Tyr Phe Val Gly Gly Ile Gly Ala Ser Ala
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 Ala Val Ile Trp Met Asp Pro Tyr Ser Pro Thr Ala Gly Ala Ser Gly
 85 90 95
 Ala Ile Tyr Ala Met Met Ala Ile Leu Val Gly Leu Phe Val Leu Arg
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 Ser Ala Asp Ile Arg Ala Pro Leu Ile Leu Ile Ala Ile Asn Ile Ala
 115 120 125
 Tyr Thr Leu Met Ser Thr Asn Val Ser Leu Trp Gly His Leu Gly Gly
 130 135 140
 Leu Ile Thr Gly Ala Leu Ile Thr Trp Pro Met Val Lys Ala Lys Thr
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 Ile Lys Ala Ala Gly Leu Thr Gly Ile Glu Leu Asn Thr Gly Gly Phe
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Ile	Gly	Asp	Lys	His	Ala	Glu	Asp	Ile	Arg	Arg	Ser	Ile	Arg	Leu	Ala	
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Glu	Arg	Leu	Gly	Gln	Asn	Arg	Val	Val	Thr	Met	Ser	Gly	Leu	Pro	Gly	
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Ser	Ala	Ala	Leu	Asp	Val	Leu	Asp	Tyr	Gln	Trp	Asp	Ile	Ala	Ala	Glu	
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Phe	Trp	Arg	Glu	Thr	Asp	Arg	Phe	Ala	Ala	Asp	His	Gly	Val	Lys	Val	
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Asp	Ala	Ser	His	Leu	Phe	Trp	Gln	Gln	Met	Asp	Pro	Ile	Ala	Val	Ile	
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Asp	His	Leu	Gly	Glu	Leu	Ile	Phe	His	Ala	Ala	Ala	Lys	Asp	Val	Arg	
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Arg	Arg	Leu	Asp	Pro	Ser	Glu	Asn	Arg	Thr	Asn	Leu	Gly	Gly	Asp	Glu	
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Trp	Ala	Asn	Glu	Trp	Pro	Lys	Asn	Ser	Ala	Trp	Asp	Phe	Val	Ala	Leu	
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Gly	Arg	Gly	His	Asp	Val	Ala	Tyr	Trp	Thr	Glu	Phe	Leu	Arg	Ala	Leu	

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Ser Leu Gly Arg Glu Glu Gly Val Asn Glu Ala Ala Lys Val Leu Ile			
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Ile Leu Val Ser Asp Asp Ala Arg Asp Glu Phe Leu Gly Ile Phe Glu			
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Gly Thr Gly Val Asp Ile Tyr Gly Leu Asn Cys Asn Gly Asn Pro Leu			
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His Pro Asn Lys Ala Ile Gly Asp Lys His Ala Glu Asp Ile Arg Arg			
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Ser Ile Arg Leu Ala Glu Arg Leu Gly Gln Asn Arg Val Val Thr Met			
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Ser Gly Leu Pro Gly Gly Glu Pro Gly Ala Lys Tyr Thr Asn Trp Val			
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Val Asn Ala Trp Asn Ser Ala Ala Leu Asp Val Leu Asp Tyr Gln Trp			
	130	135	140
Asp Ile Ala Ala Glu Phe Trp Arg Glu Thr Asp Arg Phe Ala Ala Asp			
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His Gly Val Lys Val Ala Leu Glu Leu His Pro Gln Asn Ile Val Phe			
	165	170	175
Asn Ser Ala Asp Val His Lys Leu Ile Asp Leu Thr Gly Ala Thr His			
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Val Gly Val Glu Leu Asp Ala Ser His Leu Phe Trp Gln Gln Met Asp			
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Pro Ile Ala Val Ile Asp His Leu Gly Glu Leu Ile Phe His Ala Ala
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 Ala Lys Asp Val Arg Val Asn Lys Glu Trp Ala Gln Leu Asn Gly Val
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 Leu Asp Asn Ser Phe Arg Arg Leu Asp Pro Ser Glu Asn Arg Thr Asn
 245 250 255
 Leu Gly Gly Asp Glu Trp Ala Asn Glu Trp Pro Lys Asn Ser Ala Trp
 260 265 270
 Asp Phe Val Ala Leu Gly Arg Gly His Asp Val Ala Tyr Trp Thr Glu
 275 280 285
 Phe Leu Arg Ala Leu His Arg Val Asp Pro Asn Met Leu Val Asn Ile
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 Asn Lys Ala Val Leu His Tyr Pro Gly Gly Glu Phe Glu Met Asp Ile
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 Ile Glu Ala Ser Glu Gly Asn Asn Gly Val Val Leu Gly Lys Met Leu
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 Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly Asp Ala Gly Ile Leu
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Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala Glu Asn Ala Thr Phe	
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Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu Leu Pro Thr Pro Asp	
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Glu Leu His Lys Phe Asn Asp Glu Ile Arg His His Thr Leu Leu Asp	
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Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu Ser Thr Tyr Tyr Gln	
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Asp Gln Leu Asn Pro Leu Asp Glu Ala Gln Leu Asp Lys Ala Thr Val	
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Arg Leu Met Ala Lys Val Pro Met Leu Ala Ala Tyr Ala His Arg Ala	
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Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn Ser Leu Asn Ala Arg	
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Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys Leu Leu Ile Leu His	
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Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala Gly Gly Ile Asn Ala	
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Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln Ala Val Leu Glu Met	
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Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg Leu Met Gly Phe Gly	
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 Arg Ala Met Gly Phe Pro Thr Asp Phe Phe Thr Val Leu Phe Ala Ile
 375 380 385

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Tyr Val Ser Thr Gly Ser Thr Glu Ser Lys Ile Thr Tyr Ile Asp Gly
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Asp Ala Gly Ile Leu Arg Tyr Arg Gly Tyr Asp Ile Ala Asp Leu Ala
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Glu Asn Ala Thr Phe Asn Glu Val Ser Tyr Leu Leu Ile Asn Gly Glu
 85 90 95

Leu Pro Thr Pro Asp Glu Leu His Lys Phe Asn Asp Glu Ile Arg His
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His Thr Leu Leu Asp Glu Asp Phe Lys Ser Gln Phe Asn Val Phe Pro
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 Arg Asp Ala His Pro Met Ala Thr Leu Ala Ser Ser Val Asn Ile Leu
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 Tyr Ala His Arg Ala Arg Lys Gly Ala Pro Tyr Met Tyr Pro Asp Asn
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 Ser Leu Asn Ala Arg Glu Asn Phe Leu Arg Met Met Phe Gly Tyr Pro
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 Thr Glu Pro Tyr Glu Ile Asp Pro Ile Met Val Lys Ala Leu Asp Lys
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 Leu Leu Ile Leu His Ala Asp His Glu Gln Asn Cys Ser Thr Ser Thr
 225 230 235 240
 Val Arg Met Ile Gly Ser Ala Gln Ala Asn Met Phe Val Ser Ile Ala
 245 250 255
 Gly Gly Ile Asn Ala Leu Ser Gly Pro Leu His Gly Gly Ala Asn Gln
 260 265 270
 Ala Val Leu Glu Met Leu Glu Asp Ile Lys Ser Asn His Gly Gly Asp
 275 280 285
 Ala Thr Glu Phe Met Asn Lys Val Lys Asn Lys Glu Asp Gly Val Arg
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 305 310 315 320
 Ala Ile Val Lys Glu Thr Ala His Glu Ile Leu Glu His Leu Gly Gly
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Met Ser Glu Leu Ile 5																
tgt gga cca gct att ctc ttc gca cca gct gga cgt gct gag atc att 163																
Cys Gly Pro Ala Ile Leu Phe Ala Pro Ala Gly Arg Ala Glu Ile Ile 20																
cca aaa gca gca tcg aag gcc gat atg gtc atc att gat ttg gaa gat 211																
Pro Lys Ala Ala Ser Lys Ala Asp Met Val Ile Ile Asp Leu Glu Asp 35																
ggg gca ggg gag gta gac cgt gag gtc gcc tac agg aac att aga gaa 259																
Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr Arg Asn Ile Arg Glu 50																
tcg ggg ttg gat cct aaa cga acc att gtg aga acc gta ggg ccg agc 307																
Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg Thr Val Gly Pro Ser 65																
gat cca cac ttt ttg gct gac gtg gag atg gtg aag tcc acg gat ttc 355																
Asp Pro His Phe Leu Ala Asp Val Glu Met Val Lys Ser Thr Asp Phe 85																
aca ctt gtt atg gtt cct aaa ctt ctt ggc agc gtg cct gag gaa tta 403																
Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser Val Pro Glu Glu Leu 100																
gat ggc ctc aac att atc gcc atg att gaa acc cct cag gct gca acc 451																
Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr Pro Gln Ala Ala Thr 115																
agc att cct cag att gct gcg gac cct aaa gtc gtt gga atg ttc tgg 499																
Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val Val Gly Met Phe Trp 130																
ggc gcg gag gat ctc aca cac ctc ttg gga ggc act cat tct agg ttc 547																
Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly Thr His Ser Arg Phe 145																
ttg ggt gat gag tcc aat gaa ggc tcc tac cga gac acc atg agg ctt 595																
Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg Asp Thr Met Arg Leu 165																
aca cgc gcc ctg atg cac ctc cac gcg gcg gcg aat ggg aag ttc acc 643																
Thr Arg Ala Leu Met His Leu His Ala Ala Ala Asn Gly Lys Phe Thr 180																

att gat gcc atc cat gcg gat ttc cac gat gaa gag ggc ctc tat tta 691
 Ile Asp Ala Ile His Ala Asp Phe His Asp Glu Glu Gly Leu Tyr Leu
 185 190 195

gaa gcg gtc gat gct gcg cgg act ggt ttc gct ggc acc gca tgc att 739
 Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala Gly Thr Ala Cys Ile
 200 205 210

cac ccc aag cag atc gag att gtt cgg aga gcc tat cgg cca gag gct 787
 His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala Tyr Arg Pro Glu Ala
 215 220 225

aac cag ttg gag tgg gcg aag aaa gtg gtg gag gaa gca gaa aac cat 835
 Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu Glu Ala Glu Asn His
 230 235 240 245

cca ggt gcg ttc aaa ctg gat ggt cag atg att gat gct ccg ttg att 883
 Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile Asp Ala Pro Leu Ile
 250 255 260

tcg cag gcg cgg atg gtt att tcg cgt cag cct gct tgattagttc 929
 Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro Ala
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<210> 548

<211> 273

<212> PRT

<213> Corynebacterium glutamicum

<400> 548

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 20 25 30

Ile Asp Leu Glu Asp Gly Ala Gly Glu Val Asp Arg Glu Val Ala Tyr
 35 40 45

Arg Asn Ile Arg Glu Ser Gly Leu Asp Pro Lys Arg Thr Ile Val Arg
 50 55 60

Thr Val Gly Pro Ser Asp Pro His Phe Leu Ala Asp Val Glu Met Val
 65 70 75 80

Lys Ser Thr Asp Phe Thr Leu Val Met Val Pro Lys Leu Leu Gly Ser
 85 90 95

Val Pro Glu Glu Leu Asp Gly Leu Asn Ile Ile Ala Met Ile Glu Thr
 100 105 110

Pro Gln Ala Ala Thr Ser Ile Pro Gln Ile Ala Ala Asp Pro Lys Val
 115 120 125

Val Gly Met Phe Trp Gly Ala Glu Asp Leu Thr His Leu Leu Gly Gly
 130 135 140

Thr His Ser Arg Phe Leu Gly Asp Glu Ser Asn Glu Gly Ser Tyr Arg
 145 150 155 160
 Asp Thr Met Arg Leu Thr Arg Ala Leu Met His Leu His Ala Ala Ala
 165 170 175
 Asn Gly Lys Phe Thr Ile Asp Ala Ile His Ala Asp Phe His Asp Glu
 180 185 190
 Glu Gly Leu Tyr Leu Glu Ala Val Asp Ala Ala Arg Thr Gly Phe Ala
 195 200 205
 Gly Thr Ala Cys Ile His Pro Lys Gln Ile Glu Ile Val Arg Arg Ala
 210 215 220
 Tyr Arg Pro Glu Ala Asn Gln Leu Glu Trp Ala Lys Lys Val Val Glu
 225 230 235 240
 Glu Ala Glu Asn His Pro Gly Ala Phe Lys Leu Asp Gly Gln Met Ile
 245 250 255
 Asp Ala Pro Leu Ile Ser Gln Ala Arg Met Val Ile Ser Arg Gln Pro
 260 265 270

Ala

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 <211> 2337
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(2314)
 <223> RXN00519

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 Met Ala Lys Ile Ile
 1 5
 tgg acc cgc acc gac gaa gca ccg ctg ctc gcg acc tac tcg ctg aag 163
 Trp Thr Arg Thr Asp Glu Ala Pro Leu Leu Ala Thr Tyr Ser Leu Lys
 10 15 20
 ccg gtc gtc gag gca ttt gct gct acc gcg ggc att gag gtc gag acc 211
 Pro Val Val Glu Ala Phe Ala Ala Thr Ala Gly Ile Glu Val Glu Thr
 25 30 35
 cgg gac att tca ctc gct gga cgc atc ctc gcc cag ttc cca gag cgc 259
 Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala Gln Phe Pro Glu Arg
 40 45 50
 ctc acc gaa gat cag aag gta ggc aac gca ctc gca gaa ctc ggc gag 307
 Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu Ala Glu Leu Gly Glu
 55 60 65

ctt gct aag act cct gaa gca aac atc att aag ctt cca aac atc tcc	355
Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys Leu Pro Asn Ile Ser	
70 75 80 85	
gct tct gtt cca cag ctc aag gct gct att aag gaa ctg cag gac cag	403
Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys Glu Leu Gln Asp Gln	
90 95 100	
ggc tac gac atc cca gaa ctg cct gat aac gcc acc acc gac gag gaa	451
Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala Thr Thr Asp Glu Glu	
105 110 115	
aaa gac atc ctc gca cgc tac aac gct gtt aag ggt tcc gct gtg aac	499
Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys Gly Ser Ala Val Asn	
120 125 130	
cca gtg ctg cgt gaa ggc aac tct gac cgc cgc gca cca atc gct gtc	547
Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg Ala Pro Ile Ala Val	
135 140 145	
aag aac ttt gtt aag aag ttc cca cac cgc atg ggc gag tgg tct gca	595
Lys Asn Phe Val Lys Lys Phe Pro His Arg Met Gly Glu Trp Ser Ala	
150 155 160 165	
gat tcc aag acc aac gtt gca acc atg gat gca aac gac ttc cgc cac	643
Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala Asn Asp Phe Arg His	
170 175 180	
aac gag aag tcc atc atc ctc gac gct gct gat gaa gtt cag atc aag	691
Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp Glu Val Gln Ile Lys	
185 190 195	
cac atc gca gct gac ggc acc gag acc atc ctc aag gac agc ctc aag	739
His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu Lys Asp Ser Leu Lys	
200 205 210	
ctt ctt gaa ggc gaa gtt cta gac gga acc gtt ctg tcc gca aag gca	787
Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val Leu Ser Ala Lys Ala	
215 220 225	
ctg gac gca ttc ctt ctc gag cag gtc gct cgc gca aag gca gaa ggt	835
Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg Ala Lys Ala Glu Gly	
230 235 240 245	
atc ctc ttc tcc gca cac ctg aag gcc acc atg atg aag gtc tcc gac	883
Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met Met Lys Val Ser Asp	
250 255 260	
cca atc atc ttc ggc cac gtt gtg cgc gct tac ttc gca gac gtt ttc	931
Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr Phe Ala Asp Val Phe	
265 270 275	
gca cag tac ggt gag cag ctg ctc gca gct ggc ctc aac ggc gaa aac	979
Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn	
280 285 290	
ggc ctc gct gca atc ctc tcc ggc ttg gag tcc ctg gac aac ggc gaa	1027
Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu	
295 300 305	
gaa atc aag gct gca ttc gag aag ggc ttg gaa gac ggc cca gac ctg	1075

Glu 310	Ile	Lys	Ala	Ala	Phe 315	Glu	Lys	Gly	Leu	Glu 320	Asp	Gly	Pro	Asp	Leu 325	
gcc	atg	gtt	aac	tcc	gct	cgc	ggc	atc	acc	aac	ctg	cat	gtc	cct	tcc	1123
Ala	Met	Val	Asn	Ser	Ala	Arg	Gly	Ile	Thr	Asn	Leu	His	Val	Pro	Ser	
				330					335						340	
gat	gtc	atc	gtg	gac	gct	tcc	atg	cca	gca	atg	att	cgt	acc	tcc	ggc	1171
Asp	Val	Ile	Val	Asp	Ala	Ser	Met	Pro	Ala	Met	Ile	Arg	Thr	Ser	Gly	
			345					350					355			
cac	atg	tgg	aac	aaa	gac	gac	cag	gag	cag	gac	acc	ctg	gca	atc	atc	1219
His	Met	Trp	Asn	Lys	Asp	Asp	Gln	Glu	Gln	Asp	Thr	Leu	Ala	Ile	Ile	
		360					365					370				
cca	gac	tcc	tcc	tac	gct	ggc	gtc	tac	cag	acc	gtt	atc	gaa	gac	tgc	1267
Pro	Asp	Ser	Ser	Tyr	Ala	Gly	Val	Tyr	Gln	Thr	Val	Ile	Glu	Asp	Cys	
		375				380					385					
cgc	aag	aac	ggc	gca	ttc	gat	cca	acc	acc	atg	ggt	acc	gtc	cct	aac	1315
Arg	Lys	Asn	Gly	Ala	Phe	Asp	Pro	Thr	Thr	Met	Gly	Thr	Val	Pro	Asn	
390					395					400					405	
gtt	ggt	ctg	atg	gct	cag	aag	gct	gaa	gag	tac	ggc	tcc	cat	gac	aag	1363
Val	Gly	Leu	Met	Ala	Gln	Lys	Ala	Glu	Glu	Tyr	Gly	Ser	His	Asp	Lys	
				410				415						420		
acc	ttc	cgc	atc	gaa	gca	gac	ggt	gtg	gtt	cag	gtt	gtt	tcc	tcc	aac	1411
Thr	Phe	Arg	Ile	Glu	Ala	Asp	Gly	Val	Val	Gln	Val	Val	Ser	Ser	Asn	
			425					430					435			
ggc	gac	gtt	ctc	atc	gag	cac	gac	gtt	gag	gca	aat	gac	atc	tgg	cgt	1459
Gly	Asp	Val	Leu	Ile	Glu	His	Asp	Val	Glu	Ala	Asn	Asp	Ile	Trp	Arg	
		440					445					450				
gca	tgc	cag	gtc	aag	gat	gcc	cca	atc	cag	gat	tgg	gta	aag	ctt	gct	1507
Ala	Cys	Gln	Val	Lys	Asp	Ala	Pro	Ile	Gln	Asp	Trp	Val	Lys	Leu	Ala	
		455				460					465					
gtc	acc	cgc	tcc	cgt	ctc	tcc	gga	atg	cct	gca	gtg	ttc	tgg	ttg	gat	1555
Val	Thr	Arg	Ser	Arg	Leu	Ser	Gly	Met	Pro	Ala	Val	Phe	Trp	Leu	Asp	
470					475				480						485	
cca	gag	cgc	gca	cac	gac	cgc	aac	ctg	gct	tcc	ctc	gtt	gag	aag	tac	1603
Pro	Glu	Arg	Ala	His	Asp	Arg	Asn	Leu	Ala	Ser	Leu	Val	Glu	Lys	Tyr	
				490				495						500		
ctg	gct	gac	cac	gac	acc	gag	ggc	ctg	gac	atc	cag	atc	ctc	tcc	cct	1651
Leu	Ala	Asp	His	Asp	Thr	Glu	Gly	Leu	Asp	Ile	Gln	Ile	Leu	Ser	Pro	
			505					510					515			
gtt	gag	gca	acc	cag	ctc	tcc	atc	gac	cgc	atc	cgc	cgt	ggc	gag	gac	1699
Val	Glu	Ala	Thr	Gln	Leu	Ser	Ile	Asp	Arg	Ile	Arg		Gly	Glu	Asp	
		520					525					530				
acc	atc	tct	gtc	acc	ggt	aac	gtt	ctg	cgt	gac	tac	aac	acc	gac	ctc	1747
Thr	Ile	Ser	Val	Thr	Gly	Asn	Val	Leu	Arg	Asp	Tyr	Asn	Thr	Asp	Leu	
		535				540					545					
ttc	cca	atc	ctg	gag	ctg	ggc	acc	tct	gca	aag	atg	ctg	tct	gtc	gtt	1795
Phe	Pro	Ile	Leu	Glu	Leu	Gly	Thr	Ser	Ala	Lys	Met	Leu	Ser	Val	Val	

550	555	560	565	
cct ttg atg gct ggc ggc gga ctg ttc gag acc ggt gct ggt gga tct				1843
Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr Gly Ala Gly Gly Ser	570	575	580	
gct cct aag cac gtc cag cag gtt cag gaa gaa aac cac ctg cgt tgg				1891
Ala Pro Lys His Val Gln Gln Val Gln Glu Glu Asn His Leu Arg Trp	585	590	595	
gat tcc ctc ggt gag ttc ctc gca ctg gct gag tcc ttc cgc cac gag				1939
Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu Ser Phe Arg His Glu	600	605	610	
ctc aac aac aac ggc aac acc aag gcc ggc gtt ctg gct gac gct ctg				1987
Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val Leu Ala Asp Ala Leu	615	620	625	
gac aag gca act gag aag ctg ctg aac gaa gag aag tcc cca tcc cgc				2035
Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu Lys Ser Pro Ser Arg	630	635	640	645
aag gtt ggc gag atc gac aac cgt ggc tcc cac ttc tgg ctg acc aag				2083
Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His Phe Trp Leu Thr Lys	650	655	660	
ttc tgg gct gac gag ctc gct gct cag acc gag gac gca gat ctg gct				2131
Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu Asp Ala Asp Leu Ala	665	670	675	
gct acc ttc gca cca gtc gca gaa gca ctg aac aca ggc gct gca gac				2179
Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn Thr Gly Ala Ala Asp	680	685	690	
atc gat gct gca ctg ctc gca gtt cag ggt gga gca act gac ctt ggt				2227
Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly Ala Thr Asp Leu Gly	695	700	705	
ggc tac tac tcc cct aac gag gag aag ctc acc aac atc atg cgc cca				2275
Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr Asn Ile Met Arg Pro	710	715	720	725
gtc gca cag ttc aac gag atc gtt gac gca ctg aag aag taaagtctct				2324
Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu Lys Lys	730	735		
tcacaaaaag cgc				2337

<210> 550
 <211> 738
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 550
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Ile Glu Val Glu Thr Arg Asp Ile Ser Leu Ala Gly Arg Ile Leu Ala
 35 40 45
 Gln Phe Pro Glu Arg Leu Thr Glu Asp Gln Lys Val Gly Asn Ala Leu
 50 55 60
 Ala Glu Leu Gly Glu Leu Ala Lys Thr Pro Glu Ala Asn Ile Ile Lys
 65 70 75 80
 Leu Pro Asn Ile Ser Ala Ser Val Pro Gln Leu Lys Ala Ala Ile Lys
 85 90 95
 Glu Leu Gln Asp Gln Gly Tyr Asp Ile Pro Glu Leu Pro Asp Asn Ala
 100 105 110
 Thr Thr Asp Glu Glu Lys Asp Ile Leu Ala Arg Tyr Asn Ala Val Lys
 115 120 125
 Gly Ser Ala Val Asn Pro Val Leu Arg Glu Gly Asn Ser Asp Arg Arg
 130 135 140
 Ala Pro Ile Ala Val Lys Asn Phe Val Lys Lys Phe Pro His Arg Met
 145 150 155 160
 Gly Glu Trp Ser Ala Asp Ser Lys Thr Asn Val Ala Thr Met Asp Ala
 165 170 175
 Asn Asp Phe Arg His Asn Glu Lys Ser Ile Ile Leu Asp Ala Ala Asp
 180 185 190
 Glu Val Gln Ile Lys His Ile Ala Ala Asp Gly Thr Glu Thr Ile Leu
 195 200 205
 Lys Asp Ser Leu Lys Leu Leu Glu Gly Glu Val Leu Asp Gly Thr Val
 210 215 220
 Leu Ser Ala Lys Ala Leu Asp Ala Phe Leu Leu Glu Gln Val Ala Arg
 225 230 235 240
 Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His Leu Lys Ala Thr Met
 245 250 255
 Met Lys Val Ser Asp Pro Ile Ile Phe Gly His Val Val Arg Ala Tyr
 260 265 270
 Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln Leu Leu Ala Ala Gly
 275 280 285
 Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu Ser Gly Leu Glu Ser
 290 295 300
 Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe Glu Lys Gly Leu Glu
 305 310 315 320
 Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala Arg Gly Ile Thr Asn
 325 330 335
 Leu His Val Pro Ser Asp Val Ile Val Asp Ala Ser Met Pro Ala Met
 340 345 350
 Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp Asp Gln Glu Gln Asp

355	360	365
Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala Gly Val Tyr Gln Thr		
370	375	380
Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe Asp Pro Thr Thr Met		
385	390	400
Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln Lys Ala Glu Glu Tyr		
	405	410
		415
Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala Asp Gly Val Val Gln		
	420	425
		430
Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu His Asp Val Glu Ala		
	435	440
		445
Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp Ala Pro Ile Gln Asp		
	450	455
		460
Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu Ser Gly Met Pro Ala		
	465	470
		475
Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp Arg Asn Leu Ala Ser		
	485	490
		495
Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr Glu Gly Leu Asp Ile		
	500	505
		510
Gln Ile Leu Ser Pro Val Glu Ala Thr Gln Leu Ser Ile Asp Arg Ile		
	515	520
		525
Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly Asn Val Leu Arg Asp		
	530	535
		540
Tyr Asn Thr Asp Leu Phe Pro Ile Leu Glu Leu Gly Thr Ser Ala Lys		
	545	550
		555
Met Leu Ser Val Val Pro Leu Met Ala Gly Gly Gly Leu Phe Glu Thr		
	565	570
		575
Gly Ala Gly Gly Ser Ala Pro Lys His Val Gln Gln Val Gln Glu Glu		
	580	585
		590
Asn His Leu Arg Trp Asp Ser Leu Gly Glu Phe Leu Ala Leu Ala Glu		
	595	600
		605
Ser Phe Arg His Glu Leu Asn Asn Asn Gly Asn Thr Lys Ala Gly Val		
	610	615
		620
Leu Ala Asp Ala Leu Asp Lys Ala Thr Glu Lys Leu Leu Asn Glu Glu		
	625	630
		635
Lys Ser Pro Ser Arg Lys Val Gly Glu Ile Asp Asn Arg Gly Ser His		
	645	650
		655
Phe Trp Leu Thr Lys Phe Trp Ala Asp Glu Leu Ala Ala Gln Thr Glu		
	660	665
		670
Asp Ala Asp Leu Ala Ala Thr Phe Ala Pro Val Ala Glu Ala Leu Asn		
	675	680
		685

Thr Gly Ala Ala Asp Ile Asp Ala Ala Leu Leu Ala Val Gln Gly Gly
 690 695 700

Ala Thr Asp Leu Gly Gly Tyr Tyr Ser Pro Asn Glu Glu Lys Leu Thr
 705 710 715 720

Asn Ile Met Arg Pro Val Ala Gln Phe Asn Glu Ile Val Asp Ala Leu
 725 730 735

Lys Lys

<210> 551
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1059)
 <223> FRXA00521

<400> 551

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Leu	Asp	Ala	Ala	Asp	Glu	Val	Gln	Ile	Lys	His	Ile	Ala	Ala	Asp	Gly	
1				5					10					15		
acc	gag	acc	atc	ctc	aag	gac	agc	ctc	aag	ctt	ctt	gaa	ggc	gaa	gtt	96
Thr	Glu	Thr	Ile	Leu	Lys	Asp	Ser	Leu	Lys	Leu	Leu	Glu	Gly	Glu	Val	
			20					25					30			
cta	gac	gga	acc	gtt	ctg	tcc	gca	aag	gca	ctg	gac	gca	ttc	ctt	ctc	144
Leu	Asp	Gly	Thr	Val	Leu	Ser	Ala	Lys	Ala	Leu	Asp	Ala	Phe	Leu	Leu	
		35					40					45				
gag	cag	gtc	gct	cgc	gca	aag	gca	gaa	ggt	atc	ctc	ttc	tcc	gca	cac	192
Glu	Gln	Val	Ala	Arg	Ala	Lys	Ala	Glu	Gly	Ile	Leu	Phe	Ser	Ala	His	
	50					55					60					
ctg	aag	gcc	acc	atg	atg	aag	gtc	tcc	gac	cca	atc	atc	ttc	ggc	cac	240
Leu	Lys	Ala	Thr	Met	Met	Lys	Val	Ser	Asp	Pro	Ile	Ile	Phe	Gly	His	
	65				70				75						80	
gtt	gtg	cgc	gct	tac	ttc	gca	gac	gtt	ttc	gca	cag	tac	ggt	gag	cag	288
Val	Val	Arg	Ala	Tyr	Phe	Ala	Asp	Val	Phe	Ala	Gln	Tyr	Gly	Glu	Gln	
				85					90					95		
ctg	ctc	gca	gct	ggc	ctc	aac	ggc	gaa	aac	ggc	ctc	gct	gca	atc	ctc	336
Leu	Leu	Ala	Ala	Gly	Leu	Asn	Gly	Glu	Asn	Gly	Leu	Ala	Ala	Ile	Leu	
			100					105					110			
tcc	ggc	ttg	gag	tcc	ctg	gac	aac	ggc	gaa	gaa	atc	aag	gct	gca	ttc	384
Ser	Gly	Leu	Glu	Ser	Leu	Asp	Asn	Gly	Glu	Glu	Ile	Lys	Ala	Ala	Phe	
		115					120					125				
gag	aag	ggc	ttg	gaa	gac	ggc	cca	gac	ctg	gcc	atg	gtt	aac	tcc	gct	432
Glu	Lys	Gly	Leu	Glu	Asp	Gly	Pro	Asp	Leu	Ala	Met	Val	Asn	Ser	Ala	
	130					135					140					

cgc ggc atc acc aac ctg cat gtc cct tcc gat gtc atc gtg gac gct	480
Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala	
145 150 155 160	
tcc atg cca gca atg att cgt acc tcc ggc cac atg tgg aac aaa gac	528
Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp	
165 170 175	
gac cag gag cag gac acc ctg gca atc atc cca gac tcc tcc tac gct	576
Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala	
180 185 190	
ggc gtc tac cag acc gtt atc gaa gac tgc cgc aag aac ggc gca ttc	624
Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe	
195 200 205	
gat cca acc acc atg ggt acc gtc cct aac gtt ggt ctg atg gct cag	672
Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln	
210 215 220	
aag gct gaa gag tac ggc tcc cat gac aag acc ttc cgc atc gaa gca	720
Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala	
225 230 235 240	
gac ggt gtg gtt cag gtt gtt tcc tcc aac ggc gac gtt ctc atc gag	768
Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu	
245 250 255	
cac gac gtt gag gca aat gac atc tgg cgt gca tgc cag gtc aag gat	816
His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp	
260 265 270	
gcc cca atc cag gat tgg gta aag ctt gct gtc acc cgc tcc cgt ctc	864
Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu	
275 280 285	
tcc gga atg cct gca gtg ttc tgg ttg gat cca gag cgc gca cac gac	912
Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp	
290 295 300	
cgc aac ctg gct tcc ctc gtt gag aag tac ctg gct gac cac gac acc	960
Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr	
305 310 315 320	
gag ggc ctg gac atc cag atc ctc tac cct gtt gag gca acc cag ctc	1008
Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu	
325 330 335	
tcc atc gac cgc atc cgc cgt ggc gag gac acc atc tct gtc acc ggt	1056
Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly	
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aac	1059
Asn	

<210> 552

<211> 353

<212> PRT

<213> Corynebacterium glutamicum

<400> 552

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 35 40 45
 Glu Gln Val Ala Arg Ala Lys Ala Glu Gly Ile Leu Phe Ser Ala His
 50 55 60
 Leu Lys Ala Thr Met Met Lys Val Ser Asp Pro Ile Ile Phe Gly His
 65 70 75 80
 Val Val Arg Ala Tyr Phe Ala Asp Val Phe Ala Gln Tyr Gly Glu Gln
 85 90 95
 Leu Leu Ala Ala Gly Leu Asn Gly Glu Asn Gly Leu Ala Ala Ile Leu
 100 105 110
 Ser Gly Leu Glu Ser Leu Asp Asn Gly Glu Glu Ile Lys Ala Ala Phe
 115 120 125
 Glu Lys Gly Leu Glu Asp Gly Pro Asp Leu Ala Met Val Asn Ser Ala
 130 135 140
 Arg Gly Ile Thr Asn Leu His Val Pro Ser Asp Val Ile Val Asp Ala
 145 150 155 160
 Ser Met Pro Ala Met Ile Arg Thr Ser Gly His Met Trp Asn Lys Asp
 165 170 175
 Asp Gln Glu Gln Asp Thr Leu Ala Ile Ile Pro Asp Ser Ser Tyr Ala
 180 185 190
 Gly Val Tyr Gln Thr Val Ile Glu Asp Cys Arg Lys Asn Gly Ala Phe
 195 200 205
 Asp Pro Thr Thr Met Gly Thr Val Pro Asn Val Gly Leu Met Ala Gln
 210 215 220
 Lys Ala Glu Glu Tyr Gly Ser His Asp Lys Thr Phe Arg Ile Glu Ala
 225 230 235 240
 Asp Gly Val Val Gln Val Val Ser Ser Asn Gly Asp Val Leu Ile Glu
 245 250 255
 His Asp Val Glu Ala Asn Asp Ile Trp Arg Ala Cys Gln Val Lys Asp
 260 265 270
 Ala Pro Ile Gln Asp Trp Val Lys Leu Ala Val Thr Arg Ser Arg Leu
 275 280 285
 Ser Gly Met Pro Ala Val Phe Trp Leu Asp Pro Glu Arg Ala His Asp
 290 295 300
 Arg Asn Leu Ala Ser Leu Val Glu Lys Tyr Leu Ala Asp His Asp Thr
 305 310 315 320

Glu Gly Leu Asp Ile Gln Ile Leu Tyr Pro Val Glu Ala Thr Gln Leu
 325 330 335

Ser Ile Asp Arg Ile Arg Arg Gly Glu Asp Thr Ile Ser Val Thr Gly
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Asn

<210> 553

<211> 1694

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1671)

<223> RXN02209

<400> 553

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 Asp Arg Ile Leu Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu
 20 25 30

cca acc tac acc gac gac gct gtt tcc gta gac acc tcc atc cct gca 144
 Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala
 35 40 45

acc cgc atg gtt aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa 192
 Thr Arg Met Val Asn Glu Gly Gly Gln Pro Glu Gly Gly Val Glu
 50 55 60

gct gac aac tac aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct 240
 Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
 65 70 75 80

act ggc gca gaa gga cgt cct tcc aag cca gtc acc gtt gca tcc cca 288
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
 85 90 95

cag ggt ggc gag tac acc atc gac cac ggc atg gtt gca att gca tcc 336
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
 100 105 110

atc acc tct tgc acc aac acc tct aac cca tcc gtg atg atc ggc gct 384
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
 115 120 125

ggc ctg atc gca cgt aag gca gca gaa aag ggc ctc aag tcc aag cct 432
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
 130 135 140

tgg gtt aag acc atc tgt gca cca ggt tcc cag gtt gtc gac ggc tac 480
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
 145 150 155 160

tac cag cgc gca gac ctc tgg aag gac ctt gag gcc atg ggc ttc tac	528
Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr	
165 170 175	
ctc tcc ggc ttc ggc tgc acc acc tgt att ggt aac tcc ggc cca ctg	576
Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu	
180 185 190	
cca gag gaa atc tcc gct gcg atc aac gag cac gac ctg acc gca acc	624
Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr	
195 200 205	
gca gtt ttg tcc ggt aac cgt aac ttc gag gga cgt atc tcc cct gac	672
Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp	
210 215 220	
gtt aag atg aac tac ctg gca tcc cca atc atg gtc att gct tac gca	720
Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala	
225 230 235 240	
atc gct ggc acc atg gac ttc gac ttc gag aac gaa gct ctt gga cag	768
Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln	
245 250 255	
gac cag gac ggc aac gac gtc ttc ctg aag gac atc tgg cct tcc acc	816
Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr	
260 265 270	
gag gaa atc gaa gac acc atc cag cag gca atc tcc cgt gag ctt tac	864
Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr	
275 280 285	
gaa gct gac tac gca gat gtc ttc aag ggt gac aag cag tgg cag gaa	912
Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu	
290 295 300	
ctc gat gtt cct acc ggt gac acc ttc gag tgg gac gag aac tcc acc	960
Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr	
305 310 315 320	
tac atc cgc aag gca cct tac ttc gac ggc atg cct gtc gag cca gtg	1008
Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val	
325 330 335	
gca gtc acc gac atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac	1056
Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp	
340 345 350	
tct gtc acc acc gac cac atc tcc cct gct tcc tcc att aag cca ggt	1104
Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly	
355 360 365	
acc cct gca gct cag tac ttg gat gag cac ggt gtg gaa cgc cac gac	1152
Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp	
370 375 380	
tac aac tcc ctg ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc	1200
Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg	
385 390 395 400	

ggc acc ttc gcc aac atc cgc ctc cag aac cag ctg gtt gac atc gca 1248
 Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
 405 410 415
 ggt ggc tac acc cgc gac ttc acc cag gag ggt gct cca cag gcg ttc 1296
 Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
 420 425 430
 atc tac gac gct tcc gtc aac tac aag gct gct ggc att ccg ctg gtc 1344
 Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
 435 440 445
 gtc ttg ggc ggc aag gag tac ggc acc ggt tct tcc cgt gac tgg gca 1392
 Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
 450 455 460
 gct aag ggc act aac ctg ctc gga att cgc gca gtt atc acc gag tcc 1440
 Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
 465 470 475 480
 ttc gag cgt att cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca 1488
 Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
 485 490 495
 ctg cag ttc cct gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc 1536
 Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
 500 505 510
 acc gag acc ttc gac atc acc gga ctg acc gca ctt aac gag ggc gag 1584
 Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
 515 520 525
 act cct aag act gtc aag gtc acc gca acc aag gag aac ggc gac gtc 1632
 Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
 530 535 540
 gtc gag ttc gac gca att tgt ccg cat cga cac ccc agg tgaggctgac 1681
 Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
 545 550 555
 tactaccgcc acg 1694

<210> 554

<211> 557

<212> PRT

<213> Corynebacterium glutamicum

<400> 554

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Pro Thr Tyr Thr Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala
 35 40 45

Thr Arg Met Val Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu
 50 55 60

Ala Asp Asn Tyr Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala
 65 70 75 80
 Thr Gly Ala Glu Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro
 85 90 95
 Gln Gly Gly Glu Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser
 100 105 110
 Ile Thr Ser Cys Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala
 115 120 125
 Gly Leu Ile Ala Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro
 130 135 140
 Trp Val Lys Thr Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr
 145 150 155 160
 Tyr Gln Arg Ala Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr
 165 170 175
 Leu Ser Gly Phe Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu
 180 185 190
 Pro Glu Glu Ile Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr
 195 200 205
 Ala Val Leu Ser Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp
 210 215 220
 Val Lys Met Asn Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala
 225 230 235 240
 Ile Ala Gly Thr Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln
 245 250 255
 Asp Gln Asp Gly Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr
 260 265 270
 Glu Glu Ile Glu Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr
 275 280 285
 Glu Ala Asp Tyr Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu
 290 295 300
 Leu Asp Val Pro Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr
 305 310 315 320
 Tyr Ile Arg Lys Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val
 325 330 335
 Ala Val Thr Asp Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp
 340 345 350
 Ser Val Thr Thr Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly
 355 360 365
 Thr Pro Ala Ala Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp
 370 375 380
 Tyr Asn Ser Leu Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg

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385              390              395              400
Gly Thr Phe Ala Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala
              405              410              415
Gly Gly Tyr Thr Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe
              420              425              430
Ile Tyr Asp Ala Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val
              435              440              445
Val Leu Gly Gly Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala
              450              455              460
Ala Lys Gly Thr Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser
465              470              475              480
Phe Glu Arg Ile His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro
              485              490              495
Leu Gln Phe Pro Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly
              500              505              510
Thr Glu Thr Phe Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu
              515              520              525
Thr Pro Lys Thr Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val
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Val Glu Phe Asp Ala Ile Cys Pro His Arg His Pro Arg
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<210> 555

<211> 1682

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(1659)

<223> FRXA02209

<400> 555

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ctc tcc gag gca aag gag cag ttc cgt aag gat ctg cca acc tac acc      96
Leu Ser Glu Ala Lys Glu Gln Phe Arg Lys Asp Leu Pro Thr Tyr Thr
              20              25              30
gac gac gct gtt tcc gta gac acc tcc atc cct gca acc cgc atg gtt      144
Asp Asp Ala Val Ser Val Asp Thr Ser Ile Pro Ala Thr Arg Met Val
              35              40              45
aac gaa ggt ggc gga cag cct gaa ggc ggc gtc gaa gct gac aac tac      192
Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
              50              55              60
aac gct tcc tgg gct ggc tcc ggc gag tcc ttg gct act ggc gca gaa      240

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tac Tyr	acc Thr	atc Ile	gac Asp	cac His	ggc Gly	atg Met	gtt Val	gca Ala	att Ile	gca Ala	tcc Ser	atc Ile	acc Thr	tct Ser	tgc Cys	336
acc Thr	aac Asn	acc Thr	tct Ser	aac Asn	cca Pro	tcc Ser	gtg Val	atg Met	atc Ile	ggc Gly	gct Ala	ggc Gly	ctg Leu	atc Ile	gca Ala	384
cgt Arg	aag Lys	gca Ala	gca Ala	gaa Glu	aag Lys	ggc Gly	ctc Leu	aag Lys	tcc Ser	aag Lys	cct Pro	tgg Trp	gtt Val	aag Lys	acc Thr	432
atc Ile	tgt Cys	gca Ala	cca Pro	ggc Gly	tcc Ser	cag Gln	gtt Val	gtc Val	gac Asp	ggc Gly	tac Tyr	tac Tyr	cag Gln	cgc Arg	gca Ala	480
gac Asp	ctc Leu	tgg Trp	aag Lys	gac Asp	ctt Leu	gag Glu	gcc Ala	atg Met	ggc Gly	ttc Phe	tac Tyr	ctc Leu	tcc Ser	ggc Gly	ttc Phe	528
ggc Gly	tgc Cys	acc Thr	acc Thr	tgt Cys	att Ile	ggc Gly	aac Asn	tcc Ser	ggc Gly	cca Pro	ctg Leu	cca Pro	gag Glu	gaa Glu	atc Ile	576
tcc Ser	gct Ala	gcg Ala	atc Ile	aac Asn	gag Glu	cac His	gac Asp	ctg Leu	acc Thr	gca Ala	acc Thr	gca Ala	gtt Val	ttg Leu	tcc Ser	624
ggc Gly	aac Asn	cgt Arg	aac Asn	ttc Phe	gag Glu	gga Gly	cgt Arg	atc Ile	tcc Ser	cct Pro	gac Asp	gtt Val	aag Lys	atg Met	aac Asn	672
tac Tyr	ctg Leu	gca Ala	tcc Ser	cca Pro	atc Ile	atg Met	gtc Val	att Ile	gct Ala	tac Tyr	gca Ala	atc Ile	gct Ala	ggc Gly	acc Thr	720
atg Met	gac Asp	ttc Phe	gac Asp	ttc Phe	gag Glu	aac Asn	gaa Glu	gct Ala	ctt Leu	gga Gly	cag Gln	gac Asp	cag Gln	gac Asp	ggc Gly	768
aac Asn	gac Asp	gtc Val	ttc Phe	ctg Leu	aag Lys	gac Asp	atc Ile	tgg Trp	cct Pro	tcc Ser	acc Thr	gag Glu	gaa Glu	atc Ile	gaa Glu	816
gac Asp	acc Thr	atc Ile	cag Gln	cag Gln	gca Ala	atc Ile	tcc Ser	cgt Arg	gag Glu	ctt Leu	tac Tyr	gaa Glu	gct Ala	gac Asp	tac Tyr	864
gca Ala	gat Asp	gtc Val	ttc Phe	aag Lys	ggc Gly	gac Asp	aag Lys	cag Gln	tgg Trp	cag Gln	gaa Glu	ctc Leu	gat Asp	gtt Val	cct Pro	912
acc Thr	ggc Gly	gac Asp	acc Thr	ttc Phe	gag Glu	tgg Trp	gac Asp	gag Glu	aac Asn	tcc Ser	acc Thr	tac Tyr	atc Ile	cgc Arg	aag Lys	960

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atc cag ggc gca cgc gtt ctg gct aag ctc ggc gac tct gtc acc acc Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr 340 345 350				1056
gac cac atc tcc cct gct tcc tcc att aag cca ggt acc cct gca gct Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala 355 360 365				1104
cag tac ttg gat gag cac ggt gtg gaa cgc cac gac tac aac tcc ctg Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu 370 375 380				1152
ggt tcc agg cgt ggt aac cac gag gtc atg atg cgc ggc acc ttc gcc Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala 385 390 395 400				1200
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cgc gac ttc acc cag gag ggt gct cca cag gcg ttc atc tac gac gct Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala 420 425 430				1296
tcc gtc aac tac aag gct gct ggc att ccg ctg gtc gtc ttg ggc ggc Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly 435 440 445				1344
aag gag tac ggc acc ggt tct tcc cgt gac tgg gca gct aag ggc act Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr 450 455 460				1392
aac ctg ctc gga att cgc gca gtt atc acc gag tcc ttc gag cgt att Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile 465 470 475 480				1440
cac cgc tcc aac ctc atc ggt atg ggc gtt gtc cca ctg cag ttc cct His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro 485 490 495				1488
gca ggc gaa tcc cac gag tcc ctg ggc ctt gac ggc acc gag acc ttc Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe 500 505 510				1536
gac atc acc gga ctg acc gca ctt aac gag ggc gag act cct aag act Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr 515 520 525				1584
gtc aag gtc acc gca acc aag gag aac ggc gac gtc gtc gag ttc gac Val Lys Val Thr Ala Thr Lys Glu Asn Gly Asp Val Val Glu Phe Asp 530 535 540				1632
gca att tgt ccg cat cga cac ccc agg tgaggctgac tactaccgcc Ala Ile Cys Pro His Arg His Pro Arg 545 550				1679

acg

1682

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 <211> 553
 <212> PRT
 <213> Corynebacterium glutamicum

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 35 40 45
 Asn Glu Gly Gly Gly Gln Pro Glu Gly Gly Val Glu Ala Asp Asn Tyr
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 Asn Ala Ser Trp Ala Gly Ser Gly Glu Ser Leu Ala Thr Gly Ala Glu
 65 70 75 80
 Gly Arg Pro Ser Lys Pro Val Thr Val Ala Ser Pro Gln Gly Gly Glu
 85 90 95
 Tyr Thr Ile Asp His Gly Met Val Ala Ile Ala Ser Ile Thr Ser Cys
 100 105 110
 Thr Asn Thr Ser Asn Pro Ser Val Met Ile Gly Ala Gly Leu Ile Ala
 115 120 125
 Arg Lys Ala Ala Glu Lys Gly Leu Lys Ser Lys Pro Trp Val Lys Thr
 130 135 140
 Ile Cys Ala Pro Gly Ser Gln Val Val Asp Gly Tyr Tyr Gln Arg Ala
 145 150 155 160
 Asp Leu Trp Lys Asp Leu Glu Ala Met Gly Phe Tyr Leu Ser Gly Phe
 165 170 175
 Gly Cys Thr Thr Cys Ile Gly Asn Ser Gly Pro Leu Pro Glu Glu Ile
 180 185 190
 Ser Ala Ala Ile Asn Glu His Asp Leu Thr Ala Thr Ala Val Leu Ser
 195 200 205
 Gly Asn Arg Asn Phe Glu Gly Arg Ile Ser Pro Asp Val Lys Met Asn
 210 215 220
 Tyr Leu Ala Ser Pro Ile Met Val Ile Ala Tyr Ala Ile Ala Gly Thr
 225 230 235 240
 Met Asp Phe Asp Phe Glu Asn Glu Ala Leu Gly Gln Asp Gln Asp Gly
 245 250 255
 Asn Asp Val Phe Leu Lys Asp Ile Trp Pro Ser Thr Glu Glu Ile Glu
 260 265 270

Asp Thr Ile Gln Gln Ala Ile Ser Arg Glu Leu Tyr Glu Ala Asp Tyr
 275 280 285
 Ala Asp Val Phe Lys Gly Asp Lys Gln Trp Gln Glu Leu Asp Val Pro
 290 295 300
 Thr Gly Asp Thr Phe Glu Trp Asp Glu Asn Ser Thr Tyr Ile Arg Lys
 305 310 315 320
 Ala Pro Tyr Phe Asp Gly Met Pro Val Glu Pro Val Ala Val Thr Asp
 325 330 335
 Ile Gln Gly Ala Arg Val Leu Ala Lys Leu Gly Asp Ser Val Thr Thr
 340 345 350
 Asp His Ile Ser Pro Ala Ser Ser Ile Lys Pro Gly Thr Pro Ala Ala
 355 360 365
 Gln Tyr Leu Asp Glu His Gly Val Glu Arg His Asp Tyr Asn Ser Leu
 370 375 380
 Gly Ser Arg Arg Gly Asn His Glu Val Met Met Arg Gly Thr Phe Ala
 385 390 395 400
 Asn Ile Arg Leu Gln Asn Gln Leu Val Asp Ile Ala Gly Gly Tyr Thr
 405 410 415
 Arg Asp Phe Thr Gln Glu Gly Ala Pro Gln Ala Phe Ile Tyr Asp Ala
 420 425 430
 Ser Val Asn Tyr Lys Ala Ala Gly Ile Pro Leu Val Val Leu Gly Gly
 435 440 445
 Lys Glu Tyr Gly Thr Gly Ser Ser Arg Asp Trp Ala Ala Lys Gly Thr
 450 455 460
 Asn Leu Leu Gly Ile Arg Ala Val Ile Thr Glu Ser Phe Glu Arg Ile
 465 470 475 480
 His Arg Ser Asn Leu Ile Gly Met Gly Val Val Pro Leu Gln Phe Pro
 485 490 495
 Ala Gly Glu Ser His Glu Ser Leu Gly Leu Asp Gly Thr Glu Thr Phe
 500 505 510
 Asp Ile Thr Gly Leu Thr Ala Leu Asn Glu Gly Glu Thr Pro Lys Thr
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 Ala Ile Cys Pro His Arg His Pro Arg
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<210> 557

<211> 874

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS
 <222> (101)..(874)
 <223> RXN02213

<400> 557

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                               Val Thr Glu Ser Lys
                               1      5

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Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
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Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
                25                30                35

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Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
                40                45                50

aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
                55                60                65

tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
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Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
                90                95                100

gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg 451
Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
                105                110                115

aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc 499
Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
                120                125                130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc 547
Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
                135                140                145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc 595
Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
                150                155                160                165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac 643
Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
                170                175                180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac 691
Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
                185                190                195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc 739
Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly

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200										205										210										
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Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala																														
215 220 225																														
atg ctc ggc cag cca gtg tcc atg ctg atc cct cgc gtt gtt ggc ttc	835																													
Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro Arg Val Val Gly Phe																														
230 235 240 245																														
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Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr Ala Thr																														
250 255																														

<210> 558

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<212> PRT

<213> Corynebacterium glutamicum

<400> 558

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Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
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Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
115 120 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
145 150 155 160

Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
165 170 175

Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
180 185 190

Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
195 200 205

Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile

210	215	220
Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile Pro		
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Arg Val Val Gly Phe Lys Leu Thr Gly Glu Ile Pro Val Gly Val Thr		
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Ala Thr

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 Val Thr Glu Ser Lys
 1 5
 aac tcc ttc aat gct aag agc acc ctt gaa gtt ggc gac aag tcc tat 163
 Asn Ser Phe Asn Ala Lys Ser Thr Leu Glu Val Gly Asp Lys Ser Tyr
 10 15 20
 gac tac ttc gcc ctc tct gca gtg cct ggc atg gag aag ctg ccg tac 211
 Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met Glu Lys Leu Pro Tyr
 25 30 35
 tcc ctc aag gtt ctc gga gag aac ctt ctt cgt acc gaa gac ggc gca 259
 Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg Thr Glu Asp Gly Ala
 40 45 50
 aac atc acc aac gag cac att gag gct atc gcc aac tgg gat gca tct 307
 Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala Asn Trp Asp Ala Ser
 55 60 65
 tcc gat cca agc atc gaa atc cag ttc acc cca gcc cgt gtt ctc atg 355
 Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro Ala Arg Val Leu Met
 70 75 80 85
 cag gac ttc acc ggt gtc cct tgt gta gtt gac ctc gca acc atg cgt 403
 Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp Leu Ala Thr Met Arg
 90 95 100
 gag gca gtt gct gca ctc ggt ggc gac cct aac gac gtc aac cca ctg 451
 Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn Asp Val Asn Pro Leu
 105 110 115
 aac cca gcc gag atg gtc att gac cac tcc gtc atc gtg gag gct ttc 499
 Asn Pro Ala Glu Met Val Ile Asp His Ser Val Ile Val Glu Ala Phe
 120 125 130

ggc cgc cca gat gca ctg gct aag aac gtt gag atc gag tac gag cgc 547
 Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu Ile Glu Tyr Glu Arg
 135 140 145

aac gag gag cgt tac cag ttc ctg cgt tgg ggt tcc gag tcc ttc tcc 595
 Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly Ser Glu Ser Phe Ser
 150 155 160 165

aac ttc cgc gtt gtt cct cca gga acc ggt atc gtc cac cag gtc aac 643
 Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile Val His Gln Val Asn
 170 175 180

att gag tac ttg gct cgc gtc gtc ttc gac aac gag ggc ctt gca tac 691
 Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn Glu Gly Leu Ala Tyr
 185 190 195

cca gat acc tgc atc ggt acc gac tcc cac acc acc atg gaa aac ggc 739
 Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr Thr Met Glu Asn Gly
 200 205 210

ctg ggc atc ctg ggc tgg ggc gtt ggt ggc att gag gct gaa gca gca 787
 Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile Glu Ala Glu Ala Ala
 215 220 225

atg ctc ggc cag cca gtg tcc atg ctg atc 817
 Met Leu Gly Gln Pro Val Ser Met Leu Ile
 230 235

<210> 560

<211> 239

<212> PRT

<213> Corynebacterium glutamicum

<400> 560

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Gly Asp Lys Ser Tyr Asp Tyr Phe Ala Leu Ser Ala Val Pro Gly Met
 20 25 30

Glu Lys Leu Pro Tyr Ser Leu Lys Val Leu Gly Glu Asn Leu Leu Arg
 35 40 45

Thr Glu Asp Gly Ala Asn Ile Thr Asn Glu His Ile Glu Ala Ile Ala
 50 55 60

Asn Trp Asp Ala Ser Ser Asp Pro Ser Ile Glu Ile Gln Phe Thr Pro
 65 70 75 80

Ala Arg Val Leu Met Gln Asp Phe Thr Gly Val Pro Cys Val Val Asp
 85 90 95

Leu Ala Thr Met Arg Glu Ala Val Ala Ala Leu Gly Gly Asp Pro Asn
 100 105 110

Asp Val Asn Pro Leu Asn Pro Ala Glu Met Val Ile Asp His Ser Val
 115 120 125

Ile Val Glu Ala Phe Gly Arg Pro Asp Ala Leu Ala Lys Asn Val Glu
 130 135 140

Ile Glu Tyr Glu Arg Asn Glu Glu Arg Tyr Gln Phe Leu Arg Trp Gly
 145 150 155 160
 Ser Glu Ser Phe Ser Asn Phe Arg Val Val Pro Pro Gly Thr Gly Ile
 165 170 175
 Val His Gln Val Asn Ile Glu Tyr Leu Ala Arg Val Val Phe Asp Asn
 180 185 190
 Glu Gly Leu Ala Tyr Pro Asp Thr Cys Ile Gly Thr Asp Ser His Thr
 195 200 205
 Thr Met Glu Asn Gly Leu Gly Ile Leu Gly Trp Gly Val Gly Gly Ile
 210 215 220
 Glu Ala Glu Ala Ala Met Leu Gly Gln Pro Val Ser Met Leu Ile
 225 230 235

<210> 561
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (1)..(2868)
 <223> RXA02056

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 gtc ggt tcc atg gat tac cca gca gag ttc cag ggc gct tca gaa gac 96
 Val Gly Ser Met Asp Tyr Pro Ala Glu Phe Gln Gly Ala Ser Glu Asp
 20 25 30
 cgc ctt gca gag ctc ggc gtt ggc aaa ctt gtc acc atc acc tcc acc 144
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
 35 40 45
 tac gat cac cgc gtg atc cag ggt gct gtg tcc ggt gaa ttc ctg cgc 192
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
 50 55 60
 acc atg tct cgc ctg ctc acc gat gat tcc ttc tgg gat gag atc ttc 240
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
 65 70 75 80
 gac gca atg aac gtt cct tac acc cca atg cgt tgg gca cag gac gtt 288
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
 85 90 95
 cca aac acc ggt gtt gat aag aac acc cgc gtc atg cag ctc att gag 336
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
 100 105 110
 gca tac cgc tcc cgt gga cac ctc atc gct gac acc aac cca ctt tca 384
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser

115	120	125	
tgg gtt cag cct ggc atg cca gtt cca gac cac cgc gac ctc gac atc Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile 130 135 140			432
gag acc cac aac ctg acc atc tgg gat ctg gac cgt acc ttc aac gtc Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val 145 150 155 160			480
ggg ggc ttc ggc ggc aag gag acc atg acc ctg cgc gag gta ctg tcc Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser 165 170 175			528
cgc ctc cgc gct gcg tac acc ctc aag gtc ggc tcc gaa tac acc cac Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His 180 185 190			576
atc ctg gac cgc gac gag cgc acc tgg ctg cag gac cgc ctc gag gcc Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala 195 200 205			624
gga atg cca aag cca acc cag gca gag cag aag tac atc ctg cag aag Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys 210 215 220			672
ctg aac gcc gcg gag gct ttc gag aac ttc ctg cag acc aag tac gtc Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val 225 230 235 240			720
ggc cag aag cgc ttc tcc ctc gaa ggt gca gaa gca ctt atc cca ctg Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu 245 250 255			768
atg gac tcc gcc atc gac acc gcc gca ggc caa ggc ctc gac gaa gtt Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val 260 265 270			816
gtc atc ggt atg cca cac cgt ggt cgc ctc aac gtg ctg ttc aac atc Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile 275 280 285			864
gtg ggc aag cca ctg gca tcc atc ttc aac gag ttt gaa ggc caa atg Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met 290 295 300			912
gag cag ggc cag atc ggt ggc tcc ggt gac gtg aag tac cac ctc ggt Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly 305 310 315 320			960
tcc gaa ggc cag cac ctg cag atg ttc ggc gac ggc gag atc aag gtc Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val 325 330 335			1008
tcc ctg act gct aac ccg tcc cac ctg gaa gct gtt aac cca gcg atg Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met 340 345 350			1056
gaa ggt att gtc cgc gca aag cag gac tac ctg gac aag ggc gta gac Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp 355 360 365			1104

ggc aag act gtt gtg cca ctg ctg ctc cac ggt gac gct gca ttc gca	1152
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala	
370 375 380	
ggc ctg ggc atc gtg cca gaa acc atc aac ctg gct aag ctg cgt ggc	1200
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly	
385 390 395 400	
tac gac gtc ggc ggc acc atc cac atc gtg gtg aac aac cag atc ggc	1248
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly	
405 410 415	
ttc acc acc acc cca gac tcc agc cgc tcc atg cac tac gca acc gac	1296
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp	
420 425 430	
tac gcc aag gca ttc ggc tgc cca gtc ttc cac gtc aac ggc gac gac	1344
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp	
435 440 445	
cca gag gca gtt gtc tgg gtt ggc cag ctg gcc acc gag tac cgt cgt	1392
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg	
450 455 460	
cgc ttc ggc aag gac gtc ttc atc gac ctc gtc tgc tac cgc ctc cgc	1440
Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg	
465 470 475 480	
ggc cac aac gaa gct gat gat cct tcc atg acc cag cca aag atg tat	1488
Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr	
485 490 495	
gag ctc atc acc ggc cgc gag acc gtt cgt gct cag tac acc gaa gac	1536
Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp	
500 505 510	
ctg ctc gga cgt gga gac ctc tcc aac gaa gat gca gaa gca gtc gtc	1584
Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val	
515 520 525	
cgc gac ttc cac gac cag atg gaa tct gtg ttc aac gaa gtc aag gaa	1632
Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu	
530 535 540	
ggc ggc aag aag cag gct gag gca cag acc ggc atc acc ggc tcc cag	1680
Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln	
545 550 555 560	
aag ctt cca cac ggc ctt gag acc aac atc tcc cgt gaa gag ctc ctg	1728
Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu	
565 570 575	
gaa ctg gga cag gct ttc gcc aac acc cca gaa ggc ttc aac tac cac	1776
Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His	
580 585 590	
cca cgt gtg gct ccc gtt gct aag aag cgc gtc tcc tct gtc acc gaa	1824
Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu	
595 600 605	

ggt ggc atc gac tgg gca tgg ggc gag ctc ctc gcc ttc ggt tcc ctg Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu 610 615 620	1872
gct aac tcc ggc cgc ttg gtt cgc ctt gca ggt gaa gat tcc cgc cgc Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg 625 630 635 640	1920
ggt acc ttc acc cag cgc cac gca gtt gcc atc gac cca gcg acc gct Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala 645 650 655	1968
gaa gag ttc aac cca ctc cac gag ctt gca cag tcc aag ggc aac aac Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn 660 665 670	2016
ggt aag ttc ctg gtc tac aac tcc gca ctg acc gag tac gca ggc atg Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met 675 680 685	2064
ggc ttc gag tac ggc tac tcc gta gga aac gaa gag tcc atc gtt gca Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala 690 695 700	2112
tgg gaa gca cag ttc ggc gac ttc gcc aac ggc gct cag acc atc atc Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile 705 710 715 720	2160
gat gag tac gtc tcc tca ggc gaa gct aag tgg ggc cag acc tcc aag Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys 725 730 735	2208
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tct tcc gca cgt atc gag cgc ttc ctg cag ctg tgc gct gag ggt tcc Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser 755 760 765	2304
atg act gtt gct cag cca tcc acc cca gca aac cac ttc cac cta ctg Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu 770 775 780	2352
cgt cgt cac gct ctg tcc gac ctg aag cgt cca ctg gtt atc ttc acc Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr 785 790 795 800	2400
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tac tac gaa ttg gca aag cgc aag gag aag gac gga cgc gac gac atc	2592

Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
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 gcg atc gtt cgt atc gaa atg ctc cac cca att ccg ttc aac cgc atc 2640
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
 865 870 875 880
 tcc gag gct ctt gcc ggc tac cct aac gct gag gaa gtc ctc ttc gtt 2688
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
 885 890 895
 cag gat gag cca gca aac cag ggc cca tgg ccg ttc tac cag gag cac 2736
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
 900 905 910
 ctc cca gag ctg atc ccg aac atg cca aag atg cgc cgc gtt tcc cgc 2784
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
 915 920 925
 cgc gct cag tcc tcc acc gca act ggt gtt gcc aag gtg cac cag ctg 2832
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
 930 935 940
 gag gag aag cag ctt atc gac gag gct ttc gag gct taagtcttta 2878
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<210> 562

<211> 956

<212> PRT

<213> Corynebacterium glutamicum

<400> 562

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 20 25 30
 Arg Leu Ala Glu Leu Gly Val Gly Lys Leu Val Thr Ile Thr Ser Thr
 35 40 45
 Tyr Asp His Arg Val Ile Gln Gly Ala Val Ser Gly Glu Phe Leu Arg
 50 55 60
 Thr Met Ser Arg Leu Leu Thr Asp Asp Ser Phe Trp Asp Glu Ile Phe
 65 70 75 80
 Asp Ala Met Asn Val Pro Tyr Thr Pro Met Arg Trp Ala Gln Asp Val
 85 90 95
 Pro Asn Thr Gly Val Asp Lys Asn Thr Arg Val Met Gln Leu Ile Glu
 100 105 110
 Ala Tyr Arg Ser Arg Gly His Leu Ile Ala Asp Thr Asn Pro Leu Ser
 115 120 125
 Trp Val Gln Pro Gly Met Pro Val Pro Asp His Arg Asp Leu Asp Ile

130	135	140
Glu Thr His Asn Leu Thr Ile Trp Asp Leu Asp Arg Thr Phe Asn Val 145 150 155 160		
Gly Gly Phe Gly Gly Lys Glu Thr Met Thr Leu Arg Glu Val Leu Ser 165 170 175		
Arg Leu Arg Ala Ala Tyr Thr Leu Lys Val Gly Ser Glu Tyr Thr His 180 185 190		
Ile Leu Asp Arg Asp Glu Arg Thr Trp Leu Gln Asp Arg Leu Glu Ala 195 200 205		
Gly Met Pro Lys Pro Thr Gln Ala Glu Gln Lys Tyr Ile Leu Gln Lys 210 215 220		
Leu Asn Ala Ala Glu Ala Phe Glu Asn Phe Leu Gln Thr Lys Tyr Val 225 230 235 240		
Gly Gln Lys Arg Phe Ser Leu Glu Gly Ala Glu Ala Leu Ile Pro Leu 245 250 255		
Met Asp Ser Ala Ile Asp Thr Ala Ala Gly Gln Gly Leu Asp Glu Val 260 265 270		
Val Ile Gly Met Pro His Arg Gly Arg Leu Asn Val Leu Phe Asn Ile 275 280 285		
Val Gly Lys Pro Leu Ala Ser Ile Phe Asn Glu Phe Glu Gly Gln Met 290 295 300		
Glu Gln Gly Gln Ile Gly Gly Ser Gly Asp Val Lys Tyr His Leu Gly 305 310 315 320		
Ser Glu Gly Gln His Leu Gln Met Phe Gly Asp Gly Glu Ile Lys Val 325 330 335		
Ser Leu Thr Ala Asn Pro Ser His Leu Glu Ala Val Asn Pro Ala Met 340 345 350		
Glu Gly Ile Val Arg Ala Lys Gln Asp Tyr Leu Asp Lys Gly Val Asp 355 360 365		
Gly Lys Thr Val Val Pro Leu Leu Leu His Gly Asp Ala Ala Phe Ala 370 375 380		
Gly Leu Gly Ile Val Pro Glu Thr Ile Asn Leu Ala Lys Leu Arg Gly 385 390 395 400		
Tyr Asp Val Gly Gly Thr Ile His Ile Val Val Asn Asn Gln Ile Gly 405 410 415		
Phe Thr Thr Thr Pro Asp Ser Ser Arg Ser Met His Tyr Ala Thr Asp 420 425 430		
Tyr Ala Lys Ala Phe Gly Cys Pro Val Phe His Val Asn Gly Asp Asp 435 440 445		
Pro Glu Ala Val Val Trp Val Gly Gln Leu Ala Thr Glu Tyr Arg Arg 450 455 460		

Arg Phe Gly Lys Asp Val Phe Ile Asp Leu Val Cys Tyr Arg Leu Arg
 465 470 475 480
 Gly His Asn Glu Ala Asp Asp Pro Ser Met Thr Gln Pro Lys Met Tyr
 485 490 495
 Glu Leu Ile Thr Gly Arg Glu Thr Val Arg Ala Gln Tyr Thr Glu Asp
 500 505 510
 Leu Leu Gly Arg Gly Asp Leu Ser Asn Glu Asp Ala Glu Ala Val Val
 515 520 525
 Arg Asp Phe His Asp Gln Met Glu Ser Val Phe Asn Glu Val Lys Glu
 530 535 540
 Gly Gly Lys Lys Gln Ala Glu Ala Gln Thr Gly Ile Thr Gly Ser Gln
 545 550 555 560
 Lys Leu Pro His Gly Leu Glu Thr Asn Ile Ser Arg Glu Glu Leu Leu
 565 570 575
 Glu Leu Gly Gln Ala Phe Ala Asn Thr Pro Glu Gly Phe Asn Tyr His
 580 585 590
 Pro Arg Val Ala Pro Val Ala Lys Lys Arg Val Ser Ser Val Thr Glu
 595 600 605
 Gly Gly Ile Asp Trp Ala Trp Gly Glu Leu Leu Ala Phe Gly Ser Leu
 610 615 620
 Ala Asn Ser Gly Arg Leu Val Arg Leu Ala Gly Glu Asp Ser Arg Arg
 625 630 635 640
 Gly Thr Phe Thr Gln Arg His Ala Val Ala Ile Asp Pro Ala Thr Ala
 645 650 655
 Glu Glu Phe Asn Pro Leu His Glu Leu Ala Gln Ser Lys Gly Asn Asn
 660 665 670
 Gly Lys Phe Leu Val Tyr Asn Ser Ala Leu Thr Glu Tyr Ala Gly Met
 675 680 685
 Gly Phe Glu Tyr Gly Tyr Ser Val Gly Asn Glu Asp Ser Ile Val Ala
 690 695 700
 Trp Glu Ala Gln Phe Gly Asp Phe Ala Asn Gly Ala Gln Thr Ile Ile
 705 710 715 720
 Asp Glu Tyr Val Ser Ser Gly Glu Ala Lys Trp Gly Gln Thr Ser Lys
 725 730 735
 Leu Ile Leu Leu Leu Pro His Gly Tyr Glu Gly Gln Gly Pro Asp His
 740 745 750
 Ser Ser Ala Arg Ile Glu Arg Phe Leu Gln Leu Cys Ala Glu Gly Ser
 755 760 765
 Met Thr Val Ala Gln Pro Ser Thr Pro Ala Asn His Phe His Leu Leu
 770 775 780

Arg Arg His Ala Leu Ser Asp Leu Lys Arg Pro Leu Val Ile Phe Thr
 785 790 795 800
 Pro Lys Ser Met Leu Arg Asn Lys Ala Ala Ala Ser Ala Pro Glu Asp
 805 810 815
 Phe Thr Glu Val Thr Lys Phe Gln Ser Val Ile Asn Asp Pro Asn Val
 820 825 830
 Ala Asp Ala Ala Lys Val Lys Lys Val Met Leu Val Ser Gly Lys Leu
 835 840 845
 Tyr Tyr Glu Leu Ala Lys Arg Lys Glu Lys Asp Gly Arg Asp Asp Ile
 850 855 860
 Ala Ile Val Arg Ile Glu Met Leu His Pro Ile Pro Phe Asn Arg Ile
 865 870 875 880
 Ser Glu Ala Leu Ala Gly Tyr Pro Asn Ala Glu Glu Val Leu Phe Val
 885 890 895
 Gln Asp Glu Pro Ala Asn Gln Gly Pro Trp Pro Phe Tyr Gln Glu His
 900 905 910
 Leu Pro Glu Leu Ile Pro Asn Met Pro Lys Met Arg Arg Val Ser Arg
 915 920 925
 Arg Ala Gln Ser Ser Thr Ala Thr Gly Val Ala Lys Val His Gln Leu
 930 935 940
 Glu Glu Lys Gln Leu Ile Asp Glu Ala Phe Glu Ala
 945 950 955

<210> 563
 <211> 1517
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(1494)
 <223> RXA01745

<400> 563
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 Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly Ala Val Ile Ala
 1 5 10 15
 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala
 20 25 30
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60

atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg	240
Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp	
65 70 75 80	
ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag	288
Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu	
85 90 95	
gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc	336
Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly	
100 105 110	
acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc	384
Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly	
115 120 125	
gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc	432
Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala	
130 135 140	
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag	480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu	
145 150 155 160	
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct	528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala	
165 170 175	
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac	576
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn	
180 185 190	
gtt cca tac gtc acc cca ctg gtg cgc aag ctt gct gaa aag cac ggc	624
Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly	
195 200 205	
gtt gac ttg aac acc gtg acc ggt acc ggt atc ggt ggc cgt atc cgc	672
Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg	
210 215 220	
aag cag gat gtt ttg gct gct gcg aac ggc gag gct gca cct gct gag	720
Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu	
225 230 235 240	
gct gct gct cct gtt tcc gct tgg tcc act aag tct gtt gac cct gag	768
Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu	
245 250 255	
aag gct aag ctc cgt ggt acc act cag aag gtc aac cgc atc cgt gag	816
Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu	
260 265 270	
atc acc gcg atg aag acc gtc gag gct ctg cag att tct gct cag ctc	864
Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu	
275 280 285	
acc cag ctg cac gag gtc gat atg act cgc gtt gct gag ctg cgt aag	912
Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys	
290 295 300	
aag aac aag ccc gcg ttc atc gag aag cac ggt gtg aac ctc act tac	960

Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
 305 310 315 320
 ctg cca ttc ttc gtg aag gca gtt gtc gag gct ttg gtt tcc cat cca 1008
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
 325 330 335
 aac gtc aac gcg tct ttc aac gcg aag acc aag gag atg acc tac cac 1056
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His
 340 345 350
 tcc tcc gtt aac ctc tcc atc gct gtt gat acc cca gct ggt ctg ttg 1104
 Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu
 355 360 365
 acc cca gtc att cac gat gct cag gat ctc tcc atc cca gag atc gca 1152
 Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala
 370 375 380
 aag gca att gtt gac ctg gct gat cgt tca cgc aac aac aag ctg aag 1200
 Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys
 385 390 395 400
 cca aac gat ctg tcc ggt ggc acc ttc acc atc acc aac att ggt tct 1248
 Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser
 405 410 415
 gaa ggc gca ctg tct gat acc cca atc ctg gtt cca cca cag gct ggc 1296
 Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly
 420 425 430
 atc ttg ggc acc ggc gcg atc gtg aag cgt cca gtt gtc atc acc gag 1344
 Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu
 435 440 445
 gat gga att gat tcc atc gcg atc cgt cag atg gtc ttc cta cca ctg 1392
 Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu
 450 455 460
 acc tac gac cac cag gtt gta gat ggc gca gat gct ggt cgc ttc ctg 1440
 Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu
 465 470 475 480
 acc acc atc aag gac cgc ctt gag acc gct aac ttc gaa ggc gat ctg 1488
 Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu
 485 490 495
 cag ctc taagatctct gcaagttaaa acc 1517
 Gln Leu

<210> 564

<211> 498

<212> PRT

<213> Corynebacterium glutamicum

<400> 564

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 20 25 30
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
 130 135 140
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190
 Val Pro Tyr Val Thr Pro Leu Val Arg Lys Leu Ala Glu Lys His Gly
 195 200 205
 Val Asp Leu Asn Thr Val Thr Gly Thr Gly Ile Gly Gly Arg Ile Arg
 210 215 220
 Lys Gln Asp Val Leu Ala Ala Ala Asn Gly Glu Ala Ala Pro Ala Glu
 225 230 235 240
 Ala Ala Ala Pro Val Ser Ala Trp Ser Thr Lys Ser Val Asp Pro Glu
 245 250 255
 Lys Ala Lys Leu Arg Gly Thr Thr Gln Lys Val Asn Arg Ile Arg Glu
 260 265 270
 Ile Thr Ala Met Lys Thr Val Glu Ala Leu Gln Ile Ser Ala Gln Leu
 275 280 285
 Thr Gln Leu His Glu Val Asp Met Thr Arg Val Ala Glu Leu Arg Lys
 290 295 300
 Lys Asn Lys Pro Ala Phe Ile Glu Lys His Gly Val Asn Leu Thr Tyr
 305 310 315 320
 Leu Pro Phe Phe Val Lys Ala Val Val Glu Ala Leu Val Ser His Pro
 325 330 335
 Asn Val Asn Ala Ser Phe Asn Ala Lys Thr Lys Glu Met Thr Tyr His

340	345	350
Ser Ser Val Asn Leu Ser Ile Ala Val Asp Thr Pro Ala Gly Leu Leu		
355	360	365
Thr Pro Val Ile His Asp Ala Gln Asp Leu Ser Ile Pro Glu Ile Ala		
370	375	380
Lys Ala Ile Val Asp Leu Ala Asp Arg Ser Arg Asn Asn Lys Leu Lys		
385	390	400
Pro Asn Asp Leu Ser Gly Gly Thr Phe Thr Ile Thr Asn Ile Gly Ser		
405	410	415
Glu Gly Ala Leu Ser Asp Thr Pro Ile Leu Val Pro Pro Gln Ala Gly		
420	425	430
Ile Leu Gly Thr Gly Ala Ile Val Lys Arg Pro Val Val Ile Thr Glu		
435	440	445
Asp Gly Ile Asp Ser Ile Ala Ile Arg Gln Met Val Phe Leu Pro Leu		
450	455	460
Thr Tyr Asp His Gln Val Val Asp Gly Ala Asp Ala Gly Arg Phe Leu		
465	470	475
Thr Thr Ile Lys Asp Arg Leu Glu Thr Ala Asn Phe Glu Gly Asp Leu		
485	490	495

Gln Leu

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 <211> 1005
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(982)
 <223> RXA00782

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 Met Ser Ile Phe Leu
 1 5
 aat tca gat tcc cgc atc atc att cag ggc att acc ggt tcg gaa ggt 163
 Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile Thr Gly Ser Glu Gly
 10 15 20
 tca gag cat gcg cgt cga att tta gcc tct ggt gcg aag ctc gtg ggt 211
 Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly Ala Lys Leu Val Gly
 25 30 35
 ggc acc aac ccc cgc aaa gct ggg caa acc att ttg atc aat gac act 259
 Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile Leu Ile Asn Asp Thr
 40 45 50

gag ttg cct gta ttt ggc act gtt aag gaa gca atg gag gaa acg ggt	307
Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala Met Glu Glu Thr Gly	
55 60 65	
gcg gat gtc acc gta att ttc gtt cct cca gcc ttt gcc aaa gct gcg	355
Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala Phe Ala Lys Ala Ala	
70 75 80 85	
atc att gaa gct atc gac gct cac atc cca ctg tgc gtg att att act	403
Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu Cys Val Ile Ile Thr	
90 95 100	
gag ggc atc cca gtg cgt gac gct tct gag gcg tgg gct tat gcc aag	451
Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala Trp Ala Tyr Ala Lys	
105 110 115	
aag gtg gga cac acc cgc atc att ggc cct aac tgc cca gcc att att	499
Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn Cys Pro Gly Ile Ile	
120 125 130	
act ccc ggc gaa tct ctt gcg gga att acg ccg gca aac att gca ggt	547
Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro Ala Asn Ile Ala Gly	
135 140 145	
tcc ggc ccg atc ggg ttg atc tca aag tcg gga aca ctg act tat cag	595
Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly Thr Leu Thr Tyr Gln	
150 155 160 165	
atg atg tac gaa ctt tca gat att ggc att tct acg gcg att ggt att	643
Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser Thr Ala Ile Gly Ile	
170 175 180	
ggc ggt gac cca atc atc ggt aca acc cat atc gac gct ctg gag gcc	691
Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile Asp Ala Leu Glu Ala	
185 190 195	
ttt gaa gct gat cct gag acc aag gca atc gtc atg atc ggt gag atc	739
Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val Met Ile Gly Glu Ile	
200 205 210	
ggt gga gat gca gag gaa cgc gct gct gac ttc att tct aag cac gtg	787
Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe Ile Ser Lys His Val	
215 220 225	
aca aaa cca gtt gtg ggt tac gtg gca ggc ttt acc gcc cct gaa gga	835
Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe Thr Ala Pro Glu Gly	
230 235 240 245	
aag acc atg ggg cat gct ggc gcc atc gtg aca ggt tca gaa ggc act	883
Lys Thr Met Gly His Ala Gly Ala Ile Val Thr Gly Ser Glu Gly Thr	
250 255 260	
gcg cga gca aag aag cat gca ttg gag gcc gtg ggt gtt cgc gtg gga	931
Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val Gly Val Arg Val Gly	
265 270 275	
aca act ccg agt gaa acc gcg aag ctt atg cgt gag gta gtt gca gct	979
Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg Glu Val Val Ala Ala	
280 285 290	

ttg taactaacag gccacagatc tta
Leu

1005

<210> 566
<211> 294
<212> PRT
<213> Corynebacterium glutamicum

<400> 566
Met Ser Ile Phe Leu Asn Ser Asp Ser Arg Ile Ile Ile Gln Gly Ile
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Thr Gly Ser Glu Gly Ser Glu His Ala Arg Arg Ile Leu Ala Ser Gly
20 25 30
Ala Lys Leu Val Gly Gly Thr Asn Pro Arg Lys Ala Gly Gln Thr Ile
35 40 45
Leu Ile Asn Asp Thr Glu Leu Pro Val Phe Gly Thr Val Lys Glu Ala
50 55 60
Met Glu Glu Thr Gly Ala Asp Val Thr Val Ile Phe Val Pro Pro Ala
65 70 75 80
Phe Ala Lys Ala Ala Ile Ile Glu Ala Ile Asp Ala His Ile Pro Leu
85 90 95
Cys Val Ile Ile Thr Glu Gly Ile Pro Val Arg Asp Ala Ser Glu Ala
100 105 110
Trp Ala Tyr Ala Lys Lys Val Gly His Thr Arg Ile Ile Gly Pro Asn
115 120 125
Cys Pro Gly Ile Ile Thr Pro Gly Glu Ser Leu Ala Gly Ile Thr Pro
130 135 140
Ala Asn Ile Ala Gly Ser Gly Pro Ile Gly Leu Ile Ser Lys Ser Gly
145 150 155 160
Thr Leu Thr Tyr Gln Met Met Tyr Glu Leu Ser Asp Ile Gly Ile Ser
165 170 175
Thr Ala Ile Gly Ile Gly Gly Asp Pro Ile Ile Gly Thr Thr His Ile
180 185 190
Asp Ala Leu Glu Ala Phe Glu Ala Asp Pro Glu Thr Lys Ala Ile Val
195 200 205
Met Ile Gly Glu Ile Gly Gly Asp Ala Glu Glu Arg Ala Ala Asp Phe
210 215 220
Ile Ser Lys His Val Thr Lys Pro Val Val Gly Tyr Val Ala Gly Phe
225 230 235 240
Thr Ala Pro Glu Gly Lys Thr Met Gly His Ala Gly Ala Ile Val Thr
245 250 255
Gly Ser Glu Gly Thr Ala Arg Ala Lys Lys His Ala Leu Glu Ala Val
260 265 270

Gly Val Arg Val Gly Thr Thr Pro Ser Glu Thr Ala Lys Leu Met Arg
 275 280 285

Glu Val Val Ala Ala Leu
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<210> 567
 <211> 1395
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1372)
 <223> RXA00783

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 Leu Lys His Leu Leu
 1 5
 tta cgg gaa gac ttt gtt aaa gac gca gaa ggc tct aag cat ggg ccg 163
 Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly Ser Lys His Gly Pro
 10 15 20
 gaa atg gaa ttg gca gtg gat ctt ttt gaa tac caa gca cgg gac ctc 211
 Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr Gln Ala Arg Asp Leu
 25 30 35
 ttt gaa acc cat ggt gtg cca gtg ttg aag gga att gtg gca tca aca 259
 Phe Glu Thr His Gly Val Pro Val Leu Lys Gly Ile Val Ala Ser Thr
 40 45 50
 cca gag gcg gcg agg aaa gcg gct gag gaa atc ggc gga ctg acc gtc 307
 Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile Gly Gly Leu Thr Val
 55 60 65
 gtc aag gct cag gtc aag gtg ggc gga cgt ggc aag gcg ggt ggc gtc 355
 Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly Lys Ala Gly Gly Val
 70 75 80 85
 cgt gtg gca ccg acg tcg gct cag gct ttt gat gct gcg gat gcg att 403
 Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp Ala Ala Asp Ala Ile
 90 95 100
 ctc ggc atg gat atc aaa gga cac act gtt aat cag gtg atg gtg gcg 451
 Leu Gly Met Asp Ile Lys Gly His Thr Val Asn Gln Val Met Val Ala
 105 110 115
 cag ggc gct gac att gct gag gaa tac tat ttc tcc att ttg ttg gat 499
 Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe Ser Ile Leu Leu Asp
 120 125 130
 cgc gcg aat cgt tcg tat ctg gct atg tgc tct gtt gaa ggt ggc atg 547
 Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser Val Glu Gly Gly Met
 135 140 145

gag atc gag atc ctg gcg aag gaa aag cct gaa gct ttg gca aag gtg Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu Ala Leu Ala Lys Val 150 155 160 165	595
gaa gtg gat ccc ctc act ggt att gat gag gac aaa gcg cgg gag att Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp Lys Ala Arg Glu Ile 170 175 180	643
gtc act gct gct ggc ttt gaa act gag gtg gca gag aaa gtc att ccg Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala Glu Lys Val Ile Pro 185 190 195	691
gtg ctg atc aag atc tgg cag gtg tat tac gaa gag gaa gca aca ctc Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu Glu Glu Ala Thr Leu 200 205 210	739
gtt gag gtg aac ccg ttg gtg ctc acg gat gac ggc gat gtg att gcg Val Glu Val Val Asn Pro Leu Val Leu Thr Asp Asp Gly Asp Val Ile Ala 215 220 225	787
ctt gat ggc aag atc acg ctg gat gat aac gct gat ttc cgc cat gat Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala Asp Phe Arg His Asp 230 235 240 245	835
aac cgt ggt gcg ttg gct gaa tct gcc ggt ggc ttg gac att ttg gaa Asn Arg Gly Ala Leu Ala Glu Ser Ala Gly Gly Leu Asp Ile Leu Glu 250 255 260	883
ctg aag gcc aag aag aat gat ctg aac tac gtg aaa ctt gat ggc tct Leu Lys Ala Lys Lys Asn Asp Leu Asn Tyr Val Lys Leu Asp Gly Ser 265 270 275	931
gtg ggc atc att ggc aat ggt gca ggt ttg gtg atg tcc acg ttg gat Val Gly Ile Ile Gly Asn Gly Ala Gly Leu Val Met Ser Thr Leu Asp 280 285 290	979
atc gtg gct gca gct ggt gaa cgc cat ggt ggg cag cgc ccc gcg aac Ile Val Ala Ala Ala Gly Glu Arg His Gly Gly Gln Arg Pro Ala Asn 295 300 305	1027
ttc cta gac att ggt ggc gga gca tca gct gaa tcg atg gct gct ggt Phe Leu Asp Ile Gly Gly Gly Ala Ser Ala Glu Ser Met Ala Ala Gly 310 315 320 325	1075
ctc gat gtg atc ctt ggg gat agc cag gta cgc agt gtg ttt gtg aat Leu Asp Val Ile Leu Gly Asp Ser Gln Val Arg Ser Val Phe Val Asn 330 335 340	1123
gtg ttt ggt ggc atc acc gcg tgt gat gtg gtg gca aag gga atc gtt Val Phe Gly Gly Ile Thr Ala Cys Asp Val Val Ala Lys Gly Ile Val 345 350 355	1171
gga gct ttg gat gtg ctc ggc gat caa gca acg aag cct ctt gtg gtg Gly Ala Leu Asp Val Leu Gly Asp Gln Ala Thr Lys Pro Leu Val Val 360 365 370	1219
cgc ctt gat ggc aac aac gtg gtg gaa ggc aga cga atc ctc gcg gaa Arg Leu Asp Gly Asn Asn Val Val Glu Gly Arg Arg Ile Leu Ala Glu 375 380 385	1267
tat aac cac cct ttg gtc acc gtt gtg gag ggt atg gat gca gcg gct	1315

Tyr Asn His Pro Leu Val Thr Val Val Glu Gly Met Asp Ala Ala Ala
 390 395 400 405

gat cac gct gcc cat ttg gcc aat ctt gcc cag cac ggc cag ttc gca 1363
 Asp His Ala Ala His Leu Ala Asn Leu Ala Gln His Gly Gln Phe Ala
 410 415 420

acc gct aat tagttaagga gcacctgttt aat 1395
 Thr Ala Asn

<210> 568

<211> 424

<212> PRT

<213> Corynebacterium glutamicum

<400> 568

Leu Lys His Leu Leu Leu Arg Glu Asp Phe Val Lys Asp Ala Glu Gly
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Ser Lys His Gly Pro Glu Met Glu Leu Ala Val Asp Leu Phe Glu Tyr
 20 25 30

Gln Ala Arg Asp Leu Phe Glu Thr His Gly Val Pro Val Leu Lys Gly
 35 40 45

Ile Val Ala Ser Thr Pro Glu Ala Ala Arg Lys Ala Ala Glu Glu Ile
 50 55 60

Gly Gly Leu Thr Val Val Lys Ala Gln Val Lys Val Gly Gly Arg Gly
 65 70 75 80

Lys Ala Gly Gly Val Arg Val Ala Pro Thr Ser Ala Gln Ala Phe Asp
 85 90 95

Ala Ala Asp Ala Ile Leu Gly Met Asp Ile Lys Gly His Thr Val Asn
 100 105 110

Gln Val Met Val Ala Gln Gly Ala Asp Ile Ala Glu Glu Tyr Tyr Phe
 115 120 125

Ser Ile Leu Leu Asp Arg Ala Asn Arg Ser Tyr Leu Ala Met Cys Ser
 130 135 140

Val Glu Gly Gly Met Glu Ile Glu Ile Leu Ala Lys Glu Lys Pro Glu
 145 150 155 160

Ala Leu Ala Lys Val Glu Val Asp Pro Leu Thr Gly Ile Asp Glu Asp
 165 170 175

Lys Ala Arg Glu Ile Val Thr Ala Ala Gly Phe Glu Thr Glu Val Ala
 180 185 190

Glu Lys Val Ile Pro Val Leu Ile Lys Ile Trp Gln Val Tyr Tyr Glu
 195 200 205

Glu Glu Ala Thr Leu Val Glu Val Asn Pro Leu Val Leu Thr Asp Asp
 210 215 220

Gly Asp Val Ile Ala Leu Asp Gly Lys Ile Thr Leu Asp Asp Asn Ala

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<210> 569
<211> 1623
<212> DNA
<213> Corynebacterium glutamicum
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<220>  
<221> CDS  
<222> (101)..(1600)  
<223> RXN01695
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tgttcggcag agaactcgcg gagataaaaag gaagttgaac atg tca gat tcc ccg 115
                                         Met Ser Asp Ser Pro
                                         1                               5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly
                        10                               15                               20

gcc ggt atc atg agc tcc acg ctg ggt gca atg ctg cgt cag ctg gag 211

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Ala	Gly	Ile	Met	Ser	Ser	Thr	Leu	Gly	Ala	Met	Leu	Arg	Gln	Leu	Glu	
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Pro	Ser	Trp	Thr	Gln	Ile	Val	Phe	Glu	Arg	Leu	Asp	Gly	Pro	Ala	Gln	
		40					45					50				
gag	tcg	tcc	tcc	ccg	tgg	aac	aat	gca	gga	acc	ggc	cac	tct	gct	cta	307
Glu	Ser	Ser	Ser	Pro	Trp	Asn	Asn	Ala	Gly	Thr	Gly	His	Ser	Ala	Leu	
		55				60					65					
tgc	gag	ctg	aac	tac	acc	cca	gag	gtt	aag	ggc	aag	gtt	gaa	att	gcc	355
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala	
		70			75					80					85	
aag	gct	gta	gga	atc	aac	gag	aag	ttc	cag	gtt	tcc	cgt	cag	ttc	tgg	403
Lys	Ala	Val	Gly	Ile	Asn	Glu	Lys	Phe	Gln	Val	Ser	Arg	Gln	Phe	Trp	
				90					95					100		
tct	cac	ctc	gtt	gaa	gag	gga	gtg	ctg	tct	gat	cct	aag	gaa	ttc	atc	451
Ser	His	Leu	Val	Glu	Glu	Gly	Val	Leu	Ser	Asp	Pro	Lys	Glu	Phe	Ile	
			105					110					115			
aac	cct	gtt	cct	cac	gta	tct	ttc	ggc	cag	ggc	gca	gat	cag	gtt	gca	499
Asn	Pro	Val	Pro	His	Val	Ser	Phe	Gly	Gln	Gly	Ala	Asp	Gln	Val	Ala	
		120					125					130				
tac	atc	aag	gct	cgc	tac	gaa	gct	ttg	aag	gat	cac	cca	ctc	ttc	cag	547
Tyr	Ile	Lys	Ala	Arg	Tyr	Glu	Ala	Leu	Lys	Asp	His	Pro	Leu	Phe	Gln	
		135				140					145					
ggc	atg	acc	tac	gct	gac	gat	gaa	gct	acc	ttc	acc	gag	aag	ctg	cct	595
Gly	Met	Thr	Tyr	Ala	Asp	Asp	Glu	Ala	Thr	Phe	Thr	Glu	Lys	Leu	Pro	
		150			155					160					165	
ttg	atg	gca	aag	ggc	cgt	gac	ttc	tct	gat	cca	gta	gca	atc	tct	tgg	643
Leu	Met	Ala	Lys	Gly	Arg	Asp	Phe	Ser	Asp	Pro	Val	Ala	Ile	Ser	Trp	
				170					175					180		
atc	gat	gaa	ggc	acc	gac	atc	aac	tac	ggt	gct	cag	acc	aag	cag	tac	691
Ile	Asp	Glu	Gly	Thr	Asp	Ile	Asn	Tyr	Gly	Ala	Gln	Thr	Lys	Gln	Tyr	
			185					190					195			
ctg	gat	gca	gct	gaa	gtt	gaa	ggc	act	gaa	atc	cgc	tat	ggc	cac	gaa	739
Leu	Asp	Ala	Ala	Glu	Val	Glu	Gly	Thr	Glu	Ile	Arg	Tyr	Gly	His	Glu	
		200					205					210				
gtc	aag	agc	atc	aag	gct	gat	ggc	gca	aag	tgg	atc	gtg	acc	gtc	aag	787
Val	Lys	Ser	Ile	Lys	Ala	Asp	Gly	Ala	Lys	Trp	Ile	Val	Thr	Val	Lys	
		215				220					225					
aac	gta	cac	act	ggc	gac	acc	aag	acc	atc	aag	gca	aac	ttc	gtg	ttc	835
Asn	Val	His	Thr	Gly	Asp	Thr	Lys	Thr	Ile	Lys	Ala	Asn	Phe	Val	Phe	
		230			235					240					245	
gtc	ggc	gca	ggc	gga	tac	gca	ctg	gat	ctg	ctt	cgc	agc	gca	ggc	atc	883
Val	Gly	Ala	Gly	Gly	Tyr	Ala	Leu	Asp	Leu	Leu	Arg	Ser	Ala	Gly	Ile	
				250					255					260		
cca	cag	gtc	aag	ggc	ttc	gct	gga	ttc	cca	gta	tcc	ggc	ctg	tgg	ctt	931
Pro	Gln	Val	Lys	Gly	Phe	Ala	Gly	Phe	Pro	Val	Ser	Gly	Leu	Trp	Leu	

265								270				275								
cgt	tgc	acc	aac	gag	gaa	ctg	atc	gag	cag	cac	gca	gcc	aag	gta	tat	979				
Arg	Cys	Thr	Asn	Glu	Glu	Leu	Ile	Glu	Gln	His	Ala	Ala	Lys	Val	Tyr					
280				285				290												
ggc	aag	gca	tct	gtt	ggc	gct	cct	cca	atg	tct	gtt	cct	cac	ctt	gac	1027				
Gly	Lys	Ala	Ser	Val	Gly	Ala	Pro	Pro	Met	Ser	Val	Pro	His	Leu	Asp					
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acc	cgc	gtt	atc	gag	ggc	gaa	aag	ggc	ctg	ctc	ttt	gga	cct	tac	ggc	1075				
Thr	Arg	Val	Ile	Glu	Gly	Glu	Lys	Gly	Leu	Leu	Phe	Gly	Pro	Tyr	Gly					
310				315				320												
ggc	tgg	acc	cct	aag	ttc	ttg	aag	gaa	ggc	tcc	tac	ctg	gac	ctg	ttc	1123				
Gly	Trp	Thr	Pro	Lys	Phe	Leu	Lys	Glu	Gly	Ser	Tyr	Leu	Asp	Leu	Phe					
330				335				340												
aag	tcc	atc	cgc	cca	gac	aac	att	cct	tcc	tac	ctt	ggc	gtt	gct	gct	1171				
Lys	Ser	Ile	Arg	Pro	Asp	Asn	Ile	Pro	Ser	Tyr	Leu	Gly	Val	Ala	Ala					
345				350				355												
cag	gaa	ttt	gat	ctg	acc	aag	tac	ctt	gtc	act	gaa	gtt	ctc	aag	gac	1219				
Gln	Glu	Phe	Asp	Leu	Thr	Lys	Tyr	Leu	Val	Thr	Glu	Val	Leu	Lys	Asp					
360				365				370												
cag	gac	aag	cgt	atg	gat	gct	ctt	cgc	gag	tac	atg	cca	gag	gca	caa	1267				
Gln	Asp	Lys	Arg	Met	Asp	Ala	Leu	Arg	Glu	Tyr	Met	Pro	Glu	Ala	Gln					
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Asn	Gly	Asp	Trp	Glu	Thr	Ile	Val	Ala	Gly	Gln	Arg	Val	Gln	Val	Ile					
390				395				400												
aag	cct	gca	gga	ttc	cct	aag	ttc	ggc	tcc	ctg	gaa	ttc	ggc	acc	acc	1363				
Lys	Pro	Ala	Gly	Phe	Pro	Lys	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Thr	Thr					
410				415				420												
ttg	atc	aac	aac	tcc	gaa	ggc	acc	atc	gcc	gga	ttg	ctc	ggc	gct	tcc	1411				
Leu	Ile	Asn	Asn	Ser	Glu	Gly	Thr	Ile	Ala	Gly	Leu	Leu	Gly	Ala	Ser					
425				430				435												
cct	gga	gca	tcc	atc	gca	cct	tcc	gca	atg	atc	gag	ctg	ctt	gag	cgt	1459				
Pro	Gly	Ala	Ser	Ile	Ala	Pro	Ser	Ala	Met	Ile	Glu	Leu	Leu	Glu	Arg					
440				445				450												
tgc	ttc	ggc	gac	cgc	atg	atc	gag	tgg	ggc	gac	aag	ctg	aag	gac	atg	1507				
Cys	Phe	Gly	Asp	Arg	Met	Ile	Glu	Trp	Gly	Asp	Lys	Leu	Lys	Asp	Met					
455				460				465												
atc	cct	tcc	tac	ggc	aag	aag	ctt	gct	tcc	gag	cca	gca	ctg	ttt	gag	1555				
Ile	Pro	Ser	Tyr	Gly	Lys	Lys	Leu	Ala	Ser	Glu	Pro	Ala	Leu	Phe	Glu					
470				475				480												
cag	cag	tgg	gca	cgc	acc	cag	aag	acc	ctg	aag	ctt	gag	gaa	gcc		1600				
Gln	Gln	Trp	Ala	Arg	Thr	Gln	Lys	Thr	Leu	Lys	Leu	Glu	Glu	Ala						
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 <213> Corynebacterium glutamicum

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 35 40 45
 Asp Gly Pro Ala Gln Glu Ser Ser Ser Pro Trp Asn Asn Ala Gly Thr
 50 55 60
 Gly His Ser Ala Leu Cys Glu Leu Asn Tyr Thr Pro Glu Val Lys Gly
 65 70 75 80
 Lys Val Glu Ile Ala Lys Ala Val Gly Ile Asn Glu Lys Phe Gln Val
 85 90 95
 Ser Arg Gln Phe Trp Ser His Leu Val Glu Glu Gly Val Leu Ser Asp
 100 105 110
 Pro Lys Glu Phe Ile Asn Pro Val Pro His Val Ser Phe Gly Gln Gly
 115 120 125
 Ala Asp Gln Val Ala Tyr Ile Lys Ala Arg Tyr Glu Ala Leu Lys Asp
 130 135 140
 His Pro Leu Phe Gln Gly Met Thr Tyr Ala Asp Asp Glu Ala Thr Phe
 145 150 155 160
 Thr Glu Lys Leu Pro Leu Met Ala Lys Gly Arg Asp Phe Ser Asp Pro
 165 170 175
 Val Ala Ile Ser Trp Ile Asp Glu Gly Thr Asp Ile Asn Tyr Gly Ala
 180 185 190
 Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile
 195 200 205
 Arg Tyr Gly His Glu Val Lys Ser Ile Lys Ala Asp Gly Ala Lys Trp
 210 215 220
 Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys
 225 230 235 240
 Ala Asn Phe Val Phe Val Gly Ala Gly Gly Tyr Ala Leu Asp Leu Leu
 245 250 255
 Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val
 260 265 270
 Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His
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 Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser

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<212> DNA
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<220>
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<222> (101)..(1039)
<223> FRXA01615
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tgttcggcag agaactcgcg gagataaaag gaagttgaac atg tca gat tcc ccg 115
                                         Met Ser Asp Ser Pro
                                         1                               5

aag aac gca ccg agg att acc gat gag gca gat gta gtt ctc att ggt 163
Lys Asn Ala Pro Arg Ile Thr Asp Glu Ala Asp Val Val Leu Ile Gly

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10								15					20					
gcc	ggt	atc	atg	agc	tcc	acg	ctg	ggt	gca	atg	ctg	cgt	cag	ctg	gag	211		
Ala	Gly	Ile	Met	Ser	Ser	Thr	Leu	Gly	Ala	Met	Leu	Arg	Gln	Leu	Glu			
25								30		35								
cca	agc	tgg	act	cag	atc	gtc	ttc	gag	cgt	ttg	gat	gga	ccg	gca	caa	259		
Pro	Ser	Trp	Thr	Gln	Ile	Val	Phe	Glu	Arg	Leu	Asp	Gly	Pro	Ala	Gln			
40								45		50								
gag	tcg	tcc	tcc	ccg	tgg	aac	aat	gca	gga	acc	ggc	cac	tct	gct	cta	307		
Glu	Ser	Ser	Ser	Pro	Trp	Asn	Asn	Ala	Gly	Thr	Gly	His	Ser	Ala	Leu			
55								60		65								
tgc	gag	ctg	aac	tac	acc	cca	gag	gtt	aag	ggc	aag	ggt	gaa	att	gcc	355		
Cys	Glu	Leu	Asn	Tyr	Thr	Pro	Glu	Val	Lys	Gly	Lys	Val	Glu	Ile	Ala			
70								75		80				85				
aag	gct	gta	gga	atc	aac	gag	aag	ttc	cag	gtt	tcc	cgt	cag	ttc	tgg	403		
Lys	Ala	Val	Gly	Ile	Asn	Glu	Lys	Phe	Gln	Val	Ser	Arg	Gln	Phe	Trp			
				90								100						
tct	cac	ctc	gtt	gaa	gag	gga	gtg	ctg	tct	gat	cct	aag	gaa	ttc	atc	451		
Ser	His	Leu	Val	Glu	Glu	Gly	Val	Leu	Ser	Asp	Pro	Lys	Glu	Phe	Ile			
				105				110				115						
aac	cct	gtt	cct	cac	gta	tct	ttc	ggc	cag	ggc	gca	gat	cag	gtt	gca	499		
Asn	Pro	Val	Pro	His	Val	Ser	Phe	Gly	Gln	Gly	Ala	Asp	Gln	Val	Ala			
120								125		130								
tac	atc	aag	gct	cgc	tac	gaa	gct	ttg	aag	gat	cac	cca	ctc	ttc	cag	547		
Tyr	Ile	Lys	Ala	Arg	Tyr	Glu	Ala	Leu	Lys	Asp	His	Pro	Leu	Phe	Gln			
135								140		145								
ggc	atg	acc	tac	gct	gac	gat	gaa	gct	acc	ttc	acc	gag	aag	ctg	cct	595		
Gly	Met	Thr	Tyr	Ala	Asp	Asp	Glu	Ala	Thr	Phe	Thr	Glu	Lys	Leu	Pro			
150				155				160				165						
ttg	atg	gca	aag	ggc	cgt	gac	ttc	tct	gat	cca	gta	gca	atc	tct	tgg	643		
Leu	Met	Ala	Lys	Gly	Arg	Asp	Phe	Ser	Asp	Pro	Val	Ala	Ile	Ser	Trp			
				170				175				180						
atc	gat	gaa	ggc	acc	gac	atc	aac	tac	ggt	gct	cag	acc	aag	cag	tac	691		
Ile	Asp	Glu	Gly	Thr	Asp	Ile	Asn	Tyr	Gly	Ala	Gln	Thr	Lys	Gln	Tyr			
				185				190				195						
ctg	gat	gca	gct	gaa	gtt	gaa	ggc	act	gaa	atc	cgc	tat	ggc	cac	gaa	739		
Leu	Asp	Ala	Ala	Glu	Val	Glu	Gly	Thr	Glu	Ile	Arg	Tyr	Gly	His	Glu			
200								205		210								
gtc	aag	agc	atc	aag	gct	gat	ggc	gca	aag	tgg	atc	gtg	acc	gtc	aag	787		
Val	Lys	Ser	Ile	Lys	Ala	Asp	Gly	Ala	Lys	Trp	Ile	Val	Thr	Val	Lys			
215								220		225								
aac	gta	cac	act	ggc	gac	acc	aag	acc	atc	aag	gca	aac	ttc	gtg	ttc	835		
Asn	Val	His	Thr	Gly	Asp	Thr	Lys	Thr	Ile	Lys	Ala	Asn	Phe	Val	Phe			
230				235				240				245						
gtc	ggc	gca	ggc	gga	tac	gca	ctg	gat	ctg	ctt	cgc	agc	gca	ggc	atc	883		
Val	Gly	Ala	Gly	Gly	Tyr	Ala	Leu	Asp	Leu	Leu	Arg	Ser	Ala	Gly	Ile			
				250				255				260						

Gln Thr Lys Gln Tyr Leu Asp Ala Ala Glu Val Glu Gly Thr Glu Ile

195	200	205
Arg Tyr Gly His Glu Val 210	Lys Ser Ile Lys Ala 215	Asp Gly Ala Lys Trp 220
Ile Val Thr Val Lys Asn Val His Thr Gly Asp Thr Lys Thr Ile Lys 225	230	235
Ala Asn Phe Val Phe Val Gly Ala Gly Tyr Ala Leu Asp Leu Leu 245	250	255
Arg Ser Ala Gly Ile Pro Gln Val Lys Gly Phe Ala Gly Phe Pro Val 260	265	270
Ser Gly Leu Trp Leu Arg Cys Thr Asn Glu Glu Leu Ile Glu Gln His 275	280	285
Ala Ala Lys Val Tyr Gly Lys Ala Ser Val Gly Ala Pro Pro Met Ser 290	295	300
Val Pro His Leu Asp Thr Arg Val Ile 305	310	

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 <213> Corynebacterium glutamicum

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 <222> (1)..(210)
 <223> FRXA01695

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atg atc gag ctg ctt gag cgt tgc ttc ggt gac cgc atg atc gag tgg	96
Met Ile Glu Leu Leu Glu Arg Cys Phe Gly Asp Arg Met Ile Glu Trp	
20 25 30	
ggc gac aag ctg aag gac atg atc cct tcc tac ggc aag aag ctt gct	144
Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala	
35 40 45	
tcc gag cca gca ctg ttt gag cag cag tgg gca cgc acc cag aag acc	192
Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr	
50 55 60	
ctg aag ctt gag gaa gcc taaatcttct aactgctttc ttt	233
Leu Lys Leu Glu Glu Ala	
65 70	

<210> 574
 <211> 70
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 574

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 20 25 30
 Gly Asp Lys Leu Lys Asp Met Ile Pro Ser Tyr Gly Lys Lys Leu Ala
 35 40 45
 Ser Glu Pro Ala Leu Phe Glu Gln Gln Trp Ala Arg Thr Gln Lys Thr
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 Leu Lys Leu Glu Glu Ala
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<210> 575

<211> 1063

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

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<222> (101)..(1063)

<223> RXA00290

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 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
 55 60 65
 aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
 70 75 80 85
 gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
 90 95 100
 ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
 105 110 115

gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499
 Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
 120 125 130

tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547
 Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
 135 140 145

gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165

gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn
 170 175 180

tcc ctg aag ctg ctg gat cgc aag atc gaa gac ctc aag att gtt att 691
 Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp Leu Lys Ile Val Ile
 185 190 195

tcc ggc gca ggc gca gcg ggc gtt gca gct gta gat atg ctg acc aac 739
 Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val Asp Met Leu Thr Asn
 200 205 210

gct gga gca acc gac atc gtg gtt ctt gat tcc cga ggc atc atc cac 787
 Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser Arg Gly Ile Ile His
 215 220 225

gac agc cgt gag gat ctt tcc cca gtt aag gct gct ctt gca gag aag 835
 Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala Ala Leu Ala Glu Lys
 230 235 240 245

acc aac cct cgt ggc atc agc ggt ggc atc aat gag gct ttc acc ggc 883
 Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn Glu Ala Phe Thr Gly
 250 255 260

gcg gac ctg ttc att ggc gtg tcc ggc ggc aac atc ggc gag gac gct 931
 Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn Ile Gly Glu Asp Ala
 265 270 275

ctc aaa ctc atg gcc ccg gag cca atc ctg ttc acc ctg gcg aac cca 979
 Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe Thr Leu Ala Asn Pro
 280 285 290

acc cca gag atc gat cct gag ctg tct cag aag tac ggc gcc atc gtc 1027
 Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys Tyr Gly Ala Ile Val
 295 300 305

gcg acc ggg ccg gtc ttg acc tgc cta acc aga tca 1063
 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
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<210> 576

<211> 321

<212> PRT

<213> Corynebacterium glutamicum

<400> 576

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Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val	35	40	45
Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr	50	55	60
His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala	65	70	75
Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met	85	90	95
Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile	100	105	110
Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile	115	120	125
Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser	130	135	140
Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp	145	150	155
Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu	165	170	175
Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp	180	185	190
Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val	195	200	205
Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser	210	215	220
Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala	225	230	235
Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn	245	250	255
Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn	260	265	270
Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe	275	280	285
Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys	290	295	300
Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg	305	310	315
Ser			320

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 <212> DNA
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<220>
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 <223> RXN01048

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 Met Thr Ile Asp Leu
 1 5
 cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
 Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
 10 15 20
 gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
 Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
 25 30 35
 cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
 Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
 40 45 50
 gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307
 Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr His Thr Gly Ile Gly
 55 60 65
 aac acc gtc gcg gtt att tcc gac ggc acc gct gtt ctt ggc ctt ggc 355
 Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala Val Leu Gly Leu Gly
 70 75 80 85
 gat atc gga cct cag gcc tcc ctt ccc gtc atg gag ggc aag gct cag 403
 Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met Glu Gly Lys Ala Gln
 90 95 100
 ctg ttt agc tct ttc gct ggc ctg aag gct atc cct atc gtt ttg gac 451
 Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile Pro Ile Val Leu Asp
 105 110 115
 gtt cac gat gtt gac gct ttg gtt gag acc atc gca gcc atc gcg cct 499
 Val His Asp Val Asp Ala Leu Val Glu Thr Ile Ala Ala Ile Ala Pro
 120 125 130
 tct ttc ggt gct atc aac ttg gag gac atc tcc gct cct cgt tgc ttc 547
 Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser Ala Pro Arg Cys Phe
 135 140 145
 gag gtg gag cgc cgc ctc atc gag cgt ctc gat att cca gtt atg cac 595
 Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp Ile Pro Val Met His
 150 155 160 165
 gat gac cag cac ggc acc gct gtg gtt atc ctc gct gcg ctg cgc aac 643
 Asp Asp Gln His Gly Thr Ala Val Val Ile Leu Ala Ala Leu Arg Asn

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<211> 408

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 578

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			20					25					30		

Pro	Leu	Arg	Asp	Met	Arg	Asp	Leu	Ser	Leu	Ala	Tyr	Thr	Pro	Gly	Val
		35					40					45			

Ala	Gln	Val	Cys	Glu	Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr
	50					55					60				

His	Thr	Gly	Ile	Gly	Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala
65					70					75					80

Val	Leu	Gly	Leu	Gly	Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met
			85						90					95	

Glu	Gly	Lys	Ala	Gln	Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile
		100						105					110		

Pro	Ile	Val	Leu	Asp	Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile
		115					120						125		

Ala	Ala	Ile	Ala	Pro	Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser
	130						135					140			

Ala	Pro	Arg	Cys	Phe	Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp
145					150					155					160

Ile	Pro	Val	Met	His	Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu
				165					170					175	

Ala	Ala	Leu	Arg	Asn	Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp
			180					185					190		

Leu	Lys	Ile	Val	Ile	Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val
	195						200					205			

Asp	Met	Leu	Thr	Asn	Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser
	210					215					220				

Arg	Gly	Ile	Ile	His	Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala
225					230					235					240

Ala	Leu	Ala	Glu	Lys	Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn
				245					250					255	

Glu	Ala	Phe	Thr	Gly	Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn
			260					265					270		

Ile	Gly	Glu	Asp	Ala	Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe
		275					280					285			

Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Arg Ser Asp Leu Pro Asn Gln Ile
 305 310 315 320
 Asn Asn Val Leu Ala Phe Pro Gly Ile Phe Ala Gly Ala Leu Ala Ala
 325 330 335
 Lys Ala Lys Lys Ile Thr Pro Glu Met Lys Leu Ala Ala Gln Arg Gln
 340 345 350
 Ser Gln Thr Ser Gln Leu Arg Thr Ser Arg Ser Ala Ala Ser Cys Leu
 355 360 365
 Pro Pro Trp Ile Pro Ala Leu Pro Gln Gln Ser Arg Gln Leu Ser Arg
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 Pro Ser Pro Lys Arg Lys Thr Leu Lys Asn Leu Leu Ile Asp Ala Ser
 385 390 395 400
 Leu Pro Val Glu Ala Pro Ile Phe
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 Arg Ser Asp Leu Pro Asn Gln Ile Asn Asn Val Leu Ala Phe Pro Gly
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 att ttc gcc ggc gct ctc gca gcc aag gct aag aag atc acc ccc gag 96
 Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
 20 25 30
 atg aag ctc gcc gct cag agg caa tcg cag aca tcg cag ctg agg acc 144
 Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
 35 40 45
 tcg agg tcg gcc gca tcg tgc cta ccg ccc tgg atc ccc gcg ttg ccc 192
 Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
 50 55 60
 caa cag tca agg cag ctg tcc agg ccg tcg cca aag cgc aaa acg ctt 240
 Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
 65 70 75 80
 aaa aat ttg ctt atc gac gcc tcc ctc ccc gtc gag gcg cca ata ttt 288
 Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
 85 90 95

taagagcaaa cttgaggccc aca

311

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<211> 96

<212> PRT

<213> Corynebacterium glutamicum

<400> 580

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Ile Phe Ala Gly Ala Leu Ala Ala Lys Ala Lys Lys Ile Thr Pro Glu
20 25 30

Met Lys Leu Ala Ala Gln Arg Gln Ser Gln Thr Ser Gln Leu Arg Thr
35 40 45

Ser Arg Ser Ala Ala Ser Cys Leu Pro Pro Trp Ile Pro Ala Leu Pro
50 55 60

Gln Gln Ser Arg Gln Leu Ser Arg Pro Ser Pro Lys Arg Lys Thr Leu
65 70 75 80

Lys Asn Leu Leu Ile Asp Ala Ser Leu Pro Val Glu Ala Pro Ile Phe
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<223> FRXA00290

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gagcttcccg caaaaacacc gattaacaag gctaaatgat atg acc atc gac ctg 115
Met Thr Ile Asp Leu
1 5

cag cgt tcc acc caa aac ctc acc cat gag gaa atc ttc gag gca cac 163
Gln Arg Ser Thr Gln Asn Leu Thr His Glu Glu Ile Phe Glu Ala His
10 15 20

gag ggc gga aag ctc tcc att agt tcc act cgt ccg ctc cgc gac atg 211
Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg Pro Leu Arg Asp Met
25 30 35

cgc gat ctt tcc ctt gct tac acc cct ggt gtt gct cag gtt tgt gaa 259
Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val Ala Gln Val Cys Glu
40 45 50

gca atc aag gaa gat cca gag gtt gcg cgc acc cac acg ggc att gga 307

Ala	Ile	Lys	Glu	Asp	Pro	Glu	Val	Ala	Arg	Thr	His	Thr	Gly	Ile	Gly		
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Asn	Thr	Val	Ala	Val	Ile	Ser	Asp	Gly	Thr	Ala	Val	Leu	Gly	Leu	Gly	85	
70					75				80								
gat	atc	gga	cct	cag	gcc	tcc	ctt	ccc	gtc	atg	gag	ggc	aag	gct	cag	403	
Asp	Ile	Gly	Pro	Gln	Ala	Ser	Leu	Pro	Val	Met	Glu	Gly	Lys	Ala	Gln	100	
				90				95									
ctg	ttt	agc	tct	ttc	gct	ggc	ctg	aag	gct	atc	cct	atc	gtt	ttg	gac	451	
Leu	Phe	Ser	Ser	Phe	Ala	Gly	Leu	Lys	Ala	Ile	Pro	Ile	Val	Leu	Asp	115	
			105				110										
gtt	cac	gat	gtt	gac	gct	ttg	gtt	gag	acc	atc	gca	gcc	atc	gcg	cct	499	
Val	His	Asp	Val	Asp	Ala	Leu	Val	Glu	Thr	Ile	Ala	Ala	Ile	Ala	Pro	130	
			120				125										
tct	ttc	ggg	gct	atc	aac	ttg	gag	gac	atc	tcc	gct	cct	cgt	tgc	ttc	547	
Ser	Phe	Gly	Ala	Ile	Asn	Leu	Glu	Asp	Ile	Ser	Ala	Pro	Arg	Cys	Phe	145	
	135					140											
gag	gtg	gag	cgc	cgc	ctc	atc	gag	cgt	ctc	gat	att	cca	gtt	atg	cac	595	
Glu	Val	Glu	Arg	Arg	Leu	Ile	Glu	Arg	Leu	Asp	Ile	Pro	Val	Met	His	165	
	150				155					160							
gat	gac	cag	cac	ggc	acc	gct	gtg	gtt	atc	ctc	gct	gcg	ctg	cgc	aac	643	
Asp	Asp	Gln	His	Gly	Thr	Ala	Val	Val	Ile	Leu	Ala	Ala	Leu	Arg	Asn	180	
				170					175								
tcc	ctg	aag	ctg	ctg	gat	cgc	aag	atc	gaa	gac	ctc	aag	att	gtt	att	691	
Ser	Leu	Lys	Leu	Leu	Asp	Arg	Lys	Ile	Glu	Asp	Leu	Lys	Ile	Val	Ile	195	
			185					190									
tcc	ggc	gca	ggc	gca	gcg	ggc	gtt	gca	gct	gta	gat	atg	ctg	acc	aac	739	
Ser	Gly	Ala	Gly	Ala	Ala	Gly	Val	Ala	Ala	Val	Asp	Met	Leu	Thr	Asn	210	
		200					205										
gct	gga	gca	acc	gac	atc	gtg	gtt	ctt	gat	tcc	cga	ggc	atc	atc	cac	787	
Ala	Gly	Ala	Thr	Asp	Ile	Val	Val	Leu	Asp	Ser	Arg	Gly	Ile	Ile	His	225	
	215					220											
gac	agc	cgt	gag	gat	ctt	tcc	cca	gtt	aag	gct	gct	ctt	gca	gag	aag	835	
Asp	Ser	Arg	Glu	Asp	Leu	Ser	Pro	Val	Lys	Ala	Ala	Leu	Ala	Glu	Lys	245	
	230				235					240							
acc	aac	cct	cgt	ggc	atc	agc	ggg	ggc	atc	aat	gag	gct	ttc	acc	ggc	883	
Thr	Asn	Pro	Arg	Gly	Ile	Ser	Gly	Gly	Ile	Asn	Glu	Ala	Phe	Thr	Gly	260	
				250				255									
gcg	gac	ctg	ttc	att	ggc	gtg	tcc	ggc	ggc	aac	atc	ggc	gag	gac	gct	931	
Ala	Asp	Leu	Phe	Ile	Gly	Val	Ser	Gly	Gly	Asn	Ile	Gly	Glu	Asp	Ala	275	
			265					270									
ctc	aaa	ctc	atg	gcc	ccg	gag	cca	atc	ctg	ttc	acc	ctg	gcg	aac	cca	979	
Leu	Lys	Leu	Met	Ala	Pro	Glu	Pro	Ile	Leu	Phe	Thr	Leu	Ala	Asn	Pro	290	
			280				285										
acc	cca	gag	atc	gat	cct	gag	ctg	tct	cag	aag	tac	ggc	gcc	atc	gtc	1027	
Thr	Pro	Glu	Ile	Asp	Pro	Glu	Leu	Ser	Gln	Lys	Tyr	Gly	Ala	Ile	Val		

295 300 305 1063
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 Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg Ser
 310 315 320

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 582
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 Ile Phe Glu Ala His Glu Gly Gly Lys Leu Ser Ile Ser Ser Thr Arg
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 Pro Leu Arg Asp Met Arg Asp Leu Ser Leu Ala Tyr Thr Pro Gly Val
 35 40 45
 Ala Gln Val Cys Glu Ala Ile Lys Glu Asp Pro Glu Val Ala Arg Thr
 50 55 60
 His Thr Gly Ile Gly Asn Thr Val Ala Val Ile Ser Asp Gly Thr Ala
 65 70 75 80
 Val Leu Gly Leu Gly Asp Ile Gly Pro Gln Ala Ser Leu Pro Val Met
 85 90 95
 Glu Gly Lys Ala Gln Leu Phe Ser Ser Phe Ala Gly Leu Lys Ala Ile
 100 105 110
 Pro Ile Val Leu Asp Val His Asp Val Asp Ala Leu Val Glu Thr Ile
 115 120 125
 Ala Ala Ile Ala Pro Ser Phe Gly Ala Ile Asn Leu Glu Asp Ile Ser
 130 135 140
 Ala Pro Arg Cys Phe Glu Val Glu Arg Arg Leu Ile Glu Arg Leu Asp
 145 150 155 160
 Ile Pro Val Met His Asp Asp Gln His Gly Thr Ala Val Val Ile Leu
 165 170 175
 Ala Ala Leu Arg Asn Ser Leu Lys Leu Leu Asp Arg Lys Ile Glu Asp
 180 185 190
 Leu Lys Ile Val Ile Ser Gly Ala Gly Ala Ala Gly Val Ala Ala Val
 195 200 205
 Asp Met Leu Thr Asn Ala Gly Ala Thr Asp Ile Val Val Leu Asp Ser
 210 215 220
 Arg Gly Ile Ile His Asp Ser Arg Glu Asp Leu Ser Pro Val Lys Ala
 225 230 235 240
 Ala Leu Ala Glu Lys Thr Asn Pro Arg Gly Ile Ser Gly Gly Ile Asn
 245 250 255

Glu Ala Phe Thr Gly Ala Asp Leu Phe Ile Gly Val Ser Gly Gly Asn
 260 265 270
 Ile Gly Glu Asp Ala Leu Lys Leu Met Ala Pro Glu Pro Ile Leu Phe
 275 280 285
 Thr Leu Ala Asn Pro Thr Pro Glu Ile Asp Pro Glu Leu Ser Gln Lys
 290 295 300
 Tyr Gly Ala Ile Val Ala Thr Gly Pro Val Leu Thr Cys Leu Thr Arg
 305 310 315 320
 Ser

<210> 583
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<220>
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 <222> (1)..(582)
 <223> RXN03101

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 cgc atc ggt gac gca aac gca gct gca gca cct gcc gaa gag gaa gca 96
 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala
 20 25 30
 gct cct gcc gaa gag gaa gaa cca gtt aag gaa gag cca aag aag gag 144
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 gca gct cct gaa gct cca gca gca act ggc gcc gca acc gat gtg gaa 192
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60
 atg cca gaa ctc ggc gaa tcc gtc acc gaa ggc acc att acc cag tgg 240
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80
 ctc aag gct gtc ggc gac acc gtc gaa gta gac gaa cca ctt ctt gag 288
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95
 gtc tcc acc gac aag gtc gac acc gaa atc cca tcc cca gta gca ggc 336
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110
 acc atc gtg gag atc ctt gca gac gaa gac gac acc gtc gac gtc ggc 384
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125
 gca gtc atc gcc cgc atc ggt gac gca aac gca gct gca gca cct gcc 432
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala

130	135	140	
gaa gag gaa gca gct cct gcc gaa gag gag gaa cca gtt aag gaa gag			480
Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu			
145	150	155	160
cca aag aag gaa gag ccc aag aag gaa gag ccc aag aag gaa gca gct			528
Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala			
	165	170	175
act aca cct gct gcg gca tcc gca act gtg tcc gct tct ggc gac aac			576
Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn			
	180	185	190
ggt cca			582
Val Pro			

<210> 584
 <211> 194
 <212> PRT
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<400> 584
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 Arg Ile Gly Asp Ala Asn Ala Ala Ala Pro Ala Glu Glu Glu Ala
 20 25 30
 Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu Pro Lys Lys Glu
 35 40 45
 Ala Ala Pro Glu Ala Pro Ala Ala Thr Gly Ala Ala Thr Asp Val Glu
 50 55 60
 Met Pro Glu Leu Gly Glu Ser Val Thr Glu Gly Thr Ile Thr Gln Trp
 65 70 75 80
 Leu Lys Ala Val Gly Asp Thr Val Glu Val Asp Glu Pro Leu Leu Glu
 85 90 95
 Val Ser Thr Asp Lys Val Asp Thr Glu Ile Pro Ser Pro Val Ala Gly
 100 105 110
 Thr Ile Val Glu Ile Leu Ala Asp Glu Asp Asp Thr Val Asp Val Gly
 115 120 125
 Ala Val Ile Ala Arg Ile Gly Asp Ala Asn Ala Ala Ala Ala Pro Ala
 130 135 140
 Glu Glu Glu Ala Ala Pro Ala Glu Glu Glu Glu Pro Val Lys Glu Glu
 145 150 155 160
 Pro Lys Lys Glu Glu Pro Lys Lys Glu Glu Pro Lys Lys Glu Ala Ala
 165 170 175
 Thr Thr Pro Ala Ala Ala Ser Ala Thr Val Ser Ala Ser Gly Asp Asn
 180 185 190

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<211>	139
<212>	PRT

<213> Corynebacterium glutamicum

<400> 586

Met Lys Glu Thr Leu Thr Thr Gly Leu Thr His Gln Met Thr Tyr Ile
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Val Pro Ala Asn Arg Thr Val Pro His Leu Leu Pro Glu Ala Ala Glu
 20 25 30

Phe Glu Thr Met Pro Asp Val Leu Ala Thr Gly Tyr Met Val Gly Ile
 35 40 45

Ile Glu Trp Ala Cys Met Glu Leu Leu Arg Pro His Leu Asp Asp Gly
 50 55 60

Glu Ile Ser Leu Gly Thr His Val Asn Phe Ser His Ala Ala Pro Thr
 65 70 75 80

Val Pro Gly Ser Thr Val Thr Ile Asp Val Glu Val Thr Glu Ile Asn
 85 90 95

Arg Arg Ala Val Thr Phe Asn Ile Thr Ala Ala Asp Glu Phe Ala Thr
 100 105 110

Ile Ser Thr Gly Thr His Gln Arg Gly Val Val Asn Arg Glu Lys Phe
 115 120 125

Val Ser Arg Leu Pro Glu Ala Pro Lys Glu Asn
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<210> 587

<211> 1683

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1660)

<223> RXN00389

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tctggcgcag gttcctaccg ccttcagttg aggtgaaagc atg atc acc gca acc 115
 Met Ile Thr Ala Thr
 1 5

gca ctg cat ggg tgt tca ctg att gat ggc gag tgg gtc gct gga aaa 163
 Ala Leu His Gly Cys Ser Leu Ile Asp Gly Glu Trp Val Ala Gly Lys
 10 15 20

aat ggt gag att aca gga ttc gat ccg cgc acc aat gcg agt ctg aac 211
 Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr Asn Ala Ser Leu Asn
 25 30 35

cct tcc tac tct tta gca aac agc gca cag ctg cgc gcc gcc aca aca 259
 Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu Arg Ala Ala Thr Thr
 40 45 50

tcg gcg aag cga gct ttt gaa agc tac cga ctc act act cca gag gtt 307

Ser	Ala	Lys	Arg	Ala	Phe	Glu	Ser	Tyr	Arg	Leu	Thr	Thr	Pro	Glu	Val		
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aga	gca	gat	ttc	ctg	gat	tcc	atc	gct	gac	aac	atc	gat	gcg	cta	tcc	355	
Arg	Ala	Asp	Phe	Leu	Asp	Ser	Ile	Ala	Asp	Asn	Ile	Asp	Ala	Leu	Ser	85	
70					75					80							
ggc	gag	atc	gtg	caa	cgg	gcg	agc	ctg	gag	aca	ggc	ttg	gga	act	acc	403	
Gly	Glu	Ile	Val	Gln	Arg	Ala	Ser	Leu	Glu	Thr	Gly	Leu	Gly	Thr	Thr		
				90					95					100			
cga	ctc	aca	ggc	gaa	gta	gcc	cgc	acc	agc	aac	cag	ctc	cgc	ctg	ttt	451	
Arg	Leu	Thr	Gly	Glu	Val	Ala	Arg	Thr	Ser	Asn	Gln	Leu	Arg	Leu	Phe		
			105					110					115				
gca	gaa	acc	gtg	aga	agc	gga	cag	ttc	cac	cga	gta	cgc	att	gaa	cga	499	
Ala	Glu	Thr	Val	Arg	Ser	Gly	Gln	Phe	His	Arg	Val	Arg	Ile	Glu	Arg		
		120					125					130					
gga	ccg	cgg	att	gat	ctt	cgc	cag	cgt	cag	ggt	ccg	ttg	gga	cca	gtc	547	
Gly	Pro	Arg	Ile	Asp	Leu	Arg	Gln	Arg	Gln	Val	Pro	Leu	Gly	Pro	Val		
	135					140					145						
gcg	gta	ttc	ggg	gca	agc	aac	ttc	ccc	gtc	gct	ttc	tct	act	gct	ggc	595	
Ala	Val	Phe	Gly	Ala	Ser	Asn	Phe	Pro	Val	Ala	Phe	Ser	Thr	Ala	Gly		
150					155				160						165		
ggc	gat	aca	gca	tca	gcg	ttg	gct	gca	ggc	tgc	cct	gtg	ggt	ttt	aag	643	
Gly	Asp	Thr	Ala	Ser	Ala	Leu	Ala	Ala	Gly	Cys	Pro	Val	Val	Phe	Lys		
			170						175					180			
gcg	cat	aat	gcg	cac	cct	gga	aca	gct	gag	ctc	gtc	ggg	caa	gcg	gtg	691	
Ala	His	Asn	Ala	His	Pro	Gly	Thr	Ala	Glu	Leu	Val	Gly	Gln	Ala	Val		
			185					190					195				
cgg	gga	gcc	gtc	gaa	aag	cat	gag	ttt	gat	gct	ggc	gtg	ttt	aac	ctt	739	
Arg	Gly	Ala	Val	Glu	Lys	His	Glu	Phe	Asp	Ala	Gly	Val	Phe	Asn	Leu		
		200					205					210					
gtc	tac	ggc	cgt	ggc	gtg	gaa	att	ggc	cag	gag	ctg	gct	gcg	gat	ccg	787	
Val	Tyr	Gly	Arg	Gly	Val	Glu	Ile	Gly	Gln	Glu	Leu	Ala	Ala	Asp	Pro		
	215					220					225						
aat	atc	acg	gca	atc	ggc	ttt	acc	ggc	tca	cgc	cag	ggc	ggc	ttg	gca	835	
Asn	Ile	Thr	Ala	Ile	Gly	Phe	Thr	Gly	Ser	Arg	Gln	Gly	Gly	Leu	Ala		
230					235					240					245		
ctg	tca	cag	act	gcg	ttt	agc	cgc	cca	ggt	ccc	ggt	cca	gtc	ttt	gca	883	
Leu	Ser	Gln	Thr	Ala	Phe	Ser	Arg	Pro	Val	Pro	Val	Pro	Val	Phe	Ala		
				250					255					260			
gaa	atg	agt	gcc	acc	aac	cct	gtg	ttc	gtc	ttc	ccc	ggc	gcg	ctg	gcg	931	
Glu	Met	Ser	Ala	Thr	Asn	Pro	Val	Phe	Val	Phe	Pro	Gly	Ala	Leu	Ala		
			265				270						275				
gat	ttg	gat	gca	tcg	agt	tcc	ttg	gct	gag	gcg	ttt	acc	gct	tcc	gtc	979	
Asp	Leu	Asp	Ala	Ser	Ser	Ser	Leu	Ala	Glu	Ala	Phe	Thr	Ala	Ser	Val		
		280					285					290					
acc	ggc	agt	tcc	ggg	caa	ttg	tgc	acc	aag	cct	ggc	ctc	ggt	ttc	atc	1027	
Thr	Gly	Ser	Ser	Gly	Gln	Leu	Cys	Thr	Lys	Pro	Gly	Leu	Val	Phe	Ile		

295	300	305	
ccg cgc ggt gtt gtt ggt gat gct ttt gtg gcg ctc gta gca gcc aaa			1075
Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala Leu Val Ala Ala Lys			
310	315	320	325
ttt aaa gaa acc acg ggt caa acg atg ctc acg caa ggc atc gct cag			1123
Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr Gln Gly Ile Ala Gln			
	330	335	340
gca tgg cag cgc gga gtc gac aac ctt gca gca cag cca agt gta aaa			1171
Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala Gln Pro Ser Val Lys			
	345	350	355
atc ctc gcc caa ggc acc ccc gga gat gga gag aac gcg ccg ggc ccg			1219
Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu Asn Ala Pro Gly Pro			
	360	365	370
gtg gtg ttt gaa agt gat gtg cag gcg ttg cta aat aat gtg gtg ttg			1267
Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu Asn Asn Val Val Leu			
	375	380	385
cag gaa gaa atc ttc ggt gcg gca tcg ctg gtg gtg cgt tat gat tcc			1315
Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val Val Arg Tyr Asp Ser			
390	395	400	405
ccg gat caa ctc cac caa gta gcc aat tca ctc gag gga caa tta aca			1363
Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu Glu Gly Gln Leu Thr			
	410	415	420
gcc acg atc cac gca tcc cag gat gat ttc cag gaa gtc tcg aaa ctt			1411
Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln Glu Val Ser Lys Leu			
	425	430	435
atc ccc ctc ttg gag gat ctc gcg ggc cgt gtt ctt tac ggc ggc tgg			1459
Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val Leu Tyr Gly Gly Trp			
	440	445	450
cca acg ggt gtg gaa gtt ggg cac acg gtt atc cat gga ggc cct tat			1507
Pro Thr Gly Val Glu Val Gly His Thr Val Ile His Gly Gly Pro Tyr			
	455	460	465
ccg gcg acc tca aat gcg cag tcg aca agt gtt gga acc ctg gca atc			1555
Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val Gly Thr Leu Ala Ile			
470	475	480	485
gag aga ttt atg cgc ccg gtt tct tat caa act ttc ccg gct gag ctg			1603
Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr Phe Pro Ala Glu Leu			
	490	495	500
ctt cca gat cca gtt tct gag gcg aat aaa tgg gct gta cct cgg gaa			1651
Leu Pro Asp Pro Val Ser Glu Ala Asn Lys Trp Ala Val Pro Arg Glu			
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Ile Asp Arg			
520			

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<212> PRT

<213> *Corynebacterium glutamicum*

<400> 588

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Trp Val Ala Gly Lys Asn Gly Glu Ile Thr Gly Phe Asp Pro Arg Thr
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Asn Ala Ser Leu Asn Pro Ser Tyr Ser Leu Ala Asn Ser Ala Gln Leu
      35           40           45

Arg Ala Ala Thr Thr Ser Ala Lys Arg Ala Phe Glu Ser Tyr Arg Leu
      50           55           60

Thr Thr Pro Glu Val Arg Ala Asp Phe Leu Asp Ser Ile Ala Asp Asn
 65           70           75           80

Ile Asp Ala Leu Ser Gly Glu Ile Val Gln Arg Ala Ser Leu Glu Thr
      85           90           95

Gly Leu Gly Thr Thr Arg Leu Thr Gly Glu Val Ala Arg Thr Ser Asn
     100           105           110

Gln Leu Arg Leu Phe Ala Glu Thr Val Arg Ser Gly Gln Phe His Arg
     115           120           125

Val Arg Ile Glu Arg Gly Pro Arg Ile Asp Leu Arg Gln Arg Gln Val
     130           135           140

Pro Leu Gly Pro Val Ala Val Phe Gly Ala Ser Asn Phe Pro Val Ala
     145           150           155           160

Phe Ser Thr Ala Gly Gly Asp Thr Ala Ser Ala Leu Ala Ala Gly Cys
     165           170           175

Pro Val Val Phe Lys Ala His Asn Ala His Pro Gly Thr Ala Glu Leu
     180           185           190

Val Gly Gln Ala Val Arg Gly Ala Val Glu Lys His Glu Phe Asp Ala
     195           200           205

Gly Val Phe Asn Leu Val Tyr Gly Arg Gly Val Glu Ile Gly Gln Glu
     210           215           220

Leu Ala Ala Asp Pro Asn Ile Thr Ala Ile Gly Phe Thr Gly Ser Arg
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Gln Gly Gly Leu Ala Leu Ser Gln Thr Ala Phe Ser Arg Pro Val Pro
     245           250           255

Val Pro Val Phe Ala Glu Met Ser Ala Thr Asn Pro Val Phe Val Phe
     260           265           270

Pro Gly Ala Leu Ala Asp Leu Asp Ala Ser Ser Ser Leu Ala Glu Ala
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Phe Thr Ala Ser Val Thr Gly Ser Ser Gly Gln Leu Cys Thr Lys Pro
     290           295           300

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Gly Leu Val Phe Ile Pro Arg Gly Val Val Gly Asp Ala Phe Val Ala
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Leu Val Ala Ala Lys Phe Lys Glu Thr Thr Gly Gln Thr Met Leu Thr
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Gln Gly Ile Ala Gln Ala Trp Gln Arg Gly Val Asp Asn Leu Ala Ala
340 345 350

Gln Pro Ser Val Lys Ile Leu Ala Gln Gly Thr Pro Gly Asp Gly Glu
355 360 365

Asn Ala Pro Gly Pro Val Val Phe Glu Ser Asp Val Gln Ala Leu Leu
370 375 380

Asn Asn Val Val Leu Gln Glu Glu Ile Phe Gly Ala Ala Ser Leu Val
385 390 395 400

Val Arg Tyr Asp Ser Pro Asp Gln Leu His Gln Val Ala Asn Ser Leu
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Glu Gly Gln Leu Thr Ala Thr Ile His Ala Ser Gln Asp Asp Phe Gln
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Glu Val Ser Lys Leu Ile Pro Leu Leu Glu Asp Leu Ala Gly Arg Val
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Leu Tyr Gly Gly Trp Pro Thr Gly Val Glu Val Gly His Thr Val Ile
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His Gly Gly Pro Tyr Pro Ala Thr Ser Asn Ala Gln Ser Thr Ser Val
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Gly Thr Leu Ala Ile Glu Arg Phe Met Arg Pro Val Ser Tyr Gln Thr
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Ala Val Pro Arg Glu Ile Asp Arg
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Val Val Gly Thr Ala
1 5

cat tgc gaa tca gca ctt aag gaa gtg act ttg atg tca aac gtt gga 163

His	Cys	Glu	Ser	Ala	Leu	Lys	Glu	Val	Thr	Leu	Met	Ser	Asn	Val	Gly	
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aag	cca	cgt	acc	gca	cag	gaa	atc	cag	cag	gat	tgg	gac	acc	aac	cct	211
Lys	Pro	Arg	Thr	Ala	Gln	Glu	Ile	Gln	Gln	Asp	Trp	Asp	Thr	Asn	Pro	
			25					30					35			
cgt	tgg	aac	ggc	atc	acc	cgc	gac	tac	acc	gca	gac	cag	gta	gct	gat	259
Arg	Trp	Asn	Gly	Ile	Thr	Arg	Asp	Tyr	Thr	Ala	Asp	Gln	Val	Ala	Asp	
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ctg	cag	ggg	tcc	gtc	atc	gag	gag	cac	act	ctt	gct	cgc	cgc	ggc	tca	307
Leu	Gln	Gly	Ser	Val	Ile	Glu	Glu	His	Thr	Leu	Ala	Arg	Arg	Gly	Ser	
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Glu	Ile	Leu	Trp	Asp	Ala	Val	Thr	Gln	Glu	Gly	Asp	Gly	Tyr	Ile	Asn	
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gcg	ctt	ggc	gca	ctc	acc	ggg	aac	cag	gct	gtt	cag	cag	gtt	cgt	gca	403
Ala	Leu	Gly	Ala	Leu	Thr	Gly	Asn	Gln	Ala	Val	Gln	Gln	Val	Arg	Ala	
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ggc	ctg	aag	gct	gtc	tac	ctg	tcc	ggg	tgg	cag	gtc	gca	ggg	gac	gcc	451
Gly	Leu	Lys	Ala	Val	Tyr	Leu	Ser	Gly	Trp	Gln	Val	Ala	Gly	Asp	Ala	
			105					110					115			
aac	ctc	tcc	ggc	cac	acc	tac	cct	gac	cag	tcc	ctc	tac	cca	gcg	aac	499
Asn	Leu	Ser	Gly	His	Thr	Tyr	Pro	Asp	Gln	Ser	Leu	Tyr	Pro	Ala	Asn	
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tcc	gtt	cca	agc	gtc	gtt	cgt	cgc	atc	aac	aac	gca	ctg	ctg	cgt	tcc	547
Ser	Val	Pro	Ser	Val	Val	Arg	Arg	Ile	Asn	Asn	Ala	Leu	Leu	Arg	Ser	
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gat	gaa	atc	gca	cgc	acc	gaa	ggc	gac	acc	tcc	gtt	gac	aac	tgg	gtt	595
Asp	Glu	Ile	Ala	Arg	Thr	Glu	Gly	Asp	Thr	Ser	Val	Asp	Asn	Trp	Val	
	150				155					160					165	
gtc	cca	atc	gtc	gcg	gac	ggc	gaa	gct	ggc	ttc	ggg	gga	gca	ctc	aac	643
Val	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe	Gly	Gly	Ala	Leu	Asn	
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gtc	tac	gaa	ctc	cag	aag	gca	atg	atc	gca	gct	ggc	gct	gca	ggc	acc	691
Val	Tyr	Glu	Leu	Gln	Lys	Ala	Met	Ile	Ala	Ala	Gly	Ala	Ala	Gly	Thr	
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cac	tgg	gaa	gac	cag	ctc	gct	tct	gaa	aag	aag	tgt	ggc	cac	ctc	ggc	739
His	Trp	Glu	Asp	Gln	Leu	Ala	Ser	Glu	Lys	Lys	Cys	Gly	His	Leu	Gly	
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Gly	Lys	Val	Leu	Ile	Pro	Thr	Gln	Gln	His	Ile	Arg	Thr	Leu	Asn	Ser	
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gcc	cgc	ctt	gca	gca	gac	gtt	gca	aac	acc	cca	act	gtt	gtt	atc	gca	835
Ala	Arg	Leu	Ala	Ala	Asp	Val	Ala	Asn	Thr	Pro	Thr	Val	Val	Ile	Ala	
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cgt	acc	gac	gct	gag	gca	gca	acc	ctg	atc	acc	tct	gac	gtt	gat	gag	883
Arg	Thr	Asp	Ala	Glu	Ala	Ala	Thr	Leu	Ile	Thr	Ser	Asp	Val	Asp	Glu	

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Arg	Asp	Gln	Pro	Phe	Ile	Thr	Gly	Glu	Arg	Thr	Ala	Glu	Gly	Tyr	Tyr	
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cac	gtc	aag	aat	ggt	ctc	gag	cca	tgt	atc	gca	cgt	gca	aag	tcc	tac	979
His	Val	Lys	Asn	Gly	Leu	Glu	Pro	Cys	Ile	Ala	Arg	Ala	Lys	Ser	Tyr	
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Ala	Pro	Tyr	Ala	Asp	Met	Ile	Trp	Met	Glu	Thr	Gly	Thr	Pro	Asp	Leu	
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gag	ctc	gct	aag	aag	ttc	gct	gaa	ggc	gtt	cgc	tct	gag	ttc	cca	gac	1075
Glu	Leu	Ala	Lys	Lys	Phe	Ala	Glu	Gly	Val	Arg	Ser	Glu	Phe	Pro	Asp	
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Gln	Leu	Leu	Ser	Tyr	Asn	Cys	Ser	Pro	Ser	Phe	Asn	Trp	Ser	Ala	His	
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ctc	gag	gca	gat	gag	atc	gct	aag	ttc	cag	aag	gaa	ctc	ggc	gca	atg	1171
Leu	Glu	Ala	Asp	Glu	Ile	Ala	Lys	Phe	Gln	Lys	Glu	Leu	Gly	Ala	Met	
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Gly	Phe	Lys	Phe	Gln	Phe	Ile	Thr	Leu	Ala	Gly	Phe	His	Ser	Leu	Asn	
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tac	ggc	atg	ttc	gac	ctg	gct	tac	gga	tac	gct	cgc	gaa	ggc	atg	acc	1267
Tyr	Gly	Met	Phe	Asp	Leu	Ala	Tyr	Gly	Tyr	Ala	Arg	Glu	Gly	Met	Thr	
		375				380				385						
tcc	ttc	gtt	gac	ctg	cag	aac	cgt	gag	ttc	aag	gca	gct	gaa	gag	cgt	1315
Ser	Phe	Val	Asp	Leu	Gln	Asn	Arg	Glu	Phe	Lys	Ala	Ala	Glu	Glu	Arg	
390					395					400				405		
ggc	ttc	acc	gct	gtt	aag	cac	cag	cgt	gag	gtt	ggc	gca	ggc	tac	ttc	1363
Gly	Phe	Thr	Ala	Val	Lys	His	Gln	Arg	Glu	Val	Gly	Ala	Gly	Tyr	Phe	
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gac	cag	atc	gca	acc	acc	gtt	gac	cgc	aac	tct	tct	acc	acc	gct	ttg	1411
Asp	Gln	Ile	Ala	Thr	Thr	Val	Asp	Pro	Asn	Ser	Ser	Thr	Thr	Ala	Leu	
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 Ala Arg Arg Gly Ser Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly
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 Asp Gly Tyr Ile Asn Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val
 85 90 95
 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
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 Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
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 Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
 130 135 140
 Ala Leu Leu Arg Ser Asp Glu Ile Ala Arg Thr Glu Gly Asp Thr Ser
 145 150 155 160
 Val Asp Asn Trp Val Val Pro Ile Val Ala Asp Gly Glu Ala Gly Phe
 165 170 175
 Gly Gly Ala Leu Asn Val Tyr Glu Leu Gln Lys Ala Met Ile Ala Ala
 180 185 190
 Gly Ala Ala Gly Thr His Trp Glu Asp Gln Leu Ala Ser Glu Lys Lys
 195 200 205
 Cys Gly His Leu Gly Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile
 210 215 220
 Arg Thr Leu Asn Ser Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro
 225 230 235 240
 Thr Val Val Ile Ala Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr
 245 250 255
 Ser Asp Val Asp Glu Arg Asp Gln Pro Phe Ile Thr Gly Glu Arg Thr
 260 265 270
 Ala Glu Gly Tyr Tyr His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala
 275 280 285
 Arg Ala Lys Ser Tyr Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr
 290 295 300
 Gly Thr Pro Asp Leu Glu Leu Ala Lys Lys Phe Ala Glu Gly Val Arg
 305 310 315 320
 Ser Glu Phe Pro Asp Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe
 325 330 335

Asn Trp Ser Ala His Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys
 340 345 350
 Glu Leu Gly Ala Met Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly
 355 360 365
 Phe His Ser Leu Asn Tyr Gly Met Phe Asp Leu Ala Tyr Gly Tyr Ala
 370 375 380
 Arg Glu Gly Met Thr Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys
 385 390 395 400
 Ala Ala Glu Glu Arg Gly Phe Thr Ala Val Lys His Gln Arg Glu Val
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 Met Ser Asn Val Gly
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 Arg Trp Asn Gly Ile Thr Arg Asp Tyr Thr Ala Asp Gln Val Ala Asp
 25 30 35
 ctg cag ggt tcc gtc atc gag gag cac act ctt gct cgc cgc ggc tca 259
 Leu Gln Gly Ser Val Ile Glu Glu His Thr Leu Ala Arg Arg Gly Ser
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 gag atc ctc tgg gac gca gtc acc cag gaa ggt gac gga tac atc aac 307
 Glu Ile Leu Trp Asp Ala Val Thr Gln Glu Gly Asp Gly Tyr Ile Asn
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 gcg ctt ggc gca ctc acc ggt aac cag gct gtt cag cag gtt cgt gca 355
 Ala Leu Gly Ala Leu Thr Gly Asn Gln Ala Val Gln Gln Val Arg Ala
 70 75 80 85

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90 95 100	
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105 110 115	
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170 175 180	
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185 190 195	
ggc aag gtt ctg atc cca acc cag cag cac atc cgc acc ctg aac tct Gly Lys Val Leu Ile Pro Thr Gln Gln His Ile Arg Thr Leu Asn Ser	739
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gcc cgc ctt gca gca gac gtt gca aac acc cca act gtt gtt atc gca Ala Arg Leu Ala Ala Asp Val Ala Asn Thr Pro Thr Val Val Ile Ala	787
215 220 225	
cgt acc gac gct gag gca gca acc ctg atc acc tct gac gtt gat gag Arg Thr Asp Ala Glu Ala Ala Thr Leu Ile Thr Ser Asp Val Asp Glu	835
230 235 240 245	
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250 255 260	
cac gtc aag aat ggt ctc gag cca tgt atc gca cgt gca aag tcc tac His Val Lys Asn Gly Leu Glu Pro Cys Ile Ala Arg Ala Lys Ser Tyr	931
265 270 275	
gca cca tac gca gat atg atc tgg atg gag acc ggc acc cct gac ctg Ala Pro Tyr Ala Asp Met Ile Trp Met Glu Thr Gly Thr Pro Asp Leu	979
280 285 290	
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295 300 305	
cag ctg ctg tcc tac aac tgc tcc cca tcc ttc aac tgg tct gca cac Gln Leu Leu Ser Tyr Asn Cys Ser Pro Ser Phe Asn Trp Ser Ala His	1075
310 315 320 325	

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 Leu Glu Ala Asp Glu Ile Ala Lys Phe Gln Lys Glu Leu Gly Ala Met
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 Gly Phe Lys Phe Gln Phe Ile Thr Leu Ala Gly Phe His Ser Leu Asn
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 Ser Phe Val Asp Leu Gln Asn Arg Glu Phe Lys Ala Ala Glu Glu Arg
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 Gly Phe Thr Ala Val Lys His Gln Arg Glu Val Gly Ala Gly Tyr Phe
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 Asp Gln Ile Ala Thr Thr Val Asp Pro Asn Ser Ser Thr Thr Ala Leu
 410 415 420
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 65 70 75 80
 Gln Gln Val Arg Ala Gly Leu Lys Ala Val Tyr Leu Ser Gly Trp Gln
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 Val Ala Gly Asp Ala Asn Leu Ser Gly His Thr Tyr Pro Asp Gln Ser
 100 105 110
 Leu Tyr Pro Ala Asn Ser Val Pro Ser Val Val Arg Arg Ile Asn Asn
 115 120 125

Ala	Leu	Leu	Arg	Ser	Asp	Glu	Ile	Ala	Arg	Thr	Glu	Gly	Asp	Thr	Ser	130	135	140
Val	Asp	Asn	Trp	Val	Val	Pro	Ile	Val	Ala	Asp	Gly	Glu	Ala	Gly	Phe	145	150	155
Gly	Gly	Ala	Leu	Asn	Val	Tyr	Glu	Leu	Gln	Lys	Ala	Met	Ile	Ala	Ala	165	170	175
Gly	Ala	Ala	Gly	Thr	His	Trp	Glu	Asp	Gln	Leu	Ala	Ser	Glu	Lys	Lys	180	185	190
Cys	Gly	His	Leu	Gly	Gly	Lys	Val	Leu	Ile	Pro	Thr	Gln	Gln	His	Ile	195	200	205
Arg	Thr	Leu	Asn	Ser	Ala	Arg	Leu	Ala	Ala	Asp	Val	Ala	Asn	Thr	Pro	210	215	220
Thr	Val	Val	Ile	Ala	Arg	Thr	Asp	Ala	Glu	Ala	Ala	Thr	Leu	Ile	Thr	225	230	235
Ser	Asp	Val	Asp	Glu	Arg	Asp	Gln	Pro	Phe	Ile	Thr	Gly	Glu	Arg	Thr	245	250	255
Ala	Glu	Gly	Tyr	Tyr	His	Val	Lys	Asn	Gly	Leu	Glu	Pro	Cys	Ile	Ala	260	265	270
Arg	Ala	Lys	Ser	Tyr	Ala	Pro	Tyr	Ala	Asp	Met	Ile	Trp	Met	Glu	Thr	275	280	285
Gly	Thr	Pro	Asp	Leu	Glu	Leu	Ala	Lys	Lys	Phe	Ala	Glu	Gly	Val	Arg	290	295	300
Ser	Glu	Phe	Pro	Asp	Gln	Leu	Leu	Ser	Tyr	Asn	Cys	Ser	Pro	Ser	Phe	305	310	315
Asn	Trp	Ser	Ala	His	Leu	Glu	Ala	Asp	Glu	Ile	Ala	Lys	Phe	Gln	Lys	325	330	335
Glu	Leu	Gly	Ala	Met	Gly	Phe	Lys	Phe	Gln	Phe	Ile	Thr	Leu	Ala	Gly	340	345	350
Phe	His	Ser	Leu	Asn	Tyr	Gly	Met	Phe	Asp	Leu	Ala	Tyr	Gly	Tyr	Ala	355	360	365
Arg	Glu	Gly	Met	Thr	Ser	Phe	Val	Asp	Leu	Gln	Asn	Arg	Glu	Phe	Lys	370	375	380
Ala	Ala	Glu	Glu	Arg	Gly	Phe	Thr	Ala	Val	Lys	His	Gln	Arg	Glu	Val	385	390	395
Gly	Ala	Gly	Tyr	Phe	Asp	Gln	Ile	Ala	Thr	Thr	Val	Asp	Pro	Asn	Ser	405	410	415
Ser	Thr	Thr	Ala	Leu	Lys	Gly	Ser	Thr	Glu	Glu	Gly	Gln	Phe	His	Asn	420	425	430

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Met Thr Glu Gln Glu 1 5																
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Leu Leu Ser Ala Gln Thr Ala Asp Asn Ala Gly Thr Asp Ser Thr Glu 10 15 20																
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Trp Ser Gly Phe Ala Ala Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg 55 60 65																
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 Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu Trp Gly Arg Glu Phe

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			580					585					590				
ctc	gga	tac	gtt	gtg	cgc	tgg	gtt	gag	cac	ggt	gtt	ggt	tgc	tcc	aag	1824	
Leu	Gly	Tyr	Val	Val	Arg	Trp	Val	Glu	His	Gly	Val	Gly	Cys	Ser	Lys		
		595					600					605					
gtt	cca	gac	atc	cat	gac	atc	gac	ctc	atg	gaa	gac	cgc	gca	acg	ctg	1872	
Val	Pro	Asp	Ile	His	Asp	Ile	Asp	Leu	Met	Glu	Asp	Arg	Ala	Thr	Leu		
	610					615					620						
cgt	att	tcc	tcg	cag	atg	ctg	gcc	aac	tgg	atc	cgc	cat	gat	gtt	gtc	1920	
Arg	Ile	Ser	Ser	Gln	Met	Leu	Ala	Asn	Trp	Ile	Arg	His	Asp	Val	Val		
625					630					635					640		
tcg	aag	gag	cag	gtc	ttg	gag	tca	ctg	gaa	cga	atg	gca	gtg	gtc	gtc	1968	
Ser	Lys	Glu	Gln	Val	Leu	Glu	Ser	Leu	Glu	Arg	Met	Ala	Val	Val	Val		
				645					650					655			
gac	aag	caa	aat	gcg	ggc	gac	gag	gcc	tac	cgc	gat	atg	gcg	ccg	aag	2016	
Asp	Lys	Gln	Asn	Ala	Gly	Asp	Glu	Ala	Tyr	Arg	Asp	Met	Ala	Pro	Lys		
			660					665					670				
tac	gac	gcc	tcc	ctc	gcc	ttc	cag	gcg	gct	aag	gac	ttg	att	ttc	gaa	2064	
Tyr	Asp	Ala	Ser	Leu	Ala	Phe	Gln	Ala	Ala	Lys	Asp	Leu	Ile	Phe	Glu		
		675					680					685					
ggc	acc	aag	tcc	cca	tcg	ggc	tac	acc	gag	ccc	atc	ttg	cac	gca	cgc	2112	
Gly	Thr	Lys	Ser	Pro	Ser	Gly	Tyr	Thr	Glu	Pro	Ile	Leu	His	Ala	Arg		
		690				695					700						
cgc	cgc	gag	ttc	aaa	gca	aaa	aac	taagc	cagct	tttcg	acgct	tac				2159	
Arg	Arg	Glu	Phe	Lys	Ala	Lys	Asn										
705						710											

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<213> Corynebacterium glutamicum

<400> 596

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 20 25 30
 Ile Ala Arg Asp Leu Thr Pro Arg Asn Arg Glu Leu Leu Ala Arg Arg
 35 40 45
 Asp Glu Leu Gln Met Leu Ile Asp Asp Tyr His Arg Asn Asn Ser Gly
 50 55 60
 Thr Ile Asp Gln Glu Ala Tyr Glu Asp Phe Leu Lys Glu Ile Gly Tyr
 65 70 75 80
 Leu Val Glu Glu Pro Glu Ala Ala Glu Ile Arg Thr Gln Asn Val Asp
 85 90 95
 Thr Glu Ile Ser Ser Thr Ala Gly Pro Gln Leu Val Val Pro Ile Leu
 100 105 110
 Asn Ala Arg Phe Ala Leu Asn Ala Ala Asn Ala Arg Trp Gly Ser Leu
 115 120 125
 Tyr Asp Ala Leu Tyr Gly Thr Asn Ala Ile Pro Glu Thr Asp Gly Ala
 130 135 140
 Glu Lys Gly Lys Glu Tyr Asn Pro Val Arg Gly Gln Lys Val Ile Glu
 145 150 155 160
 Trp Gly Arg Glu Phe Leu Asp Ser Val Val Pro Leu Asp Gly Ala Ser
 165 170 175
 His Ala Asp Val Glu Lys Tyr Asn Ile Thr Asp Gly Lys Leu Ala Ala
 180 185 190
 His Ile Gly Asp Ser Val Tyr Arg Leu Lys Asn Arg Glu Ser Tyr Arg
 195 200 205
 Gly Phe Thr Gly Asn Phe Leu Asp Pro Glu Ala Ile Leu Leu Glu Thr
 210 215 220
 Asn Gly Leu His Ile Glu Leu Gln Ile Asp Pro Val His Pro Ile Gly
 225 230 235 240
 Lys Ala Asp Lys Thr Gly Leu Lys Asp Ile Val Leu Glu Ser Ala Ile
 245 250 255
 Thr Thr Ile Met Asp Phe Glu Asp Ser Val Ala Ala Val Asp Ala Glu
 260 265 270
 Asp Lys Thr Leu Gly Tyr Ser Asn Trp Phe Gly Leu Asn Thr Gly Glu
 275 280 285
 Leu Lys Glu Glu Met Ser Lys Asn Gly Arg Ile Phe Thr Arg Glu Leu
 290 295 300
 Asn Lys Asp Arg Val Tyr Ile Gly Arg Asn Gly Thr Glu Leu Val Leu
 305 310 315 320

His Gly Arg Ser Leu Leu Phe Val Arg Asn Val Gly His Leu Met Gln
 325 330 335
 Asn Pro Ser Ile Leu Ile Asp Gly Glu Glu Ile Phe Glu Gly Ile Met
 340 345 350
 Asp Ala Val Leu Thr Thr Val Cys Ala Ile Pro Gly Ile Ala Pro Gln
 355 360 365
 Asn Lys Met Arg Asn Ser Arg Lys Gly Ser Ile Tyr Ile Val Lys Pro
 370 375 380
 Lys Gln His Gly Pro Glu Glu Val Ala Phe Thr Asn Glu Leu Phe Gly
 385 390 395 400
 Arg Val Glu Asp Leu Leu Asp Leu Pro Arg His Thr Leu Lys Val Gly
 405 410 415
 Val Met Asp Glu Glu Arg Arg Thr Ser Val Asn Leu Asp Ala Ser Ile
 420 425 430
 Met Glu Val Ala Asp Arg Leu Ala Phe Ile Asn Thr Gly Phe Leu Asp
 435 440 445
 Arg Thr Gly Asp Glu Ile His Thr Ser Met Glu Ala Gly Ala Met Val
 450 455 460
 Arg Lys Ala Asp Met Gln Thr Ala Pro Trp Lys Gln Ala Tyr Glu Asn
 465 470 475 480
 Asn Asn Val Asp Ala Gly Ile Gln Arg Gly Leu Pro Gly Lys Ala Gln
 485 490 495
 Ile Gly Lys Gly Met Trp Ala Met Thr Glu Leu Met Ala Glu Met Leu
 500 505 510
 Glu Lys Lys Ile Gly Gln Pro Arg Glu Gly Ala Asn Thr Ala Trp Val
 515 520 525
 Pro Ser Pro Thr Gly Ala Thr Leu His Ala Thr His Tyr His Leu Val
 530 535 540
 Asp Val Phe Lys Val Gln Asp Glu Leu Arg Ala Ala Gly Arg Arg Asp
 545 550 555 560
 Ser Leu Arg Asn Ile Leu Thr Ile Ser Thr Ala Pro Asn Thr Asn Trp
 565 570 575
 Ser Glu Glu Glu Lys Lys Glu Glu Met Asp Asn Asn Cys Gln Ser Ile
 580 585 590
 Leu Gly Tyr Val Val Arg Trp Val Glu His Gly Val Gly Cys Ser Lys
 595 600 605
 Val Pro Asp Ile His Asp Ile Asp Leu Met Glu Asp Arg Ala Thr Leu
 610 615 620
 Arg Ile Ser Ser Gln Met Leu Ala Asn Trp Ile Arg His Asp Val Val
 625 630 635 640
 Ser Lys Glu Gln Val Leu Glu Ser Leu Glu Arg Met Ala Val Val Val

				645						650						655			
Asp	Lys	Gln	Asn	Ala	Gly	Asp	Glu	Ala	Tyr	Arg	Asp	Met	Ala	Pro	Lys				
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Tyr	Asp	Ala	Ser	Leu	Ala	Phe	Gln	Ala	Ala	Lys	Asp	Leu	Ile	Phe	Glu				
		675					680					685							
Gly	Thr	Lys	Ser	Pro	Ser	Gly	Tyr	Thr	Glu	Pro	Ile	Leu	His	Ala	Arg				
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Arg	Arg	Glu	Phe	Lys	Ala	Lys	Asn												
705					710														

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 <223> RXA01089

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 Leu Ser Arg Phe Ala
 1 5
 gcc aac ctg tca ttg act ttt act gag cta gat ttc ctg gat cgt ttt 163
 Ala Asn Leu Ser Leu Thr Phe Thr Glu Leu Asp Phe Leu Asp Arg Phe
 10 15 20
 gat gcc gct tcg aag cat gct ttc agt gcc gtg gag ttt cag tac cct 211
 Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val Glu Phe Gln Tyr Pro
 25 30 35
 tac gat ttc gat gtt caa gag att aaa cag cgt gct gat tcc gca ggt 259
 Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg Ala Asp Ser Ala Gly
 40 45 50
 ctg ccc att gaa ctg ttc aat gcc cca cct ggg gat act ttt ggt ctt 307
 Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly Asp Thr Phe Gly Leu
 55 60 65
 gcg gca ctg gct tcc cct gaa gac ttt caa caa tcc atc gag cag gcc 355
 Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln Ser Ile Glu Gln Ala
 70 75 80 85
 atc acg tac gcc aca gtg ttg aag cca aag aag atg cat gtc atg gct 403
 Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys Met His Val Met Ala
 90 95 100
 ggc atc gcg gac gta acc tca gaa acc acg gcg cgc tat gtg gag aat 451
 Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala Arg Tyr Val Glu Asn
 105 110 115
 att cgc tgg gct gcg cag caa cta gac aag ctc gac gtt gtc gtt gtt 499

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Ile Arg Trp Ala Ala Gln Gln Leu Asp Lys Leu Asp Val Val Val Val
120                               125                               130

att gaa cca att aat cac tat tcg gtt ccc ggt tat ttc ctg cac act 547
Ile Glu Pro Ile Asn His Tyr Ser Val Pro Gly Tyr Phe Leu His Thr
135                               140                               145

tta gag cag gcg tat tgg ctt atc gac agc att gcc cac ccc aat gtg 595
Leu Glu Gln Ala Tyr Trp Leu Ile Asp Ser Ile Ala His Pro Asn Val
150                               155                               160                               165

aag atc tta ttc gat act ttc cac ctt cag cag att cat ggc aat ctc 643
Lys Ile Leu Phe Asp Thr Phe His Leu Gln Gln Ile His Gly Asn Leu
170                               175                               180

acc cgc cgc ctg cgc gag gtt cat ggc gca ggt ctt ttg gga cac gtg 691
Thr Arg Arg Leu Arg Glu Val His Gly Ala Gly Leu Leu Gly His Val
185                               190                               195

caa gtg gcc tca gtt cct gat cga cac gaa cct ggc act ggc gaa gtc 739
Gln Val Ala Ser Val Pro Asp Arg His Glu Pro Gly Thr Gly Glu Val
200                               205                               210

aat gcg gcg tat atc ttc caa ctc cta agc gaa ctg gga tat gac ggt 787
Asn Ala Ala Tyr Ile Phe Gln Leu Leu Ser Glu Leu Gly Tyr Asp Gly
215                               220                               225

gtc atc gct ggc gaa tac cac cct gct ggt gaa act aca gcc ggt ttg 835
Val Ile Ala Gly Glu Tyr His Pro Ala Gly Glu Thr Thr Ala Gly Leu
230                               235                               240                               245

ggc tgg ttg gag ctc tagatcgtaa gtggtgtcgt acc 873
Gly Trp Leu Glu Leu
250

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<210> 598
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 <212> PRT
 <213> Corynebacterium glutamicum

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Phe Leu Asp Arg Phe Asp Ala Ala Ser Lys His Ala Phe Ser Ala Val
20           25           30

Glu Phe Gln Tyr Pro Tyr Asp Phe Asp Val Gln Glu Ile Lys Gln Arg
35           40           45

Ala Asp Ser Ala Gly Leu Pro Ile Glu Leu Phe Asn Ala Pro Pro Gly
50           55           60

Asp Thr Phe Gly Leu Ala Ala Leu Ala Ser Pro Glu Asp Phe Gln Gln
65           70           75           80

Ser Ile Glu Gln Ala Ile Thr Tyr Ala Thr Val Leu Lys Pro Lys Lys
85           90           95

Met His Val Met Ala Gly Ile Ala Asp Val Thr Ser Glu Thr Thr Ala

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100					105					110					
Arg	Tyr	Val	Glu	Asn	Ile	Arg	Trp	Ala	Ala	Gln	Gln	Leu	Asp	Lys	Leu
		115					120					125			
Asp	Val	Val	Val	Val	Ile	Glu	Pro	Ile	Asn	His	Tyr	Ser	Val	Pro	Gly
	130					135					140				
Tyr	Phe	Leu	His	Thr	Leu	Glu	Gln	Ala	Tyr	Trp	Leu	Ile	Asp	Ser	Ile
145					150					155					160
Ala	His	Pro	Asn	Val	Lys	Ile	Leu	Phe	Asp	Thr	Phe	His	Leu	Gln	Gln
				165					170					175	
Ile	His	Gly	Asn	Leu	Thr	Arg	Arg	Leu	Arg	Glu	Val	His	Gly	Ala	Gly
			180					185					190		
Leu	Leu	Gly	His	Val	Gln	Val	Ala	Ser	Val	Pro	Asp	Arg	His	Glu	Pro
	195						200					205			
Gly	Thr	Gly	Glu	Val	Asn	Ala	Ala	Tyr	Ile	Phe	Gln	Leu	Leu	Ser	Glu
	210					215					220				
Leu	Gly	Tyr	Asp	Gly	Val	Ile	Ala	Gly	Glu	Tyr	His	Pro	Ala	Gly	Glu
225					230					235					240
Thr	Thr	Ala	Gly	Leu	Gly	Trp	Leu	Glu	Leu						
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 <212> DNA
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 <223> RXA01886

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 Met Thr Phe Lys Leu 5
 gca gca tgc gca gag atg atc tac cag gac ctg cct ttc gag gag agg 163
 Ala Ala Cys Ala Glu Met Ile Tyr Gln Asp Leu Pro Phe Glu Glu Arg 20
 gtc aag acg atc tct gat cag gga ttc ctc gtg gaa att tgg gac tgg 211
 Val Lys Thr Ile Ser Asp Gln Gly Phe Leu Val Glu Ile Trp Asp Trp 35
 tcc aca aaa gac atc gat gcg ctc gtg gca aca ggc gcg gaa ttt tcc 259
 Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr Gly Ala Glu Phe Ser 50
 tcc atg acg ggc tac ctg cgc ggg gat ctg att act gaa cag ggc cgc 307
 Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile Thr Glu Gln Gly Arg

55	60	65	
gcg gag ctc ttg gca acc gct tcg gag tcc ttg gcg gtg gcg gaa aag			355
Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu Ala Val Ala Glu Lys			
70	75	80	85
ctc aac tgc ccc cgg ctg aat ctg cat gga act ggc ctt gga ccg cag			403
Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr Gly Leu Gly Pro Gln			
	90	95	100
gga cta cct gtt act ccc att gaa gtg gtt acc cca gaa atg tgg ctc			451
Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr Pro Glu Met Trp Leu			
	105	110	115
tac gct gct gaa acg ctc cgc cag atc gct gag ctg ggg gag cgc gca			499
Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu Leu Gly Glu Arg Ala			
	120	125	130
ggc aag gtt ttc gtg ctg gaa aac ctc aac ctc gca gtc gat cac ccc			547
Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu Ala Val Asp His Pro			
	135	140	145
ggc act cct ttt gcc aag gcc act gac act ttg gcg ctg gtc aag gct			595
Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu Ala Leu Val Lys Ala			
	150	155	160
gtc aat cac ccg aat ctg cgc ctc aac ctg gat ttg tac cac gcc cag			643
Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp Leu Tyr His Ala Gln			
	170	175	180
att ggc gaa gga aac ctc att gag ctg ctc cgt gag gcg cag cca ttc			691
Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg Glu Ala Gln Pro Phe			
	185	190	195
atc ggc gaa atc cag gtt gcc gat gtc ccc ggc cgc atg gaa ccc ggc			739
Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly Arg Met Glu Pro Gly			
	200	205	210
acc ggc gag atc aac tac cag ggc gtc gcg aaa gct ctc gcc gcg atg			787
Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys Ala Leu Ala Ala Met			
	215	220	225
ggc tac gac ggc gtc atc ggc atg gag gcg tgg gca tcg ggc gac tcc			835
Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp Ala Ser Gly Asp Ser			
	230	235	240
agc gac gcg ctg cag gcg ttg aag tca gcg ttc acg gtc taaattgctt			884
Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe Thr Val			
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<211> 258

<212> PRT

<213> Corynebacterium glutamicum

<400> 600

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 Glu Ile Trp Asp Trp Ser Thr Lys Asp Ile Asp Ala Leu Val Ala Thr
 35 40 45
 Gly Ala Glu Phe Ser Ser Met Thr Gly Tyr Leu Arg Gly Asp Leu Ile
 50 55 60
 Thr Glu Gln Gly Arg Ala Glu Leu Leu Ala Thr Ala Ser Glu Ser Leu
 65 70 75 80
 Ala Val Ala Glu Lys Leu Asn Cys Pro Arg Leu Asn Leu His Gly Thr
 85 90 95
 Gly Leu Gly Pro Gln Gly Leu Pro Val Thr Pro Ile Glu Val Val Thr
 100 105 110
 Pro Glu Met Trp Leu Tyr Ala Ala Glu Thr Leu Arg Gln Ile Ala Glu
 115 120 125
 Leu Gly Glu Arg Ala Gly Lys Val Phe Val Leu Glu Asn Leu Asn Leu
 130 135 140
 Ala Val Asp His Pro Gly Thr Pro Phe Ala Lys Ala Thr Asp Thr Leu
 145 150 155 160
 Ala Leu Val Lys Ala Val Asn His Pro Asn Leu Arg Leu Asn Leu Asp
 165 170 175
 Leu Tyr His Ala Gln Ile Gly Glu Gly Asn Leu Ile Glu Leu Leu Arg
 180 185 190
 Glu Ala Gln Pro Phe Ile Gly Glu Ile Gln Val Ala Asp Val Pro Gly
 195 200 205
 Arg Met Glu Pro Gly Thr Gly Glu Ile Asn Tyr Gln Gly Val Ala Lys
 210 215 220
 Ala Leu Ala Ala Met Gly Tyr Asp Gly Val Ile Gly Met Glu Ala Trp
 225 230 235 240
 Ala Ser Gly Asp Ser Ser Asp Ala Leu Gln Ala Leu Lys Ser Ala Phe
 245 250 255
 Thr Val

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 <212> DNA
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 <223> RXN03117

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	1 5	
gtg cgc acc cac cgt tct gcg gaa gag ttc ccg tac aag aag cac ctg	103	
Val Arg Thr His Arg Ser Ala Glu Glu Phe Pro Tyr Lys Lys His Leu		
	10 15 20	
gct cac aag atg gct cgc gtt gca gcc gac cca gtt gag gtt gct gcg	151	
Ala His Lys Met Ala Arg Val Ala Ala Asp Pro Val Glu Val Ala Ala		
	25 30 35	
gac act cag gaa atg atc atc acc cgc atc atc gac aat gca tcg gtg	199	
Asp Thr Gln Glu Met Ile Ile Thr Arg Ile Ile Asp Asn Ala Ser Val		
	40 45 50	
cag gca gct tcc gtg ttg cgt cga cca gtt agc tct gcc cgt gcg atg	247	
Gln Ala Ala Ser Val Leu Arg Arg Pro Val Ser Ser Ala Arg Ala Met		
	55 60 65	
gca cag gtc agg cca gtt acc gat ggt cgg ggt gca tct gtt ttc ggt	295	
Ala Gln Val Arg Pro Val Thr Asp Gly Arg Gly Ala Ser Val Phe Gly		
	70 75 80 85	
ctg cca gga cgt tat gcc gcg gaa tgg gct gcg ctt gct aac ggc act	343	
Leu Pro Gly Arg Tyr Ala Ala Glu Trp Ala Ala Leu Ala Asn Gly Thr		
	90 95 100	
gcg gtg cgt gag ctt gat ttc cat gac acg ttc ctc gct gcg gaa tac	391	
Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr		
	105 110 115	
tcc cac cca gga gat aac att cct ccg att ttg gct gca gca cag cag	439	
Ser His Pro Gly Asp Asn Ile Pro Pro Ile Leu Ala Ala Ala Gln Gln		
	120 125 130	
gct gga aaa ggt ggc aag gat ctg atc cgt ggc atc gct act ggg tat	487	
Ala Gly Lys Gly Gly Lys Asp Leu Ile Arg Gly Ile Ala Thr Gly Tyr		
	135 140 145	
gag att cag gtt aac ttg gtg cgt gga atg tgc ctg cat gag cac aag	535	
Glu Ile Gln Val Asn Leu Val Arg Gly Met Cys Leu His Glu His Lys		
	150 155 160 165	
att gat cac gtt gct cat ctt gga cca tca gcg gct gct ggt atc gga	583	
Ile Asp His Val Ala His Leu Gly Pro Ser Ala Ala Ala Gly Ile Gly		
	170 175 180	
acc ttg cta gac cta gat gtg gac acc atc tac cag gca att ggt cag	631	
Thr Leu Leu Asp Leu Asp Val Asp Thr Ile Tyr Gln Ala Ile Gly Gln		
	185 190 195	
gca ttg cac acc acc acg gcg acg agg cag tcc cgt aaa ggt gcg att	679	
Ala Leu His Thr Thr Thr Ala Thr Arg Gln Ser Arg Lys Gly Ala Ile		
	200 205 210	
tct tca tgg aag gca ttt gct cct gcg ttt gcg ggc aag atg tcc atc	727	
Ser Ser Trp Lys Ala Phe Ala Pro Ala Phe Ala Gly Lys Met Ser Ile		
	215 220 225	
gag gca gta gat cgc gca atg cgt ggc gag ggc gca ccg tca cca atc	775	

Glu Ala Val Asp Arg Ala Met Arg Gly Glu Gly Ala Pro Ser Pro Ile	
230 235 240 245	
tgg gaa ggc gaa gac ggc gta atc gcg tgg ctg ctg tcc ggt ctt gat	823
Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Leu Asp	
250 255 260	
cac atc tac acc att cct ttg cct gca gaa ggt gaa gcc aaa cga gca	871
His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly Glu Ala Lys Arg Ala	
265 270 275	
atc ttg gat acc tac acc aag gaa cac tcg gcg gaa tac cag tca cag	919
Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln	
280 285 290	
gca ccg atc gac ttg gcg cgc agc atg ggg gag aag ctg gca gca cag	967
Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu Lys Leu Ala Ala Gln	
295 300 305	
ggc ttg gac ctg cgt gat gtg gac tcc atc gtt ttg cac acc tcc cac	1015
Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val Leu His Thr Ser His	
310 315 320 325	
cac act cac tac gtg atc ggc acc gga tct aat gat cca cag aag ttc	1063
His Thr His Tyr Val Ile Gly Thr Gly Ser Asn Asp Pro Gln Lys Phe	
330 335 340	
gat cca gat gca tcg cga gaa acc ctt gat cac tcc atc atg tac att	1111
Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile	
345 350 355	
ttc gct gtc gcg ctg aag gat cgc gcg tgg cac cac gag cgt tcc tat	1159
Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His His Glu Arg Ser Tyr	
360 365 370	
gct cct gag cga gcc cac cgc cga gag acc atc gag ctg tgg aac aag	1207
Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile Glu Leu Trp Asn Lys	
375 380 385	
att tcc acg gtg gag gat cct gaa tgg acc agg cgt tac cac tcc gtt	1255
Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Val	
390 395 400 405	
gat cct gca gaa aag gcc ttc ggc gca cgc gca gtg atc acc ttc aag	1303
Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala Val Ile Thr Phe Lys	
410 415 420	
gat gga acc gtc gtg gaa gat gaa ctg gct gtg gcg aat gcg cat cct	1351
Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val Ala Asn Ala His Pro	
425 430 435	
ctg gga gca cgg cct ttc gct agg gag cag tac att cag aaa ttc cgc	1399
Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr Ile Gln Lys Phe Arg	
440 445 450	
acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa cag gat cgc ttc ttg	1447
Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu Gln Asp Arg Phe Leu	
455 460 465	
gat gcg gca cag cgt acg cac gag ctt gag gat ctt tca gaa ctc aac	1495
Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp Leu Ser Glu Leu Asn	

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Gly Leu Phe

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<212> PRT
<213> Corynebacterium glutamicum
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Tyr	Lys	Lys	His 20	Leu	Ala	His	Lys	Met 25	Ala	Arg	Val	Ala	Ala 30	Asp	Pro
Val	Glu	Val 35	Ala	Ala	Asp	Thr	Gln 40	Glu	Met	Ile	Ile	Thr 45	Arg	Ile	Ile
Asp	Asn 50	Ala	Ser	Val	Gln	Ala 55	Ala	Ser	Val	Leu	Arg 60	Arg	Pro	Val	Ser
Ser 65	Ala	Arg	Ala	Met	Ala 70	Gln	Val	Arg	Pro	Val 75	Thr	Asp	Gly	Arg	Gly 80
Ala	Ser	Val	Phe	Gly 85	Leu	Pro	Gly	Arg	Tyr 90	Ala	Ala	Glu	Trp	Ala 95	Ala
Leu	Ala	Asn	Gly 100	Thr	Ala	Val	Arg	Glu 105	Leu	Asp	Phe	His	Asp 110	Thr	Phe
Leu	Ala 115	Ala	Glu	Tyr	Ser	His	Pro 120	Gly	Asp	Asn	Ile	Pro 125	Pro	Ile	Leu
Ala 130	Ala	Ala	Gln	Gln	Ala	Gly 135	Lys	Gly	Gly	Lys	Asp 140	Leu	Ile	Arg	Gly
Ile 145	Ala	Thr	Gly	Tyr	Glu 150	Ile	Gln	Val	Asn 155	Leu	Val	Arg	Gly	Met	Cys 160
Leu	His	Glu	His	Lys 165	Ile	Asp	His	Val	Ala 170	His	Leu	Gly	Pro	Ser 175	Ala
Ala	Ala	Gly	Ile 180	Gly	Thr	Leu	Leu	Asp 185	Leu	Asp	Val	Asp	Thr 190	Ile	Tyr
Gln	Ala 195	Ile	Gly	Gln	Ala	Leu	His 200	Thr	Thr	Thr	Ala	Thr 205	Arg	Gln	Ser
Arg	Lys 210	Gly	Ala	Ile	Ser	Ser 215	Trp	Lys	Ala	Phe	Ala 220	Pro	Ala	Phe	Ala
Gly 225	Lys	Met	Ser	Ile	Glu 230	Ala	Val	Asp	Arg	Ala 235	Met	Arg	Gly	Glu	Gly 240

Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala Trp Leu
 245 250 255
 Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala Glu Gly
 260 265 270
 Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His Ser Ala
 275 280 285
 Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met Gly Glu
 290 295 300
 Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser Ile Val
 305 310 315 320
 Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly Ser Asn
 325 330 335
 Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu Asp His
 340 345 350
 Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Lys Asp Arg Ala Trp His
 355 360 365
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala His Arg Arg Glu Thr Ile
 370 375 380
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
 385 390 395 400
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 405 410 415
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 420 425 430
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 435 440 445
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 450 455 460
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 465 470 475 480
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 485 490 495
 Pro Val Ile Pro Glu Gly Leu Phe
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<210> 603

<211> 975

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(975)

<223> FRXA00406

<400> 603

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atc atc gac aat gca tgc gtg cag gca gct tcc gtg ttg cgt cga cca	96
Ile Ile Asp Asn Ala Ser Val Gln Ala Ser Val Leu Arg Arg Pro	
20 25 30	
gtt agc tct gcc cgt gcg atg gca cag gtc agg cca gtt acc gat ggt	144
Val Ser Ser Ala Arg Ala Met Ala Gln Val Arg Pro Val Thr Asp Gly	
35 40 45	
cgg ggt gca tct gtt ttc ggt ctg cca gga cgt tat gcc gcg gaa tgg	192
Arg Gly Ala Ser Val Phe Gly Leu Pro Gly Arg Tyr Ala Ala Glu Trp	
50 55 60	
gct gcg ctt gct aac ggc act gcg gtg cgt gag ctt gat ttc cat gac	240
Ala Ala Leu Ala Asn Gly Thr Ala Val Arg Glu Leu Asp Phe His Asp	
65 70 75 80	
acg ttc ctc gct gcg gaa tac tcc cac cca gga gat aac att cct ccg	288
Thr Phe Leu Ala Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro	
85 90 95	
att ttg gct gca gca cag cag gct gga aaa ggt ggc aag gat ctg atc	336
Ile Leu Ala Ala Ala Gln Gln Ala Gly Lys Gly Gly Lys Asp Leu Ile	
100 105 110	
cgt ggc atc gct act ggg tat gag att cag gtt aac ttg gtg cgt gga	384
Arg Gly Ile Ala Thr Gly Tyr Glu Ile Gln Val Asn Leu Val Arg Gly	
115 120 125	
atg tgc ctg cat gag cac aag att gat cac gtt gct cat ctt gga cca	432
Met Cys Leu His Glu His Lys Ile Asp His Val Ala His Leu Gly Pro	
130 135 140	
tca gcg gct gct ggt atc gga acc ttg cta gac cta gat gtg gac acc	480
Ser Ala Ala Ala Gly Ile Gly Thr Leu Leu Asp Leu Asp Val Asp Thr	
145 150 155 160	
atc tac cag gca att ggt cag gca ttg cac acc acc acg gcg acg agg	528
Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg	
165 170 175	
cag tcc cgt aaa ggt gcg att tct tca tgg aag gca ttt gct cct gcg	576
Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala	
180 185 190	
ttt gcg ggc aag atg tcc atc gag gca gta gat cgc gca atg cgt ggc	624
Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly	
195 200 205	
gag ggc gca ccg tca cca atc tgg gaa ggc gaa gac ggc gta atc gcg	672
Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala	
210 215 220	
tgg ctg ctg tcc ggt ctt gat cac atc tac acc att cct ttg cct gca	720
Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala	

225	230	235	240	
gaa ggt gaa gcc aaa cga gca atc ttg gat acc tac acc aag gaa cac				768
Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His				
	245	250	255	
tcg gcg gaa tac cag tca cag gca ccg atc gac ttg gcg cgc agc atg				816
Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met				
	260	265	270	
ggg gag aag ctg gca gca cag ggc ttg gac ctg cgt gat gtg gac tcc				864
Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser				
	275	280	285	
atc gtt ttg cac acc tcc cac cac act cac tac gtg atc ggc acc gga				912
Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly				
	290	295	300	
tct aat gat cca cag aag ttc gat cca gat gca tcg cga gaa acc ctt				960
Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu				
305	310	315	320	
gat cac tcc atc atg				975
Asp His Ser Ile Met				
	325			

<210> 604

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 604

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Ile	Ile	Asp	Asn	Ala	Ser	Val	Gln	Ala	Ala	Ser	Val	Leu	Arg	Arg	Pro
		20					25						30		
Val	Ser	Ser	Ala	Arg	Ala	Met	Ala	Gln	Val	Arg	Pro	Val	Thr	Asp	Gly
		35					40					45			
Arg	Gly	Ala	Ser	Val	Phe	Gly	Leu	Pro	Gly	Arg	Tyr	Ala	Ala	Glu	Trp
	50					55					60				
Ala	Ala	Leu	Ala	Asn	Gly	Thr	Ala	Val	Arg	Glu	Leu	Asp	Phe	His	Asp
	65				70					75					80
Thr	Phe	Leu	Ala	Ala	Glu	Tyr	Ser	His	Pro	Gly	Asp	Asn	Ile	Pro	Pro
			85					90					95		
Ile	Leu	Ala	Ala	Ala	Gln	Gln	Ala	Gly	Lys	Gly	Gly	Lys	Asp	Leu	Ile
		100						105					110		
Arg	Gly	Ile	Ala	Thr	Gly	Tyr	Glu	Ile	Gln	Val	Asn	Leu	Val	Arg	Gly
		115					120					125			
Met	Cys	Leu	His	Glu	His	Lys	Ile	Asp	His	Val	Ala	His	Leu	Gly	Pro
	130					135					140				
Ser	Ala	Ala	Ala	Gly	Ile	Gly	Thr	Leu	Leu	Asp	Leu	Asp	Val	Asp	Thr

145 150 155 160
 Ile Tyr Gln Ala Ile Gly Gln Ala Leu His Thr Thr Thr Ala Thr Arg
 165 170 175
 Gln Ser Arg Lys Gly Ala Ile Ser Ser Trp Lys Ala Phe Ala Pro Ala
 180 185 190
 Phe Ala Gly Lys Met Ser Ile Glu Ala Val Asp Arg Ala Met Arg Gly
 195 200 205
 Glu Gly Ala Pro Ser Pro Ile Trp Glu Gly Glu Asp Gly Val Ile Ala
 210 215 220
 Trp Leu Leu Ser Gly Leu Asp His Ile Tyr Thr Ile Pro Leu Pro Ala
 225 230 235 240
 Glu Gly Glu Ala Lys Arg Ala Ile Leu Asp Thr Tyr Thr Lys Glu His
 245 250 255
 Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu Ala Arg Ser Met
 260 265 270
 Gly Glu Lys Leu Ala Ala Gln Gly Leu Asp Leu Arg Asp Val Asp Ser
 275 280 285
 Ile Val Leu His Thr Ser His His Thr His Tyr Val Ile Gly Thr Gly
 290 295 300
 Ser Asn Asp Pro Gln Lys Phe Asp Pro Asp Ala Ser Arg Glu Thr Leu
 305 310 315 320
 Asp His Ser Ile Met
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<210> 605
 <211> 431
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(408)
 <223> FRXA00514

<400> 605
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 1 5 10 15
 gag ctg tgg aac aag att tcc acg gtg gag gat cct gaa tgg acc agg 96
 Glu Leu Trp Asn Lys Ile Ser Thr Val Glu Asp Pro Glu Trp Thr Arg
 20 25 30
 cgt tac cac tcc gtt gat cct gca gaa aag gcc ttc ggc gca cgc gca 144
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 gtg atc acc ttc aag gat gga acc gtc gtg gaa gat gaa ctg gct gtg 192
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val

50	55	60	
gcg aat gcg cat cct ctg gga gca cgg cct ttc gct agg gag cag tac			240
Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr			
65	70	75	80
att cag aaa ttc cgc acc ttg gct gaa ggt gtt gtg tcc gaa aag gaa			288
Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu			
	85	90	95
cag gat cgc ttc ttg gat gcg gca cag cgt acg cac gag ctt gag gat			336
Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp			
	100	105	110
ctt tca gaa ctc aac att gaa ttg gat gcc gat att ttg gcc aag gct			384
Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala			
	115	120	125
cct gtg att ccg gaa gga ctg ttc tgatggcggg tttgttttcc tct			431
Pro Val Ile Pro Glu Gly Leu Phe			
130	135		

<210> 606
 <211> 136
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 606
 His Glu Arg Ser Tyr Ala Pro Glu Arg Ala Leu Arg Arg Glu Thr Ile
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 20 25 30
 Arg Tyr His Ser Val Asp Pro Ala Glu Lys Ala Phe Gly Ala Arg Ala
 35 40 45
 Val Ile Thr Phe Lys Asp Gly Thr Val Val Glu Asp Glu Leu Ala Val
 50 55 60
 Ala Asn Ala His Pro Leu Gly Ala Arg Pro Phe Ala Arg Glu Gln Tyr
 65 70 75 80
 Ile Gln Lys Phe Arg Thr Leu Ala Glu Gly Val Val Ser Glu Lys Glu
 85 90 95
 Gln Asp Arg Phe Leu Asp Ala Ala Gln Arg Thr His Glu Leu Glu Asp
 100 105 110
 Leu Ser Glu Leu Asn Ile Glu Leu Asp Ala Asp Ile Leu Ala Lys Ala
 115 120 125
 Pro Val Ile Pro Glu Gly Leu Phe
 130 135

<210> 607
 <211> 718
 <212> DNA
 <213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(718)

<223> RXA00512

<400> 607

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cccatcttct aaccgccta tatataagga gtgaatcacc atg tcc agc gcc aca 115
                                         Met Ser Ser Ala Thr
                                         1 5
acc act gat gtt cgc aaa ggg ctc tac gga gtc atc gcc gat tac acg 163
Thr Thr Asp Val Arg Lys Gly Leu Tyr Gly Val Ile Ala Asp Tyr Thr
                        10 15 20
gcc gtt tcc aaa gtc atg cca gag acc aat tca ctg acc tac cgt ggc 211
Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser Leu Thr Tyr Arg Gly
                        25 30 35
tac gcg gtg gaa gat ttg gtg gaa aac tgc agc ttc gag gag gtg ttt 259
Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Phe
                        40 45 50
tac ctc ctg tgg cac ggc gag ctg ccc act gcg caa caa ctt gcg gag 307
Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala Gln Gln Leu Ala Glu
                        55 60 65
ttc aat gag cgt ggc cgt tcc tac cgc tcc ctg gat gcc ggt ttg atc 355
Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile
                        70 75 80 85
tcc ctg atc cac tct ttg ccc aaa gaa gcc cac ccg atg gat gtt atg 403
Ser Leu Ile His Ser Leu Pro Lys Glu Ala His Pro Met Asp Val Met
                        90 95 100
cgc acc gcg gtg tcc tac atg ggc acc aag gat tcc gag tat ttc acc 451
Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp Ser Glu Tyr Phe Thr
                        105 110 115
acc gat tct gag cac atc cgc aaa gtt ggc cac acc ttg ttg gcg cag 499
Thr Asp Ser Glu His Ile Arg Lys Val Gly His Thr Leu Leu Ala Gln
                        120 125 130
ctt ccg atg gtg cta gcc atg gat att cgt cgc cgc aag ggc ctc gat 547
Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg Arg Lys Gly Leu Asp
                        135 140 145
atc atc gcc cct gac tcc agc aag tca gtc gcc gaa aac ctg ctg tct 595
Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala Glu Asn Leu Leu Ser
                        150 155 160 165
atg gtg ttt ggt act ggc ccg gaa tca cct gca tcc aac cca gct gac 643
Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala Ser Asn Pro Ala Asp
                        170 175 180
gtc cgc gat ttt gag aaa tca ctg atc ctc tac gcc gag cac tcc ttc 691
Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr Ala Glu His Ser Phe
                        185 190 195

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aac gcc tcc acc ttc acc gcc cgc gtg
 Asn Ala Ser Thr Phe Thr Ala Arg Val
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718

<210> 608
 <211> 206
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 608
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 Ile Ala Asp Tyr Thr Ala Val Ser Lys Val Met Pro Glu Thr Asn Ser
 20 25 30
 Leu Thr Tyr Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser
 35 40 45
 Phe Glu Glu Val Phe Tyr Leu Leu Trp His Gly Glu Leu Pro Thr Ala
 50 55 60
 Gln Gln Leu Ala Glu Phe Asn Glu Arg Gly Arg Ser Tyr Arg Ser Leu
 65 70 75 80
 Asp Ala Gly Leu Ile Ser Leu Ile His Ser Leu Pro Lys Glu Ala His
 85 90 95
 Pro Met Asp Val Met Arg Thr Ala Val Ser Tyr Met Gly Thr Lys Asp
 100 105 110
 Ser Glu Tyr Phe Thr Thr Asp Ser Glu His Ile Arg Lys Val Gly His
 115 120 125
 Thr Leu Leu Ala Gln Leu Pro Met Val Leu Ala Met Asp Ile Arg Arg
 130 135 140
 Arg Lys Gly Leu Asp Ile Ile Ala Pro Asp Ser Ser Lys Ser Val Ala
 145 150 155 160
 Glu Asn Leu Leu Ser Met Val Phe Gly Thr Gly Pro Glu Ser Pro Ala
 165 170 175
 Ser Asn Pro Ala Asp Val Arg Asp Phe Glu Lys Ser Leu Ile Leu Tyr
 180 185 190
 Ala Glu His Ser Phe Asn Ala Ser Thr Phe Thr Ala Arg Val
 195 200 205

<210> 609
 <211> 320
 <212> DNA
 <213> Corynebacterium glutamicum
 <220>
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 <222> (1)..(297)
 <223> RXA00518

<400> 609

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Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
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atg tat gaa aac atg cgc gac gcc atg gac gcc cgc acc ggc atc aag 96
Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
             20             25             30

ccg aat ctc gat ttc cct gct ggc cct gcc tac cac ctg ctc ggt ttc 144
Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
             35             40             45

ccg gtc gat ttc ttc acc ccg ctg ttc gtc atc gcc cgc gtc gcc ggc 192
Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
             50             55             60

tgg acg gcc cac atc gtg gag cag tac gaa aac aac tcg ctc atc cgc 240
Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
             65             70             75             80

cca ctg tcc gag tac aac ggc gag gag cag cgc gag gtc gcg ccc att 288
Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
             85             90             95

gaa aag cgc taaaagattt tcgcttttcg acg 320
Glu Lys Arg

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<210> 610

<211> 99

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 610

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Val Leu Pro Val Leu Ala Ala Arg His Asp Gly Glu Lys Trp Val Ala
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Met Tyr Glu Asn Met Arg Asp Ala Met Asp Ala Arg Thr Gly Ile Lys
             20             25             30

Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr His Leu Leu Gly Phe
             35             40             45

Pro Val Asp Phe Phe Thr Pro Leu Phe Val Ile Ala Arg Val Ala Gly
             50             55             60

Trp Thr Ala His Ile Val Glu Gln Tyr Glu Asn Asn Ser Leu Ile Arg
             65             70             75             80

Pro Leu Ser Glu Tyr Asn Gly Glu Glu Gln Arg Glu Val Ala Pro Ile
             85             90             95

Glu Lys Arg

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<210> 611

<211> 1494

<212> DNA

<213> Corynebacterium glutamicum

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<221> CDS

$\langle 222 \rangle$ (101) . . (1471)

<223> RXA01077

$\langle 400 \rangle$ 611

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aatgaaggca agccaaactt aactagtaga taggattgca atg acc gaa tcg caa 115
Met Thr Glu Ser Gln
1 5

gat ctc gcc gca ttc gtg gaa gct gcc aaa ctc aat gat gca agc ccc 163
Asp Leu Ala Ala Phe Val Glu Ala Ala Lys Leu Asn Asp Ala Ser Pro
10 15 20

gaa gcc gta gag caa ttg aaa atc aga gtg cta gac acc gta ggc gtt 211
Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu Asp Thr Val Gly Val
25 30 35

gcc att ggc gca ctg gat gcc gaa ccg att gtc gcc att cga gga ctc 259
Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val Ala Ile Arg Gly Leu
40 45 50

ctg gaa gac ctc ggg gga acc gaa cag tca aca ctt att ggt ggt ggc 307
Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr Leu Ile Gly Gly Gly
55 60 65

aaa acc agt ccg gaa cgt gca gca ttt ttc aac agc gca tta agc cgc 355
Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn Ser Ala Leu Ser Arg
70 75 80 85

tac	ctc	gac	ttc	atg	gac	gcc	tac	cta	gca	aag	ggc	gaa	acc	aac	cac	403
Tyr	Leu	Asp	Phe	Met	Asp	Ala	Tyr	Leu	Ala	Lys	Gly	Glu	Thr	Asn	His	
				90					95					100		

ccc tcg gat aac ttc gga gca gtg ctc gct gca gcc gaa agc gtt ggc 451
Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala Ala Glu Ser Val Gly
105 110 115

gcc tct gga aaa gac ctg ctc acc gca ttc gcc gtg gcc tac cag gta 499
Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala Val Ala Tyr Gln Val
120 125 130

cac acc aga ctt tca gat gtc gca cca gtt cgc gcc aaa ggt ttc gat 547
 His Thr Arg Leu Ser Asp Val Ala Pro Val Arg Ala Lys Gly Phe Asp
 135 140 145

cac acc acc caa gga gca ttc gca gcg ggc gca tct gct gcc aag gca 595
 His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala Ser Ala Ala Lys Ala
 150 155 160 165

ctg ggt ttg cca gct gat caa atc gcc aac gca ctg gcc atc gca gga 643
Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala Leu Ala Ile Ala Gly
170 175 180

aca gcc aat gtt gca ctt cgt gtc act cgc act gga aac ttg agc cac 691
Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr Gly Asn Leu Ser His
185 190 195

tgg aaa ggc ctt gcc tac cca cac gtg tcc aaa gaa gga acc tgg gca	739
Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys Glu Gly Thr Trp Ala	
200 205 210	
gca ctg ctc gca agc cga ggt att acc ggt ccg gaa gaa gtc ttc gaa	787
Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro Glu Glu Val Phe Glu	
215 220 225	
ggc aac aag gga ttc aaa gag tcc gtc tcc gga ccg ttc gag atc gat	835
Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly Pro Phe Glu Ile Asp	
230 235 240 245	
tgg tcc aag gaa gac ttg gaa agc gtt aag cgc acc atc atc aag aaa	883
Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg Thr Ile Ile Lys Lys	
250 255 260	
cac aac gcg gaa att cac tcg cag tca gcg ctt gat gca gcc caa gaa	931
His Asn Ala Glu Ile His Ser Gln Ser Ala Leu Asp Ala Ala Gln Glu	
265 270 275	
ata cgc gca caa gaa ggc ttc aat gtg gac aac att gaa aag att cac	979
Ile Arg Ala Gln Glu Gly Phe Asn Val Asp Asn Ile Glu Lys Ile His	
280 285 290	
ctg act act ttc gac gtt gcc tac tcc atc att ggc ggc ggc gaa gaa	1027
Leu Thr Thr Phe Asp Val Ala Tyr Ser Ile Ile Gly Gly Gly Glu Glu	
295 300 305	
ggc gac aaa cag ctt att cgc acc aaa gaa gaa gcc gat cac tca ctg	1075
Gly Asp Lys Gln Leu Ile Arg Thr Lys Glu Glu Ala Asp His Ser Leu	
310 315 320 325	
ccg tgg atg ctc gct gta gtt ctg ctg gat ggt cag ctc aat ccc gaa	1123
Pro Trp Met Leu Ala Val Val Leu Leu Asp Gly Gln Leu Asn Pro Glu	
330 335 340	
cag tac gaa cca tca cgc atc gtt gct gat gat gta caa acc ttg atg	1171
Gln Tyr Glu Pro Ser Arg Ile Val Ala Asp Asp Val Gln Thr Leu Met	
345 350 355	
aag aaa atc gaa atc aca ccg tca gat gaa ttc tct gat cgc ttc cct	1219
Lys Lys Ile Glu Ile Thr Pro Ser Asp Glu Phe Ser Asp Arg Phe Pro	
360 365 370	
gac cac atg cca gct gat cta gaa gtc aca cta aac gat ggc tcg gtg	1267
Asp His Met Pro Ala Asp Leu Glu Val Thr Leu Asn Asp Gly Ser Val	
375 380 385	
ttc aaa gct tca caa gat agc tac tta ggc ttc cac gac aat ccc cta	1315
Phe Lys Ala Ser Gln Asp Ser Tyr Leu Gly Phe His Asp Asn Pro Leu	
390 395 400 405	
gat tgg gac aac gcg cgc aag aaa ttc gat gcc ctt gtc aca cca ttc	1363
Asp Trp Asp Asn Ala Arg Lys Lys Phe Asp Ala Leu Val Thr Pro Phe	
410 415 420	
acc ggt gaa gaa cta cgt gaa gaa atc gcc acg atc att cac gag ctc	1411
Thr Gly Glu Glu Leu Arg Glu Glu Ile Ala Thr Ile Ile His Glu Leu	
425 430 435	

gat agc cga cag gtt tct gaa ctc aca gaa gcc ctg gcc aaa gtc tcc 1459
 Asp Ser Arg Gln Val Ser Glu Leu Thr Glu Ala Leu Ala Lys Val Ser
 440 445 450

acc acc cgc agc taaaactttt tgaaaggagc tca 1494
 Thr Thr Arg Ser
 455

<210> 612

<211> 457

<212> PRT

<213> Corynebacterium glutamicum

<400> 612

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Asn Asp Ala Ser Pro Glu Ala Val Glu Gln Leu Lys Ile Arg Val Leu
 20 25 30

Asp Thr Val Gly Val Ala Ile Gly Ala Leu Asp Ala Glu Pro Ile Val
 35 40 45

Ala Ile Arg Gly Leu Leu Glu Asp Leu Gly Gly Thr Glu Gln Ser Thr
 50 55 60

Leu Ile Gly Gly Gly Lys Thr Ser Pro Glu Arg Ala Ala Phe Phe Asn
 65 70 75 80

Ser Ala Leu Ser Arg Tyr Leu Asp Phe Met Asp Ala Tyr Leu Ala Lys
 85 90 95

Gly Glu Thr Asn His Pro Ser Asp Asn Phe Gly Ala Val Leu Ala Ala
 100 105 110

Ala Glu Ser Val Gly Ala Ser Gly Lys Asp Leu Leu Thr Ala Phe Ala
 115 120 125

Val Ala Tyr Gln Val His Thr Arg Leu Ser Asp Val Ala Pro Val Arg
 130 135 140

Ala Lys Gly Phe Asp His Thr Thr Gln Gly Ala Phe Ala Ala Gly Ala
 145 150 155 160

Ser Ala Ala Lys Ala Leu Gly Leu Pro Ala Asp Gln Ile Ala Asn Ala
 165 170 175

Leu Ala Ile Ala Gly Thr Ala Asn Val Ala Leu Arg Val Thr Arg Thr
 180 185 190

Gly Asn Leu Ser His Trp Lys Gly Leu Ala Tyr Pro His Val Ser Lys
 195 200 205

Glu Gly Thr Trp Ala Ala Leu Leu Ala Ser Arg Gly Ile Thr Gly Pro
 210 215 220

Glu Glu Val Phe Glu Gly Asn Lys Gly Phe Lys Glu Ser Val Ser Gly
 225 230 235 240

Pro Phe Glu Ile Asp Trp Ser Lys Glu Asp Leu Glu Ser Val Lys Arg

245										250					255				
Thr	Ile	Ile	Lys	Lys	His	Asn	Ala	Glu	Ile	His	Ser	Gln	Ser	Ala	Leu				
			260					265					270						
Asp	Ala	Ala	Gln	Glu	Ile	Arg	Ala	Gln	Glu	Gly	Phe	Asn	Val	Asp	Asn				
		275					280					285							
Ile	Glu	Lys	Ile	His	Leu	Thr	Thr	Phe	Asp	Val	Ala	Tyr	Ser	Ile	Ile				
	290					295					300								
Gly	Gly	Gly	Glu	Glu	Gly	Asp	Lys	Gln	Leu	Ile	Arg	Thr	Lys	Glu	Glu				
305					310					315					320				
Ala	Asp	His	Ser	Leu	Pro	Trp	Met	Leu	Ala	Val	Val	Leu	Leu	Asp	Gly				
				325					330					335					
Gln	Leu	Asn	Pro	Glu	Gln	Tyr	Glu	Pro	Ser	Arg	Ile	Val	Ala	Asp	Asp				
			340					345					350						
Val	Gln	Thr	Leu	Met	Lys	Lys	Ile	Glu	Ile	Thr	Pro	Ser	Asp	Glu	Phe				
		355					360					365							
Ser	Asp	Arg	Phe	Pro	Asp	His	Met	Pro	Ala	Asp	Leu	Glu	Val	Thr	Leu				
	370					375					380								
Asn	Asp	Gly	Ser	Val	Phe	Lys	Ala	Ser	Gln	Asp	Ser	Tyr	Leu	Gly	Phe				
385					390				395					400					
His	Asp	Asn	Pro	Leu	Asp	Trp	Asp	Asn	Ala	Arg	Lys	Lys	Phe	Asp	Ala				
				405				410					415						
Leu	Val	Thr	Pro	Phe	Thr	Gly	Glu	Glu	Leu	Arg	Glu	Glu	Ile	Ala	Thr				
			420				425						430						
Ile	Ile	His	Glu	Leu	Asp	Ser	Arg	Gln	Val	Ser	Glu	Leu	Thr	Glu	Ala				
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<213> Corynebacterium glutamicum

<220>

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<222> (1)..(900)

<223> RXN03144

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1				5				10					15				
aag	gcg	ttc	gcg	cca	gcg	ttt	gcg	gga	aag	atg	gcc	att	gag	gcg	atg		96
Lys	Ala	Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met		
			20					25					30				

gat	cgt	gcg	atg	cgt	ggg	gag	ggt	tcg	ccc	gca	ccg	att	tgg	gag	ggc	144
Asp	Arg	Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly	
		35					40					45				
gaa	gac	ggg	gtc	atc	gcg	tgg	ctg	tta	tcg	ggc	aaa	gat	cat	gtt	tat	192
Glu	Asp	Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr	
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cat	gtg	cca	ttg	ccg	gaa	cac	ggc	gag	ccc	aag	ctg	ggg	att	cta	gag	240
His	Val	Pro	Leu	Pro	Glu	His	Gly	Glu	Pro	Lys	Leu	Gly	Ile	Leu	Glu	
	65				70					75					80	
act	tac	aca	aag	gaa	cat	tca	gcg	gaa	tat	caa	tcg	cag	gca	ccg	att	288
Thr	Tyr	Thr	Lys	Glu	His	Ser	Ala	Glu	Tyr	Gln	Ser	Gln	Ala	Pro	Ile	
			85						90					95		
gat	ctg	gcg	cgc	agg	atg	aag	cca	ctg	gtt	gac	gcg	gct	ggc	gga	acg	336
Asp	Leu	Ala	Arg	Arg	Met	Lys	Pro	Leu	Val	Asp	Ala	Ala	Gly	Gly	Thr	
			100					105					110			
gaa	cac	att	gca	gag	att	gtg	ctg	cgc	acc	agt	cac	cac	acg	cat	tat	384
Glu	His	Ile	Ala	Glu	Ile	Val	Leu	Arg	Thr	Ser	His	His	Thr	His	Tyr	
		115					120					125				
gtg	att	ggc	act	ggg	gcg	aac	gat	ccg	cag	aag	atg	gat	ccg	cag	gcc	432
Val	Ile	Gly	Thr	Gly	Ala	Asn	Asp	Pro	Gln	Lys	Met	Asp	Pro	Gln	Ala	
	130					135					140					
tcg	cgt	gaa	acc	ctg	gat	cat	tcc	atc	atg	tac	att	ttc	gcc	gtc	gcg	480
Ser	Arg	Glu	Thr	Leu	Asp	His	Ser	Ile	Met	Tyr	Ile	Phe	Ala	Val	Ala	
	145				150					155					160	
ctt	caa	gat	ggc	gtg	tgg	cac	cac	gag	ttt	tcc	tac	acc	cgc	aag	cgt	528
Leu	Gln	Asp	Gly	Val	Trp	His	His	Glu	Phe	Ser	Tyr	Thr	Arg	Lys	Arg	
				165				170						175		
tcc	acc	cgc	ccg	gaa	act	gtg	gag	ctg	tgg	cac	aag	att	cgc	acc	gtg	576
Ser	Thr	Arg	Pro	Glu	Thr	Val	Glu	Leu	Trp	His	Lys	Ile	Arg	Thr	Val	
			180					185					190			
gag	gat	cct	gaa	tgg	acg	cgc	cga	tac	cat	tct	gat	gat	cct	gca	aaa	624
Glu	Asp	Pro	Glu	Trp	Thr	Arg	Arg	Tyr	His	Ser	Asp	Asp	Pro	Ala	Lys	
		195					200					205				
aag	gcc	ttt	ggt	gcg	aaa	gca	gtg	atc	aca	atg	gct	gat	ggc	acc	gtg	672
Lys	Ala	Phe	Gly	Ala	Lys	Ala	Val	Ile	Thr	Met	Ala	Asp	Gly	Thr	Val	
	210					215					220					
att	gag	gat	gaa	ttg	gct	gtc	gcg	gat	gcc	cac	ccg	ctg	ggt	gct	cgg	720
Ile	Glu	Asp	Glu	Leu	Ala	Val	Ala	Asp	Ala	His	Pro	Leu	Gly	Ala	Arg	
	225				230					235					240	
ccg	ttt	gcg	cgg	gag	aat	tac	att	gaa	aaa	ttc	cgc	aca	ctc	gcg	cag	768
Pro	Phe	Ala	Arg	Glu	Asn	Tyr	Ile	Glu	Lys	Phe	Arg	Thr	Leu	Ala	Gln	
				245					250					255		
ggg	att	gtc	att	gat	tca	gaa	cag	gaa	cgc	ttc	ttg	cat	gcc	gtg	caa	816
Gly	Ile	Val	Ile	Asp	Ser	Glu	Gln	Glu	Arg	Phe	Leu	His	Ala	Val	Gln	
			260					265					270			
agc	ctg	cct	gac	ctg	gat	gat	ctt	gat	cag	ctc	aac	atc	gaa	gtc	gac	864

Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285

ata agc aac cag gcc gcg acg aaa gcg ggg ctg tta tgaatctctt 910
 Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
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<211> 300

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 614

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Asp Arg Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly
 35 40 45

Glu Asp Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr
 50 55 60

His Val Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu
 65 70 75 80

Thr Tyr Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile
 85 90 95

Asp Leu Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr
 100 105 110

Glu His Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr
 115 120 125

Val Ile Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala
 130 135 140

Ser Arg Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala
 145 150 155 160

Leu Gln Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg
 165 170 175

Ser Thr Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val
 180 185 190

Glu Asp Pro Glu Trp Thr Arg Arg Tyr His Ser Asp Asp Pro Ala Lys
 195 200 205

Lys Ala Phe Gly Ala Lys Ala Val Ile Thr Met Ala Asp Gly Thr Val
 210 215 220

Ile Glu Asp Glu Leu Ala Val Ala Asp Ala His Pro Leu Gly Ala Arg
 225 230 235 240

Pro Phe Ala Arg Glu Asn Tyr Ile Glu Lys Phe Arg Thr Leu Ala Gln
 245 250 255

Gly Ile Val Ile Asp Ser Glu Gln Glu Arg Phe Leu His Ala Val Gln
 260 265 270

Ser Leu Pro Asp Leu Asp Asp Leu Asp Gln Leu Asn Ile Glu Val Asp
 275 280 285

Ile Ser Asn Gln Ala Ala Thr Lys Ala Gly Leu Leu
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<211> 511

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(511)

<223> FRXA02322

<400> 615

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ctttaaggaa acagtgcaca aataaatctc aaggagcccc atg cgc atc cac gat 115
 Met Arg Ile His Asp
 1 5

gtt tat acc cac ctt tcg gcc gat aac ttt ccc aaa gca gag cac ctt 163
 Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro Lys Ala Glu His Leu
 10 15 20

gcg tgg aaa ttc tcc gag ctt gcc acc gac ccc gtg gag gtg aca ccg 211
 Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro Val Glu Val Thr Pro
 25 30 35

gat gtt tcg gag atg atc atc aac cgg atc atc gac aac gcg gcg gtg 259
 Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile Asp Asn Ala Ala Val
 40 45 50

tct gcc gcg tcg gtg ttg cgc cgg cct gtg act gtg gcc agg caa caa 307
 Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr Val Ala Arg Gln Gln
 55 60 65

gcg cag tcc cat ccg cgg gaa aag ggc gga aaa gtt ttt gga att tca 355
 Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys Val Phe Gly Ile Ser
 70 75 80 85

ggc agc tac tca cca gag tgg gct gcc ttt gct aat ggt gtg gcc gta 403
 Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala Asn Gly Val Ala Val
 90 95 100

cgt gaa ttg gac ttc cac gat aca ttt tta gca gct gaa tac tcc cat 451
 Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala Ala Glu Tyr Ser His
 105 110 115

ccc ggc gac aat att cca cca ctt ctt gca gta gcg cag gct cag aga 499
 Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val Ala Gln Ala Gln Arg
 120 125 130

agc agc ggc agg
Ser Ser Gly Arg
135

511

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<211> 137
<212> PRT
<213> Corynebacterium glutamicum

<400> 616
Met Arg Ile His Asp Val Tyr Thr His Leu Ser Ala Asp Asn Phe Pro
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Lys Ala Glu His Leu Ala Trp Lys Phe Ser Glu Leu Ala Thr Asp Pro
20 25 30
Val Glu Val Thr Pro Asp Val Ser Glu Met Ile Ile Asn Arg Ile Ile
35 40 45
Asp Asn Ala Ala Val Ser Ala Ala Ser Val Leu Arg Arg Pro Val Thr
50 55 60
Val Ala Arg Gln Gln Ala Gln Ser His Pro Arg Glu Lys Gly Gly Lys
65 70 75 80
Val Phe Gly Ile Ser Gly Ser Tyr Ser Pro Glu Trp Ala Ala Phe Ala
85 90 95
Asn Gly Val Ala Val Arg Glu Leu Asp Phe His Asp Thr Phe Leu Ala
100 105 110
Ala Glu Tyr Ser His Pro Gly Asp Asn Ile Pro Pro Leu Leu Ala Val
115 120 125
Ala Gln Ala Gln Arg Ser Ser Gly Arg
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<212> DNA
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<220>
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<222> (1)..(603)
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Thr Ala Thr Arg Gln Ser Arg Lys Gly Glu Ile Ser Ser Trp Lys Ala
1 5 10 15
ttc gcg cca gcg ttt gcg gga aag atg gcc att gag gcg atg gat cgt 96
Phe Ala Pro Ala Phe Ala Gly Lys Met Ala Ile Glu Ala Met Asp Arg
20 25 30
gcg atg cgt ggg gag ggt tcg ccc gca ccg att tgg gag ggc gaa gac 144
Ala Met Arg Gly Glu Gly Ser Pro Ala Pro Ile Trp Glu Gly Glu Asp

35	40	45	
ggg gtc atc gcg tgg ctg tta tgc ggc aaa gat cat gtt tat cat gtg			192
Gly Val Ile Ala Trp Leu Leu Ser Gly Lys Asp His Val Tyr His Val			
50	55	60	
cca ttg ccg gaa cac ggc gag ccc aag ctg ggg att cta gag act tac			240
Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr			
65	70	75	80
aca aag gaa cat tca gcg gaa tat caa tgc cag gca ccg att gat ctg			288
Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu			
	85	90	95
gcg cgc agg atg aag cca ctg gtt gac gcg gct ggc gga acg gaa cac			336
Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His			
	100	105	110
att gca gag att gtg ctg cgc acc agt cac cac acg cat tat gtg att			384
Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile			
	115	120	125
ggc act ggg gcg aac gat ccg cag aag atg gat ccg cag gcc tgc cgt			432
Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg			
	130	135	140
gaa acc ctg gat cat tcc atc atg tac att ttc gcc gtc gcg ctt caa			480
Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln			
	145	150	155
gat ggc gtg tgg cac cac gag ttt tcc tac acc cgc aag cgt tcc acc			528
Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr			
	165	170	175
cgc ccg gaa act gtg gag ctg tgg cac aag att cgc acc gtg gag gat			576
Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp			
	180	185	190
cct gaa tgg acg cgc cga tac cat tct			603
Pro Glu Trp Thr Arg Arg Tyr His Ser			
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<210> 618

<211> 201

<212> PRT

<213> Corynebacterium glutamicum

<400> 618

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Phe	Ala	Pro	Ala	Phe	Ala	Gly	Lys	Met	Ala	Ile	Glu	Ala	Met	Asp	Arg
		20						25					30		

Ala	Met	Arg	Gly	Glu	Gly	Ser	Pro	Ala	Pro	Ile	Trp	Glu	Gly	Glu	Asp
		35					40					45			

Gly	Val	Ile	Ala	Trp	Leu	Leu	Ser	Gly	Lys	Asp	His	Val	Tyr	His	Val
	50					55					60				

Pro Leu Pro Glu His Gly Glu Pro Lys Leu Gly Ile Leu Glu Thr Tyr
65 70 75 80

Thr Lys Glu His Ser Ala Glu Tyr Gln Ser Gln Ala Pro Ile Asp Leu
85 90 95

Ala Arg Arg Met Lys Pro Leu Val Asp Ala Ala Gly Gly Thr Glu His
100 105 110

Ile Ala Glu Ile Val Leu Arg Thr Ser His His Thr His Tyr Val Ile
115 120 125

Gly Thr Gly Ala Asn Asp Pro Gln Lys Met Asp Pro Gln Ala Ser Arg
130 135 140

Glu Thr Leu Asp His Ser Ile Met Tyr Ile Phe Ala Val Ala Leu Gln
145 150 155 160

Asp Gly Val Trp His His Glu Phe Ser Tyr Thr Arg Lys Arg Ser Thr
165 170 175

Arg Pro Glu Thr Val Glu Leu Trp His Lys Ile Arg Thr Val Glu Asp
180 185 190

Pro Glu Trp Thr Arg Arg Tyr His Ser
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<210> 619
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(1243)
<223> RXA02332

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Met Ser Asp Ser Gln
1 5

gtc cgc aaa gga ctc aac ggc gtc atc tct gac tac aca agc att tcc 163
Val Arg Lys Gly Leu Asn Gly Val Ile Ser Asp Tyr Thr Ser Ile Ser
10 15 20

aaa gtg atg cca gag agc aac tcg ctg act tac cgt ggc tac gcc gtg 211
Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr Arg Gly Tyr Ala Val
25 30 35

gag gat ttg gtg gaa aac tgc agc ttt gaa gaa gtg atc tac ctc ctg 259
Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu Val Ile Tyr Leu Leu
40 45 50

tgg ttt ggg gag ctg ccc acc act gaa caa ctc cgg acc ttc aac acg 307
Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu Arg Thr Phe Asn Thr
55 60 65

aca ggt cga agc tac cgc tca ctc gac gcc gga ctg att tcc ctc atc	355
Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly Leu Ile Ser Leu Ile	
70 75 80 85	
cac tcc tta ccc aac acc tgc cac ccc atg gac gtg ctg cgc acc gca	403
His Ser Leu Pro Asn Thr Cys His Pro Met Asp Val Leu Arg Thr Ala	
90 95 100	
gtg tcc tac atg ggt acc ttt gat ccc gat ccg ttt acc cgc gat gcc	451
Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro Phe Thr Arg Asp Ala	
105 110 115	
gat cat atc cga agc att gga cac aac ctg ctt gcg cag ctt ccc atg	499
Asp His Ile Arg Ser Ile Gly His Asn Leu Leu Ala Gln Leu Pro Met	
120 125 130	
gtg gtt gcc atg gat atc cgc agg cga agt ggg gaa gag atc atc gca	547
Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly Glu Glu Ile Ile Ala	
135 140 145	
cct gac cac aac aaa ggt atc gct tcg aat ttc tta tcc atg gtg ttt	595
Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe Leu Ser Met Val Phe	
150 155 160 165	
ggc aat gat gat ggt tct gta gcc aac tcc gca gat gac atc cgc gat	643
Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala Asp Asp Ile Arg Asp	
170 175 180	
ttt gaa cgc tcc ctc atc ctc tac gcc gag cac tcc ttc aac gcc tcc	691
Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His Ser Phe Asn Ala Ser	
185 190 195	
aca ttc tca gcc cgc gtg atc tca tca acg cga tcc gat acg tat tcg	739
Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg Ser Asp Thr Tyr Ser	
200 205 210	
gcg atc aca ggt gcg atc ggt gct ctc aaa ggc cca ctg cac gga ggt	787
Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly Pro Leu His Gly Gly	
215 220 225	
gcc aat gag ttt gtc atg cac acc atg ctg gat atc gac gat ccc aac	835
Ala Asn Glu Phe Val Met His Thr Met Leu Asp Ile Asp Asp Pro Asn	
230 235 240 245	
aat gct gcc gac tgg atg ggc aag gcg ttg gat cgt aaa gaa cgc atc	883
Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp Arg Lys Glu Arg Ile	
250 255 260	
atg gga ttc ggg cac cgc gtg tac aaa aac ggc gac tcc agg gtc ccc	931
Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly Asp Ser Arg Val Pro	
265 270 275	
tcc atg gag aaa tcc atg cgc tcc ctt gct gct cgt cac cgt ggt caa	979
Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala Arg His Arg Gly Gln	
280 285 290	
aaa tgg gtg cac atg tat gag tcg atg caa gaa gtc atg gag gct cgc	1027
Lys Trp Val His Met Tyr Glu Ser Met Gln Glu Val Met Glu Ala Arg	
295 300 305	
act ggc att aaa ccc aac ctc gac ttc ccg gcc ggc cct gcc tat tac	1075

Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala Gly Pro Ala Tyr Tyr
 310 315 320 325

atg ctg gga ttc ccc gtc gac ttc ttc aca cca ctg ttt gtg ctg gcc 1123
 Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro Leu Phe Val Leu Ala
 330 335 340

cga gtg tca ggg tgg acg gca cac atc gtg gag caa ttt gaa aac aat 1171
 Arg Val Ser Gly Trp Thr Ala His Ile Val Glu Gln Phe Glu Asn Asn
 345 350 355

gcg ctg atc cga cca ttg tct gcc tac aac gga gtg gaa gaa agg gag 1219
 Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly Val Glu Glu Arg Glu
 360 365 370

gtg gtg ccc att tcg gag aga acc taatcagtga ggctgatttc taa 1266
 Val Val Pro Ile Ser Glu Arg Thr
 375 380

<210> 620
 <211> 381
 <212> PRT
 <213> Corynebacterium glutamicum

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Tyr Thr Ser Ile Ser Lys Val Met Pro Glu Ser Asn Ser Leu Thr Tyr
 20 25 30

Arg Gly Tyr Ala Val Glu Asp Leu Val Glu Asn Cys Ser Phe Glu Glu
 35 40 45

Val Ile Tyr Leu Leu Trp Phe Gly Glu Leu Pro Thr Thr Glu Gln Leu
 50 55 60

Arg Thr Phe Asn Thr Thr Gly Arg Ser Tyr Arg Ser Leu Asp Ala Gly
 65 70 75 80

Leu Ile Ser Leu Ile His Ser Leu Pro Asn Thr Cys His Pro Met Asp
 85 90 95

Val Leu Arg Thr Ala Val Ser Tyr Met Gly Thr Phe Asp Pro Asp Pro
 100 105 110

Phe Thr Arg Asp Ala Asp His Ile Arg Ser Ile Gly His Asn Leu Leu
 115 120 125

Ala Gln Leu Pro Met Val Val Ala Met Asp Ile Arg Arg Arg Ser Gly
 130 135 140

Glu Glu Ile Ile Ala Pro Asp His Asn Lys Gly Ile Ala Ser Asn Phe
 145 150 155 160

Leu Ser Met Val Phe Gly Asn Asp Asp Gly Ser Val Ala Asn Ser Ala
 165 170 175

Asp Asp Ile Arg Asp Phe Glu Arg Ser Leu Ile Leu Tyr Ala Glu His
 180 185 190

Ser Phe Asn Ala Ser Thr Phe Ser Ala Arg Val Ile Ser Ser Thr Arg
 195 200 205
 Ser Asp Thr Tyr Ser Ala Ile Thr Gly Ala Ile Gly Ala Leu Lys Gly
 210 215 220
 Pro Leu His Gly Gly Ala Asn Glu Phe Val Met His Thr Met Leu Asp
 225 230 235 240
 Ile Asp Asp Pro Asn Asn Ala Ala Asp Trp Met Gly Lys Ala Leu Asp
 245 250 255
 Arg Lys Glu Arg Ile Met Gly Phe Gly His Arg Val Tyr Lys Asn Gly
 260 265 270
 Asp Ser Arg Val Pro Ser Met Glu Lys Ser Met Arg Ser Leu Ala Ala
 275 280 285
 Arg His Arg Gly Gln Lys Trp Val His Met Tyr Glu Ser Met Gln Glu
 290 295 300
 Val Met Glu Ala Arg Thr Gly Ile Lys Pro Asn Leu Asp Phe Pro Ala
 305 310 315 320
 Gly Pro Ala Tyr Tyr Met Leu Gly Phe Pro Val Asp Phe Phe Thr Pro
 325 330 335
 Leu Phe Val Leu Ala Arg Val Ser Gly Trp Thr Ala His Ile Val Glu
 340 345 350
 Gln Phe Glu Asn Asn Ala Leu Ile Arg Pro Leu Ser Ala Tyr Asn Gly
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 370 375 380

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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1015)
 <223> RXN02333

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 Met Asn Leu Phe Ser
 1 5
 aat ggt gtt gat gtg ggg agg cgt cga caa gca ttt aaa gcg gca ctc 163
 Asn Gly Val Asp Val Gly Arg Arg Arg Gln Ala Phe Lys Ala Ala Leu
 10 15 20
 gcc gca ccc cac atc gcc cgg ctg ccc ggc gca ttc tcc cct ctg att 211
 Ala Ala Pro His Ile Ala Arg Leu Pro Gly Ala Phe Ser Pro Leu Ile

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Ala	Arg	Ser	Ile	Glu	Glu	Ala	Gly	Phe	Glu	Gly	Val	Tyr	Val	Ser	Gly	
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Ala	Val	Ile	Ala	Ala	Asp	Leu	Ala	Leu	Pro	Asp	Ile	Gly	Leu	Thr	Thr	
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ctg	acc	gaa	gtc	gcc	cac	cgc	gcg	cgg	caa	att	gcg	cgc	gtc	aca	gac	355
Leu	Thr	Glu	Val	Ala	His	Arg	Ala	Arg	Gln	Ile	Ala	Arg	Val	Thr	Asp	
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cta	gga	gtg	ctt	gtc	gac	gcc	gac	acc	ggc	ttt	ggc	gaa	ccc	atg	tcg	403
Leu	Gly	Val	Leu	Val	Asp	Ala	Asp	Thr	Gly	Phe	Gly	Glu	Pro	Met	Ser	
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gcc	gca	cgc	acc	gtc	gcc	gaa	ttg	gag	gac	gcc	ggt	gtg	gcc	gga	tgc	451
Ala	Ala	Arg	Thr	Val	Ala	Glu	Leu	Glu	Asp	Ala	Gly	Val	Ala	Gly	Cys	
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His	Leu	Glu	Asp	Gln	Val	Asn	Pro	Lys	Arg	Cys	Gly	His	Leu	Asp	Gly	
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Lys	Glu	Val	Val	Arg	Thr	Asp	Val	Met	Val	Arg	Arg	Ile	Ala	Ala	Ala	
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Val	Ser	Ala	Arg	Arg	Asp	Pro	Asn	Phe	Val	Ile	Cys	Ala	Arg	Thr	Asp	
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gcc	gct	gga	gtg	gaa	gga	atc	gac	gcc	gcc	att	gag	cgc	gcg	aaa	gcc	643
Ala	Ala	Gly	Val	Glu	Gly	Ile	Asp	Ala	Ala	Ile	Glu	Arg	Ala	Lys	Ala	
				170				175						180		
tac	tta	gat	gcg	ggc	gcc	gac	atg	att	ttc	acc	gaa	gcc	ctc	cac	agc	691
Tyr	Leu	Asp	Ala	Gly	Ala	Asp	Met	Ile	Phe	Thr	Glu	Ala	Leu	His	Ser	
			185				190						195			
gaa	gcc	gac	ttc	cga	tac	ttc	cgg	cac	gcc	atc	cct	gat	gcc	ttg	ttg	739
Glu	Ala	Asp	Phe	Arg	Tyr	Phe	Arg	His	Ala	Ile	Pro	Asp	Ala	Leu	Leu	
		200					205					210				
ctg	gcg	aat	atg	acc	gaa	ttt	ggc	aaa	acg	acg	ctg	ctg	tca	gcc	gac	787
Leu	Ala	Asn	Met	Thr	Glu	Phe	Gly	Lys	Thr	Thr	Leu	Leu	Ser	Ala	Asp	
	215					220					225					
gtg	ttg	gaa	gag	att	ggc	tac	aac	gcc	gtg	atc	tac	ccc	gtg	acc	acg	835
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Val	Tyr	Val	Ser	Gly	Ala	Val	Ile	Ala	Ala	Asp	Leu	Ala	Leu	Pro	Asp	
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Ile	Gly	Leu	Thr	Thr	Leu	Thr	Glu	Val	Ala	His	Arg	Ala	Arg	Gln	Ile	
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Ala	Arg	Val	Thr	Asp	Leu	Gly	Val	Leu	Val	Asp	Ala	Asp	Thr	Gly	Phe	
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Gly	Glu	Pro	Met	Ser	Ala	Ala	Arg	Thr	Val	Ala	Glu	Leu	Glu	Asp	Ala	
			100					105					110			
Gly	Val	Ala	Gly	Cys	His	Leu	Glu	Asp	Gln	Val	Asn	Pro	Lys	Arg	Cys	
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Gly	His	Leu	Asp	Gly	Lys	Glu	Val	Val	Arg	Thr	Asp	Val	Met	Val	Arg	
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Arg	Ile	Ala	Ala	Ala	Val	Ser	Ala	Arg	Arg	Asp	Pro	Asn	Phe	Val	Ile	
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Cys	Ala	Arg	Thr	Asp	Ala	Ala	Gly	Val	Glu	Gly	Ile	Asp	Ala	Ala	Ile	
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Glu	Arg	Ala	Lys	Ala	Tyr	Leu	Asp	Ala	Gly	Ala	Asp	Met	Ile	Phe	Thr	
			180					185					190			
Glu	Ala	Leu	His	Ser	Glu	Ala	Asp	Phe	Arg	Tyr	Phe	Arg	His	Ala	Ile	
		195					200					205				
Pro	Asp	Ala	Leu	Leu	Leu	Ala	Asn	Met	Thr	Glu	Phe	Gly	Lys	Thr	Thr	
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Glu Leu Leu Arg Tyr Glu Asp Tyr Asn Val Phe Asp Gln His Ile Phe
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Thr Tyr Arg Lys Gly Glu Asn Asn Glu
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 Met Arg Ile Glu Ile
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aca agc gta ttt gtt gat gac cag gcc aaa gca ctc gat ttc tac acc 163
 Thr Ser Val Phe Val Asp Asp Gln Ala Lys Ala Leu Asp Phe Tyr Thr
 10 15 20

acg aag ctc gga ttt gag ctc aaa cac gat gta act gct ggt gac tac 211
 Thr Lys Leu Gly Phe Glu Leu Lys His Asp Val Thr Ala Gly Asp Tyr
 25 30 35

cgc tgg ttg act gtt gtt gat cca gaa aac cca gat ggt gtg cag ctt 259
 Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro Asp Gly Val Gln Leu
 40 45 50

ttg ttg gaa cca aac cag cac cca gat gca gcg act tac caa gct gga 307
 Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala Thr Tyr Gln Ala Gly
 55 60 65

att aaa cga gac ggt att ccc gct aca cag ttt tat gtt gat gat gtg 355
 Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe Tyr Val Asp Asp Val
 70 75 80 85

cag gaa gaa tat gac agc ctc aag gat aaa ggc gtg gat ttc atc atg 403
 Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly Val Asp Phe Ile Met
 90 95 100

gaa cca acc gat gtg ggc cct tca gtg att gcc att ctc gat gac acc 451
 Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala Ile Leu Asp Asp Thr
 105 110 115

gta gga aac cta att cag att gtt caa ttg aag cag aac taaccccgtg 500
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Thr Ala Gly Asp Tyr Arg Trp Leu Thr Val Val Asp Pro Glu Asn Pro
 35 40 45

Asp Gly Val Gln Leu Leu Leu Glu Pro Asn Gln His Pro Asp Ala Ala
 50 55 60

Thr Tyr Gln Ala Gly Ile Lys Arg Asp Gly Ile Pro Ala Thr Gln Phe
 65 70 75 80

Tyr Val Asp Asp Val Gln Glu Glu Tyr Asp Ser Leu Lys Asp Lys Gly
 85 90 95

Val Asp Phe Ile Met Glu Pro Thr Asp Val Gly Pro Ser Val Ile Ala
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Gln Asn
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 Met Thr Ser Ile Pro
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aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
 Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
 10 15 20

cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
 His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp

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Ala	Gly	Phe	Ser	Thr	Ala	Ala	Glu	Ser	Asn	Ala	Phe	Tyr	Arg	Arg	Asn				
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cac	cg	ggt	tat	gac	tcg	gat	aat	gag	cg	gtg	gtc	ggc	gat	gtg	ggt	499			
His	Arg	Gly	Tyr	Asp	Ser	Asp	Asn	Glu	Arg	Val	Val	Gly	Asp	Val	Gly				
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atg	gcc	ggc	gtg	gcg	att	gat	tcg	att	ttg	gat	atg	cgt	cag	ctg	ttt	547			
Met	Ala	Gly	Val	Ala	Ile	Asp	Ser	Ile	Leu	Asp	Met	Arg	Gln	Leu	Phe				
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gat	ggc	att	gat	ttg	tcc	agc	gtg	tcg	gtg	tcg	atg	acc	atg	aat	ggc	595			
Asp	Gly	Ile	Asp	Leu	Ser	Ser	Val	Ser	Val	Ser	Met	Thr	Met	Asn	Gly				
150				155				160				165							
gct	gtg	ctg	ccg	att	ctt	gcg	ttc	tat	atc	gtg	gcg	gct	gag	gaa	caa	643			
Ala	Val	Leu	Pro	Ile	Leu	Ala	Phe	Tyr	Ile	Val	Ala	Ala	Glu	Glu	Gln				
170				175				180											
ggt	gtg	ggt	ccg	gag	cag	ctt	gcg	ggc	acg	atc	cag	aat	gac	atc	ttg	691			
Gly	Val	Gly	Pro	Glu	Gln	Leu	Ala	Gly	Thr	Ile	Gln	Asn	Asp	Ile	Leu				
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Lys	Glu	Phe	Met	Val	Arg	Asn	Thr	Tyr	Ile	Tyr	Pro	Pro	Lys	Pro	Ser				
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Arg	Phe	Asn	Ser	Ile	Ser	Ile	Ser	Gly	Tyr	His	Ile	Gln	Glu	Ala	Gly				
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Ala	Thr	Ala	Asp	Leu	Glu	Leu	Ala	Tyr	Thr	Leu	Ala	Asp	Gly	Ile	Glu				
250				255				260											
tac	atc	cgt	gca	ggt	aaa	gag	gta	ggc	ctt	gac	gtg	gat	aag	ttc	gcg	93			

cct cgt ctg tcc ttc ttc tgg ggt att tct atg tac acc ttc atg gag	979
Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
280 285 290	
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Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
295 300 305	
aaa ttc gat ccg aaa aac gcc aag tcc cag tcg ctg cgc acg cac tcg	1075
Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
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Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp Val Tyr Asn Asn Val	
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Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr Gln Gly His Thr Gln	
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Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu Ala Leu Pro Thr Asp	
360 365 370	
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Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu Leu Gln Gln Glu	
375 380 385	
tct ggc acg gtg cgt cca gtt gat cca tgg gcg ggc tcc tat tac gtg	1315
Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala Gly Ser Tyr Tyr Val	
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Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala Arg Lys His Ile Asp	
410 415 420	
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Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala Thr Ala Gln Gly Ile	
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cct aag ctg cgc att gag gaa tca gcg gca cgc acc cag gct cgc att	1459
Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg Thr Gln Ala Arg Ile	
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Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn Arg Tyr Val Ala Glu	
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Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp Asn Thr Lys Val Arg	
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Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys Ala Glu Arg Asn Asp	
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gcg gaa gtc aag gct gcg ctg gat gcg ttg aca gct gct gcc cgc aac	1651
Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr Ala Ala Ala Arg Asn	
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 Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn Leu Leu Lys Leu Ala
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 535 540 545

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 Leu Glu Val Val Phe 555 Arg His Glu Ala Glu Ile Arg Thr Leu Ser 565
 550 560

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 630 635 640

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 650 655

cac ctc acc ttg ctg ccc gag ctg aag aaa gaa ctt gca gct ctt ggc 2131
 His Leu Thr Leu Leu Pro Glu Leu Lys Lys Glu Leu Ala Ala Leu Gly 675
 665 670

cgc gat gac att ctg gtc acc gtg ggc ggc gtc att ccg ccg ggc gat 2179
 Arg Asp Asp Ile Leu Val Thr Val Gly Gly Val Ile Pro Pro Gly Asp 690
 680 685

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<211> 737

<212> PRT

<213> *Corynebacterium glutamicum*

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Pro Glu Gly Ile Asp Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp
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      50           55           60

Pro Phe Met Arg Gly Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp
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Thr Ile Arg Gln Tyr Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala
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Phe Tyr Arg Arg Asn Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala
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Phe Asp Leu Ala Thr His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val
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Val Gly Asp Val Gly Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp
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Met Thr Met Asn Gly Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val
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Ala Ala Glu Glu Gln Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile
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Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr
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Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr
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Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His
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Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu
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Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp
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Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met
      275          280          285

Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp
      290          295          300

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Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser
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 Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp
 325 330 335
 Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr
 340 345 350
 Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu
 355 360 365
 Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu
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 Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala
 385 390 395 400
 Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala
 405 410 415
 Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala
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 Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg
 435 440 445
 Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn
 450 455 460
 Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp
 465 470 475 480
 Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
 485 490 495
 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr
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 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn
 515 520 525
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly
 530 535 540
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
 545 550 555 560
 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly
 565 570 575
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu
 580 585 590
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
 595 600 605
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
 610 615 620
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu

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Ser Leu Ala Ala	Gly His Leu Thr	Leu Leu Pro Glu	Leu Lys Lys Glu			
	660	665	670			
Leu Ala Ala Leu	Gly Arg Asp Asp	Ile Leu Val Thr	Val Gly Gly Val			
	675	680	685			
Ile Pro Pro Gly	Asp Phe Gln Asp	Leu Tyr Asp Met	Gly Ala Ala Ala			
	690	695	700			
Ile Tyr Pro Ser	Gly Thr Val Ile	Ala Glu Ser Ala	Ile Asp Leu Ile			
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Thr Arg Leu Ala	Ala His Leu Gly	Phe Asp Leu Asp	Val Asp Val Asn			
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 Met Thr Ser Ile Pro
 1 5
 aat ttt tca gac atc cca ttg act gct gag aca cgt gca tcg gag tca 163
 Asn Phe Ser Asp Ile Pro Leu Thr Ala Glu Thr Arg Ala Ser Glu Ser
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 cac aac gtt gac gcc ggc aag gtg tgg aac act ccc gaa ggc att gat 211
 His Asn Val Asp Ala Gly Lys Val Trp Asn Thr Pro Glu Gly Ile Asp
 25 30 35
 gtc aag cgc gta ttc acg cag gct gac cgc gac gag gcg caa gcg gcg 259
 Val Lys Arg Val Phe Thr Gln Ala Asp Arg Asp Glu Ala Gln Ala Ala
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 gga cat ccg gtg gat tct ttg cca ggt caa aag cca ttt atg cgc ggg 307
 Gly His Pro Val Asp Ser Leu Pro Gly Gln Lys Pro Phe Met Arg Gly
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 ccg tac cca act atg tac acc aat cag ccg tgg acg att cgc cag tac 355
 Pro Tyr Pro Thr Met Tyr Thr Asn Gln Pro Trp Thr Ile Arg Gln Tyr
 70 75 80 85

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Ala Gly Phe Ser Thr Ala Ala Glu Ser Asn Ala Phe Tyr Arg Arg Asn	
90 95 100	
ctt gct gcg ggt caa aaa ggt ttg tcg gtt gcg ttc gat cta gcg acc	451
Leu Ala Ala Gly Gln Lys Gly Leu Ser Val Ala Phe Asp Leu Ala Thr	
105 110 115	
cac cgc ggt tat gac tcg gat aat gag cgc gtg gtc ggc gat gtg ggt	499
His Arg Gly Tyr Asp Ser Asp Asn Glu Arg Val Val Gly Asp Val Gly	
120 125 130	
atg gcc ggc gtg gcg att gat tcg att ttg gat atg cgt cag ctg ttt	547
Met Ala Gly Val Ala Ile Asp Ser Ile Leu Asp Met Arg Gln Leu Phe	
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gat ggc att gat ttg tcc agc gtg tcg gtg tcg atg acc atg aat ggc	595
Asp Gly Ile Asp Leu Ser Ser Val Ser Val Ser Met Thr Met Asn Gly	
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Ala Val Leu Pro Ile Leu Ala Phe Tyr Ile Val Ala Ala Glu Glu Gln	
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Gly Val Gly Pro Glu Gln Leu Ala Gly Thr Ile Gln Asn Asp Ile Leu	
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Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr Pro Pro Lys Pro Ser	
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Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr Ser Leu Lys Met Pro	
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Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His Ile Gln Glu Ala Gly	
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Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu Ala Asp Gly Ile Glu	
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Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp Val Asp Lys Phe Ala	
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Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met Tyr Thr Phe Met Glu	
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Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp Ser Glu Leu Val Ala	
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Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser Leu Arg Thr His Ser	
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Gln	Thr	Ser	Gly	Trp	Ser	Leu	Thr	Ala	Gln	Asp	Val	Tyr	Asn	Asn	Val		
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Ala	Arg	Thr	Ala	Ile	Glu	Ala	Met	Ala	Ala	Thr	Gln	Gly	His	Thr	Gln		
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Ser	Leu	His	Thr	Asn	Ala	Leu	Asp	Glu	Ala	Leu	Ala	Leu	Pro	Thr	Asp		
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ttc	tct	gct	cgt	atc	gcc	cga	aac	acc	cag	ctg	ttg	ctg	cag	cag	gaa	1267	
Phe	Ser	Ala	Arg	Ile	Ala	Arg	Asn	Thr	Gln	Leu	Leu	Leu	Gln	Gln	Glu		
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tct	ggc	acg	gtg	cgt	cca	gtt	gat	cca	tgg	gcg	ggc	tcc	tat	tac	gtg	1315	
Ser	Gly	Thr	Val	Arg	Pro	Val	Asp	Pro	Trp	Ala	Gly	Ser	Tyr	Tyr	Val		
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gag	tgg	ttg	acc	aat	gag	ctg	gct	aac	cgc	gcg	cgc	aag	cac	atc	gat	1363	
Glu	Trp	Leu	Thr	Asn	Glu	Leu	Ala	Asn	Arg	Ala	Arg	Lys	His	Ile	Asp		
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Glu	Val	Glu	Glu	Ala	Gly	Gly	Met	Ala	Gln	Ala	Thr	Ala	Gln	Gly	Ile		
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cct	aag	ctg	cgc	att	gag	gaa	tca	gcg	gca	cgc	acc	cag	gct	cgc	att	1459	
Pro	Lys	Leu	Arg	Ile	Glu	Glu	Ser	Ala	Ala	Arg	Thr	Gln	Ala	Arg	Ile		
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Asp	Ser	Gly	Arg	Gln	Ala	Leu	Ile	Gly	Val	Asn	Arg	Tyr	Val	Ala	Glu		
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gaa	gat	gag	gaa	att	gaa	gtc	ctc	aag	gtt	gac	aac	acc	aag	gtt	cgc	1555	
Glu	Asp	Glu	Glu	Ile	Glu	Val	Leu	Lys	Val	Asp	Asn	Thr	Lys	Val	Arg		
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gca	gaa	cag	ttg	gct	aaa	ctc	gcg	caa	ctg	aaa	gca	gag	cgc	aac	gat	1603	
Ala	Glu	Gln	Leu	Ala	Lys	Leu	Ala	Gln	Leu	Lys	Ala	Glu	Arg	Asn	Asp		
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gcg	gaa	gtc	aag	gct	gcg	ctg	gat	gcg	ttg	aca	gct	gct	gcc	cgc	aac	1651	
Ala	Glu	Val	Lys	Ala	Ala	Leu	Asp	Ala	Leu	Thr	Ala	Ala	Ala	Arg	Asn		
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Glu	His	Lys	Glu	Pro	Gly	Asp	Leu	Asp	Gln	Asn	Leu	Leu	Lys	Leu	Ala		
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gtc	gat	gct	gcg	cgc	gca	aaa	gct	acc	att	gga	gag	atc	tcc	gat	gct	1747	
Val	Asp	Ala	Ala	Arg	Ala	Lys	Ala	Thr	Ile	Gly	Glu	Ile	Ser	Asp	Ala		
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Leu	Glu	Val	Val	Phe	Gly	Arg	His	Glu	Ala	Glu	Ile	Arg	Thr	Leu	Ser		
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Glu	Arg	Ala	Ile	Ala	Leu	Ala	Asp	Ala	Phe	Glu	Ala	Glu	Glu	Gly	Arg					
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cgc	cca	cgt	atc	ttt	att	gcc	aag	atg	ggc	cag	gat	gga	cat	gac	cgt	1939				
Arg	Pro	Arg	Ile	Phe	Ile	Ala	Lys	Met	Gly	Gln	Asp	Gly	His	Asp	Arg					
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Gly	Gln	Lys	Val	Val	Ala	Ser	Ala	Tyr	Ala	Asp	Leu	Gly	Met	Asp	Val					
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Val	Asp	Ala	Asp	Val	His	Val	Val	Gly	Met	Ser	Ser	Leu	Ala	Ala	Gly					
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His	Leu	Thr	Leu	Leu																
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<212> PRT

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Pro	Glu	Gly	Ile	Asp	Val	Lys	Arg	Val	Phe	Thr	Gln	Ala	Asp	Arg	Asp
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Glu	Ala	Gln	Ala	Ala	Gly	His	Pro	Val	Asp	Ser	Leu	Pro	Gly	Gln	Lys
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Pro	Phe	Met	Arg	Gly	Pro	Tyr	Pro	Thr	Met	Tyr	Thr	Asn	Gln	Pro	Trp
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Thr	Ile	Arg	Gln	Tyr	Ala	Gly	Phe	Ser	Thr	Ala	Ala	Glu	Ser	Asn	Ala
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Phe	Tyr	Arg	Arg	Asn	Leu	Ala	Ala	Gly	Gln	Lys	Gly	Leu	Ser	Val	Ala
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Phe	Asp	Leu	Ala	Thr	His	Arg	Gly	Tyr	Asp	Ser	Asp	Asn	Glu	Arg	Val
	115						120					125			

Val	Gly	Asp	Val	Gly	Met	Ala	Gly	Val	Ala	Ile	Asp	Ser	Ile	Leu	Asp
	130					135					140				

Met	Arg	Gln	Leu	Phe	Asp	Gly	Ile	Asp	Leu	Ser	Ser	Val	Ser	Val	Ser
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		180		185		190
Gln Asn Asp Ile Leu Lys Glu Phe Met Val Arg Asn Thr Tyr Ile Tyr						
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Pro Pro Lys Pro Ser Met Arg Ile Ile Ser Asn Ile Phe Glu Tyr Thr						
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Ser Leu Lys Met Pro Arg Phe Asn Ser Ile Ser Ile Ser Gly Tyr His						
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Ile Gln Glu Ala Gly Ala Thr Ala Asp Leu Glu Leu Ala Tyr Thr Leu						
		245		250		255
Ala Asp Gly Ile Glu Tyr Ile Arg Ala Gly Lys Glu Val Gly Leu Asp						
		260		265		270
Val Asp Lys Phe Ala Pro Arg Leu Ser Phe Phe Trp Gly Ile Ser Met						
		275		280		285
Tyr Thr Phe Met Glu Ile Ala Lys Leu Arg Ala Gly Arg Leu Leu Trp						
		290		295		300
Ser Glu Leu Val Ala Lys Phe Asp Pro Lys Asn Ala Lys Ser Gln Ser						
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Leu Arg Thr His Ser Gln Thr Ser Gly Trp Ser Leu Thr Ala Gln Asp						
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Val Tyr Asn Asn Val Ala Arg Thr Ala Ile Glu Ala Met Ala Ala Thr						
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Gln Gly His Thr Gln Ser Leu His Thr Asn Ala Leu Asp Glu Ala Leu						
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Ala Leu Pro Thr Asp Phe Ser Ala Arg Ile Ala Arg Asn Thr Gln Leu						
		370		375		380
Leu Leu Gln Gln Glu Ser Gly Thr Val Arg Pro Val Asp Pro Trp Ala						
		385		390		395
Gly Ser Tyr Tyr Val Glu Trp Leu Thr Asn Glu Leu Ala Asn Arg Ala						
		405		410		415
Arg Lys His Ile Asp Glu Val Glu Glu Ala Gly Gly Met Ala Gln Ala						
		420		425		430
Thr Ala Gln Gly Ile Pro Lys Leu Arg Ile Glu Glu Ser Ala Ala Arg						
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Thr Gln Ala Arg Ile Asp Ser Gly Arg Gln Ala Leu Ile Gly Val Asn						
		450		455		460
Arg Tyr Val Ala Glu Glu Asp Glu Glu Ile Glu Val Leu Lys Val Asp						
		465		470		475
						480

Asn Thr Lys Val Arg Ala Glu Gln Leu Ala Lys Leu Ala Gln Leu Lys
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 Ala Glu Arg Asn Asp Ala Glu Val Lys Ala Ala Leu Asp Ala Leu Thr
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 Ala Ala Ala Arg Asn Glu His Lys Glu Pro Gly Asp Leu Asp Gln Asn
 515 520 525
 Leu Leu Lys Leu Ala Val Asp Ala Ala Arg Ala Lys Ala Thr Ile Gly
 530 535 540
 Glu Ile Ser Asp Ala Leu Glu Val Val Phe Gly Arg His Glu Ala Glu
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 Ile Arg Thr Leu Ser Gly Val Tyr Lys Asp Glu Val Gly Lys Glu Gly
 565 570 575
 Thr Val Ser Asn Val Glu Arg Ala Ile Ala Leu Ala Asp Ala Phe Glu
 580 585 590
 Ala Glu Glu Gly Arg Arg Pro Arg Ile Phe Ile Ala Lys Met Gly Gln
 595 600 605
 Asp Gly His Asp Arg Gly Gln Lys Val Val Ala Ser Ala Tyr Ala Asp
 610 615 620
 Leu Gly Met Asp Val Asp Val Gly Pro Leu Phe Gln Thr Pro Ala Glu
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 aag act gcg gtg ccc gag gaa ctt tca gag aac ctc gaa act tgg tac 163
 Lys Thr Ala Val Pro Glu Glu Leu Ser Glu Asn Leu Glu Thr Trp Tyr 20
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 Lys Ala Val Ala Gly Val Phe Ala Arg Thr Gln Lys Lys Asp Ile Gly

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Lys	Phe	Thr	Glu	Val	Pro	Gly	Glu	Phe	Pro	Phe	Thr	Arg	Gly	Thr	Thr															
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Arg Thr Phe Asp Asp Ala Ile Pro Asp Gly Val Pro Gly Val Ser Arg	
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Val Glu Ser Phe Thr Asp Asp Leu Ala Glu Lys Ala Trp Ala Val Phe	
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Ser Gly Ile Glu Ala Glu Gly Gly Tyr Ser Ala Ala Cys Ala Ser Gly	
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Thr Val Thr Ala Met Leu Asp Gln Thr Trp Glu Gln Thr Arg Ala Asp	
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505 510 515	

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 520 525 530

ccc ggc act gac gct ttt gca gaa gct gca cag gcc gca ggc att gta 1747
 Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln Ala Ala Gly Ile Val
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 Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu Thr Gly Glu Gly Ala
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gtc gaa aag ctc cgc gaa gcg ggc gtt gag cgc atc ctg ctt gct ggc 1843
 Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg Ile Leu Leu Ala Gly
 570 575 580

gcg ccg aag agc ttt gag ggc agc gcg cat gcg ccc gat ggt tat ttg 1891
 Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala Pro Asp Gly Tyr Leu
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 Asn Met Thr Ile Asp Ala Ala Ala Thr Leu Ala Asp Leu Leu Asp Ala
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<211> 616

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<213> Corynebacterium glutamicum

<400> 632

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Lys Lys Asp Ile Gly Asp Ile Ala Val Asp Val Trp Lys Lys Leu Ile
 35 40 45

Val Thr Thr Pro Asp Gly Val Asp Ile Asn Pro Leu Tyr Thr Arg Ala
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Asp Glu Ser Gln Arg Lys Phe Thr Glu Val Pro Gly Glu Phe Pro Phe
 65 70 75 80

Thr Arg Gly Thr Thr Val Asp Gly Glu Arg Val Gly Trp Gly Val Thr
 85 90 95

Glu Thr Phe Gly His Asp Ser Pro Lys Asn Ile Asn Ala Ala Val Leu
 100 105 110

Asn Ala Leu Asn Ser Gly Thr Thr Thr Leu Gly Phe Glu Phe Ser Glu
 115 120 125

Glu Phe Thr Ala Ala Asp Leu Lys Val Ala Leu Glu Gly Val Tyr Leu
 130 135 140

Asn	Met	Ala	Pro	Leu	Leu	Ile	His	Ala	Gly	Gly	Ser	Thr	Ser	Glu	Val	145	150	155	160
Ala	Ala	Ala	Leu	Tyr	Thr	Leu	Ala	Glu	Glu	Ala	Gly	Thr	Phe	Phe	Ala	165	170	175	
Ala	Leu	Thr	Leu	Gly	Ser	Arg	Pro	Leu	Thr	Ala	Gln	Val	Asp	Gly	Ser	180	185	190	
His	Ser	Asp	Thr	Ile	Glu	Glu	Ala	Val	Gln	Leu	Ala	Val	Asn	Ala	Ser	195	200	205	
Lys	Arg	Ala	Asn	Val	Arg	Ala	Ile	Leu	Val	Asp	Gly	Ser	Ser	Phe	Ser	210	215	220	
Asn	Gln	Gly	Ala	Ser	Asp	Ala	Gln	Glu	Ile	Gly	Leu	Ser	Ile	Ala	Ala	225	230	235	240
Gly	Val	Asp	Tyr	Val	Arg	Arg	Leu	Val	Asp	Ala	Gly	Leu	Ser	Thr	Glu	245	250	255	
Ala	Ala	Leu	Lys	Gln	Val	Ala	Phe	Arg	Phe	Ala	Val	Thr	Asp	Glu	Gln	260	265	270	
Phe	Ala	Gln	Ile	Ser	Lys	Leu	Arg	Val	Ala	Arg	Arg	Leu	Trp	Ala	Arg	275	280	285	
Val	Cys	Glu	Val	Leu	Gly	Phe	Pro	Glu	Leu	Ala	Val	Ala	Pro	Gln	His	290	295	300	
Ala	Val	Thr	Ala	Arg	Ala	Met	Phe	Ser	Gln	Arg	Asp	Pro	Trp	Val	Asn	305	310	315	320
Met	Leu	Arg	Ser	Thr	Val	Ala	Ala	Phe	Ala	Ala	Gly	Val	Gly	Gly	Ala	325	330	335	
Thr	Asp	Val	Glu	Val	Arg	Thr	Phe	Asp	Asp	Ala	Ile	Pro	Asp	Gly	Val	340	345	350	
Pro	Gly	Val	Ser	Arg	Asn	Phe	Ala	His	Arg	Ile	Ala	Arg	Asn	Thr	Asn	355	360	365	
Leu	Leu	Leu	Leu	Glu	Glu	Ser	His	Leu	Gly	His	Val	Val	Asp	Pro	Ala	370	375	380	
Gly	Gly	Ser	Tyr	Phe	Val	Glu	Ser	Phe	Thr	Asp	Asp	Leu	Ala	Glu	Lys	385	390	395	400
Ala	Trp	Ala	Val	Phe	Ser	Gly	Ile	Glu	Ala	Glu	Gly	Gly	Tyr	Ser	Ala	405	410	415	
Ala	Cys	Ala	Ser	Gly	Thr	Val	Thr	Ala	Met	Leu	Asp	Gln	Thr	Trp	Glu	420	425	430	
Gln	Thr	Arg	Ala	Asp	Val	Ala	Ser	Arg	Lys	Lys	Lys	Leu	Thr	Gly	Ile	435	440	445	
Asn	Glu	Phe	Pro	Asn	Leu	Ala	Glu	Ser	Pro	Leu	Pro	Ala	Asp	Arg	Arg	450	455	460	

Val Glu Pro Ala Gly Val Arg Arg Trp Ala Ala Asp Phe Glu Ala Leu
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Arg Asn Arg Ser Asp Ala Phe Leu Glu Lys Asn Gly Ala Arg Pro Gln
 485 490 495

Ile Thr Met Ile Pro Leu Gly Pro Leu Ser Lys His Asn Ile Arg Thr
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Gly Phe Thr Ser Asn Leu Leu Ala Ser Gly Gly Ile Glu Ala Ile Asn
 515 520 525

Pro Gly Gln Leu Val Pro Gly Thr Asp Ala Phe Ala Glu Ala Ala Gln
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Ala Ala Gly Ile Val Val Val Cys Gly Thr Asp Gln Glu Tyr Ala Glu
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Thr Gly Glu Gly Ala Val Glu Lys Leu Arg Glu Ala Gly Val Glu Arg
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Ile Leu Leu Ala Gly Ala Pro Lys Ser Phe Glu Gly Ser Ala His Ala
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 Val Thr Thr Pro Ser
 1 5

aag aaa act ctg ctc ttt gat ctc gac gga acc ctc gtc gat tct ttc 163
 Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
 10 15 20

ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
 Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
 25 30 35

gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259
 Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
 40 45 50

gaa tgg acg ttc cag gat ttg ggc atg act cca gag cag gca caa gac 307

Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
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 Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
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 tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc cgc ttg aaa tac 403
 Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Arg Leu Lys Tyr
 90 95 100
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 Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys Gly Glu Phe Phe Ala
 105 110 115
 gag aag gta ctt cgc aaa ttc gag atg ttc gat ctc ttc gaa ttc atg 499
 Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp Leu Phe Glu Phe Met
 120 125 130
 ggt gcc gcc acc gac agc ggc aac cga cgc agc aaa tct gcc gtg atc 547
 Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser Lys Ser Ala Val Ile
 135 140 145
 aaa cat gtc ctc gac agc gtt ggg ttg gac gaa cca aat gat att ttg 595
 Lys His Val Leu Asp Ser Val Gly Leu Asp Glu Pro Asn Asp Ile Leu
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 Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly Ser Ser Glu Phe Gly
 170 175 180
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 Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly Ser Lys Thr Glu Trp
 185 190 195
 gac gct gcc cgc tac acc gtg agc acc gca gaa gaa tta gaa agg atc 739
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 Ile His Asp Trp Ala
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 35 40 45
 Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
 50 55 60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
 65 70 75 80
 Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
 85 90 95
 Ile Arg Leu Lys Tyr Glu Gly Phe Arg Leu Cys Thr Ala Thr Ser Lys
 100 105 110
 Gly Glu Phe Phe Ala Glu Lys Val Leu Arg Lys Phe Glu Met Phe Asp
 115 120 125
 Leu Phe Glu Phe Met Gly Ala Ala Thr Asp Ser Gly Asn Arg Arg Ser
 130 135 140
 Lys Ser Ala Val Ile Lys His Val Leu Asp Ser Val Gly Leu Asp Glu
 145 150 155 160
 Pro Asn Asp Ile Leu Met Ile Gly Asp Arg Ser His Asp Ile Glu Gly
 165 170 175
 Ser Ser Glu Phe Gly Ile Asp Cys Val Ala Val Thr Trp Gly Tyr Gly
 180 185 190
 Ser Lys Thr Glu Trp Asp Ala Ala Arg Tyr Thr Val Ser Thr Ala Glu
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 Val Thr Thr Pro Ser
 1 5
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 Lys Lys Thr Leu Leu Phe Asp Leu Asp Gly Thr Leu Val Asp Ser Phe
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 ccc ggt atc cgc act tca ttc ctt cac acc ctg cac gaa aag aac tgg 211
 Pro Gly Ile Arg Thr Ser Phe Leu His Thr Leu His Glu Lys Asn Trp
 25 30 35
 gaa atc ccc tct gag gaa cgc atc tcg caa gtt cca gga cct ccc atg 259
 Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val Pro Gly Pro Pro Met
 40 45 50

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 Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro Glu Gln Ala Gln Asp
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 Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln Val Gly Trp Asp Leu
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tcc gaa gca ttc ccc ggc atg cga gat ttg ctg atc ccc ttg ata tac 403
 Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu Ile Pro Leu Ile Tyr
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His Glu Lys Asn Trp Glu Ile Pro Ser Glu Glu Arg Ile Ser Gln Val
 35 40 45

Pro Gly Pro Pro Met Glu Trp Thr Phe Gln Asp Leu Gly Met Thr Pro
 50 55 60

Glu Gln Ala Gln Asp Ala Leu Gln Thr Tyr Leu Glu His Tyr Gly Gln
 65 70 75 80

Val Gly Trp Asp Leu Ser Glu Ala Phe Pro Gly Met Arg Asp Leu Leu
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Met Ile Lys Ala Ile
1 5

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Phe Trp Asp Met Asp Gly Thr Met Val Asp Ser Glu Pro Gln Trp Gly
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att gct acc tac gag ctc agc gaa gcc atg ggc cgc cgc ctc acc ccg 211
Ile Ala Thr Tyr Glu Leu Ser Glu Ala Met Gly Arg Arg Leu Thr Pro
25 30 35

gag ctc cgg gaa ctc acc gtc ggc tcg agc ctg ccg cgc acc atg cgc 259
Glu Leu Arg Glu Leu Thr Val Gly Ser Ser Leu Pro Arg Thr Met Arg
40 45 50

tta tgc gca gag cac gca ggc att aca ttg agc gac gcg gac tac gag 307
Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser Asp Ala Asp Tyr Glu
55 60 65

cgc tac cgg gct ggc atg ttc gcc cgg gtc cat gag ctt ttc gac gaa 355
Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His Glu Leu Phe Asp Glu
70 75 80 85

tcc ctc gtc cca aat cca ggc gtc acc gaa ctc ctg aca gag ttg aag 403
Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu Leu Thr Glu Leu Lys
90 95 100

gcc ctc gag atc ccc atg ttg gtc acc acc aac aca gag cgc gat ctc 451
Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn Thr Glu Arg Asp Leu
105 110 115

gcg acc cgt tca gtc gca gcc gtg gga aat gag ttc ttc atc ggt tct 499
Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu Phe Phe Ile Gly Ser
120 125 130

atc gct ggt gat gaa gtc cca aca gca aag cca gcc ccc gac atg tac 547
Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro Ala Pro Asp Met Tyr
135 140 145

ctc gaa gca gca cga cgt gtg ggc ttt gac cca tca gag tgc ctc gtg 595
Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro Ser Glu Cys Leu Val
150 155 160 165

ttc gaa gat tcc tac aac ggc atg ctg ggc gct gtt act gca ggt tgc 643
Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala Val Thr Ala Gly Cys
170 175 180

cgc gtc att ggt ctg cac cca gaa gaa gtc caa gcg cca gaa ggt gta 691
Arg Val Ile Gly Leu His Pro Glu Glu Val Gln Ala Pro Glu Gly Val
185 190 195

gtg cct ttg cgt tcc ctc cac ggt aaa aac tct ttc gaa ggt gtc acc 739
Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser Phe Glu Gly Val Thr
200 205 210

gct gag atg gtc act gcc tgg tac cac cag atc gag ccg gca ggt gtc 787
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215 220 225

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Ala Lys
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Pro Arg Thr Met Arg Leu Cys Ala Glu His Ala Gly Ile Thr Leu Ser
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Asp Ala Asp Tyr Glu Arg Tyr Arg Ala Gly Met Phe Ala Arg Val His
65 70 75 80
Glu Leu Phe Asp Glu Ser Leu Val Pro Asn Pro Gly Val Thr Glu Leu
85 90 95
Leu Thr Glu Leu Lys Ala Leu Glu Ile Pro Met Leu Val Thr Thr Asn
100 105 110
Thr Glu Arg Asp Leu Ala Thr Arg Ser Val Ala Ala Val Gly Asn Glu
115 120 125
Phe Phe Ile Gly Ser Ile Ala Gly Asp Glu Val Pro Thr Ala Lys Pro
130 135 140
Ala Pro Asp Met Tyr Leu Glu Ala Ala Arg Arg Val Gly Phe Asp Pro
145 150 155 160
Ser Glu Cys Leu Val Phe Glu Asp Ser Tyr Asn Gly Met Leu Gly Ala
165 170 175
Val Thr Ala Gly Cys Arg Val Ile Gly Leu His Pro Glu Glu Val Gln
180 185 190
Ala Pro Glu Gly Val Val Pro Leu Arg Ser Leu His Gly Lys Asn Ser
195 200 205
Phe Glu Gly Val Thr Ala Glu Met Val Thr Ala Trp Tyr His Gln Ile
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                                         Met Arg Gly Leu Ile
                                         1 5
ggt gac tac gct gga gta cta gac gga acc gat gag gac cag cgt cgc 163
Val Asp Tyr Ala Gly Val Leu Asp Gly Thr Asp Glu Asp Gln Arg Arg
          10          15          20
tgg cgc aac ctg ctc gcc gca gca aag aaa aat ggc gtc gga acc gtg 211
Trp Arg Asn Leu Leu Ala Ala Ala Lys Lys Asn Gly Val Gly Thr Val
          25          30          35
atc ctc agc aac gat cca ggt ggg ctc ggc gca gcg ccg atc cgg gaa 259
Ile Leu Ser Asn Asp Pro Gly Gly Leu Gly Ala Ala Pro Ile Arg Glu
          40          45          50
ctc gaa aca aac ggg gta gtc gat aag gtg ctg ctg tcg gga gaa ctt 307
Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu Leu Ser Gly Glu Leu
          55          60          65
ggc gtc gaa aag cca gag gaa gca gct ttc cag gcc gcc gca gac gcc 355
Gly Val Glu Lys Pro Glu Glu Ala Ala Phe Gln Ala Ala Ala Asp Ala
          70          75          80          85
atc gac ctg ccc atg cgt gac tgc gtg ctt gtc gac gac tcg atc ctc 403
Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val Asp Asp Ser Ile Leu
          90          95          100
aac gtg cgc ggc gcc gtc gaa gcc gga ctc gta ggc gtc tac tac cag 451
Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val Gly Val Tyr Tyr Gln
          105          110          115
caa ttt gac cgt gca gtc gtc gaa atc gtc gga ctg ttc ggg cta gaa 499
Gln Phe Asp Arg Ala Val Val Glu Ile Val Gly Leu Phe Gly Leu Glu
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          20          25          30

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 35 40 45
 Ala Pro Ile Arg Glu Leu Glu Thr Asn Gly Val Val Asp Lys Val Leu
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 Ala Ala Ala Asp Ala Ile Asp Leu Pro Met Arg Asp Cys Val Leu Val
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 Asp Asp Ser Ile Leu Asn Val Arg Gly Ala Val Glu Ala Gly Leu Val
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 Val Asp Val Val Asp
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 atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
 Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
 10 15 20
 gtc cca ctg acc att ggc tta gcg ccg ctg gtc gca atc atg caa acg 211
 Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
 25 30 35
 ttt tgg caa gtt acc ggc aaa gag cac tgg tat cgg gcc aca aga ttt 259
 Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr Arg Ala Thr Arg Phe
 40 45 50
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 Phe Gly Thr Val Leu Leu Ile Asn Phe Ala Val Gly Val Ala Thr Gly
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 Ile Val Gln Glu Phe Gln Phe Gly Met Asn Trp Ser Glu Tyr Ser Arg
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 Phe Val Gly Asp Val Phe Gly Gly Pro Leu Ala Leu Glu Gly Leu Ile

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Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	Ile	Val	Ala	Asn	Ser	Phe		
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Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	Leu	Thr	Ala	Gly	Thr	Phe		
185								190				195					
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Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	Arg	Ala	His	Arg	Gln	Ala		
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Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	His	Ser	Met	His	Arg	Pro		
215								220				225					
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Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	Val	Ser	Ser	Val	Ala	Leu		
230				235				240				245					
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Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	Met	Phe	Val	Gln	Gln	Pro		
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Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	Glu	Thr	Ala	Thr	Asp	Pro		
265								270				275					
aac	ttc	tcc	att	ctg	aca	att	ggg	acg	cac	aac	aac	tgc	gat	acg	gta	979	
Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	Asn	Asn	Cys	Asp	Thr	Val		
280								285				290					
acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	cca	ttc	ttg	gct	gaa	gga	1027	
Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	Pro	Phe	Leu	Ala	Glu	Gly		
295				300				305									
aaa	ttc	acc	ggg	gtg	act	ttg	cag	ggg	gta	aac	cag	ctc	caa	gct	gca	1075	
Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	Asn	Gln	Leu	Gln	Ala	Ala		
310				315</													

acc tac tgg tca ttc cgc gca atg atc ggc ctg atg ctt ggt tct ttg 1171
 Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly Leu Met Leu Gly Ser Leu
 345 350 355

 gct atc gct gcg att gcg tgg ctg ttg ctg cgt aag aag cgc aca cca 1219
 Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu Arg Lys Lys Arg Thr Pro
 360 365 370

 act gga aag att gct cgt ctg ttc cag atc ggc agc ctc att gct atc 1267
 Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly Ser Leu Ile Ala Ile
 375 380 385

 ccg ttc cca ttc ttg gcc aac tct gct ggt tgg atc ttc acc gag atg 1315
 Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp Ile Phe Thr Glu Met
 390 395 400 405

 ggc cgc cag cct tgg gtg gtg cac ccg aac cct gaa tct gcc ggc gat 1363
 Gly Arg Gln Pro Trp Val Val His Pro Asn Pro Glu Ser Ala Gly Asp
 410 415 420

 gcc cga aca gag atg atc cgg atg act gtt gat atg ggt gta tct gat 1411
 Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp Met Gly Val Ser Asp
 425 430 435

 cat gcg cca tgg caa gtc tgg ctg act ctc att ggc ttc acg att ctc 1459
 His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile Gly Phe Thr Ile Leu
 440 445 450

 tat ctc att ttg ttc gtg gtg tgg gtg tgg ctg att cgc cgc gca gtt 1507
 Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu Ile Arg Arg Ala Val
 455 460 465

 ctg atc gga cca cca gag gaa ggc gct cca tcc gtg gag gca aag act 1555
 Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser Val Glu Ala Lys Thr
 470 475 480 485

 gga ccg gca acc ccg att ggt tca gat atg ccc atg aca ccg ctg caa 1603
 Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro Met Thr Pro Leu Gln
 490 495 500

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<210> 642

<211> 513

<212> PRT

<213> Corynebacterium glutamicum

<400> 642

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Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
 20 25 30

Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His Trp Tyr

35					40					45					
Arg	Ala	Thr	Arg	Phe	Phe	Gly	Thr	Val	Leu	Leu	Ile	Asn	Phe	Ala	Val
50						55					60				
Gly	Val	Ala	Thr	Gly	Ile	Val	Gln	Glu	Phe	Gln	Phe	Gly	Met	Asn	Trp
65					70					75					80
Ser	Glu	Tyr	Ser	Arg	Phe	Val	Gly	Asp	Val	Phe	Gly	Gly	Pro	Leu	Ala
				85					90					95	
Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly	Leu
			100					105					110		
Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala	Ser
		115					120					125			
Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile	Ile
	130					135					140				
Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn	Pro
145					150					155					160
Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr	Asn
				165					170					175	
Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe	Leu
			180					185					190		
Thr	Ala	Gly	Thr	Phe	Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile	Arg
		195					200					205			
Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys	His
	210					215					220				
Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val	Val
225					230					235					240
Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu	Met
				245					250					255	
Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys	Glu
			260					265					270		
Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His	Asn
		275					280					285			
Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu	Pro
	290					295					300				
Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val	Asn
305					310					315					320
Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr	Ser
				325					330					335	
Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly	Leu
			340					345					350		
Met	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Leu	Arg
		355					360					365			

Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile Gly
 370 375 380
 Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly Trp
 385 390 395 400
 Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn Pro
 405 410 415
 Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val Asp
 420 425 430
 Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu Ile
 435 440 445
 Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp Leu
 450 455 460
 Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro Ser
 465 470 475 480
 Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met Pro
 485 490 495
 Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu Lys
 500 505 510

Glu

<210> 643
 <211> 238
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(238)
 <223> FRXA00055

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 Val Asp Val Val Asp
 1 5
 atc gca cgg tgg caa ttc gga att acc acc gtc tat cac ttc att ttt 163
 Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val Tyr His Phe Ile Phe
 10 15 20
 gtc cca ctg acc att ggc tta gca ccg ctg gtc gcg atc atg caa acg 211
 Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val Ala Ile Met Gln Thr
 25 30 35
 ttt tgg caa gtt acc ggc aaa gag cac 238
 Phe Trp Gln Val Thr Gly Lys Glu His
 40 45

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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 644
 Val Asp Val Val Asp Ile Ala Arg Trp Gln Phe Gly Ile Thr Thr Val
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 Tyr His Phe Ile Phe Val Pro Leu Thr Ile Gly Leu Ala Pro Leu Val
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 Ala Ile Met Gln Thr Phe Trp Gln Val Thr Gly Lys Glu His
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 <212> DNA
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<220>
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 <222> (1)..(1302)
 <223> FRXA01744

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 gct ttg gag ggt ctt atc gcg ttc ttc ctt gag tct gta ttc ctg gga 96
 Ala Leu Glu Gly Leu Ile Ala Phe Phe Leu Glu Ser Val Phe Leu Gly
 20 25 30
 ctg tgg att ttc gga tgg ggg aag att cct ggt tgg ttg cac act gca 144
 Leu Trp Ile Phe Gly Trp Gly Lys Ile Pro Gly Trp Leu His Thr Ala
 35 40 45
 tcc att tgg atc gtt gct att gcg acg aat att tct gcc tat ttc atc 192
 Ser Ile Trp Ile Val Ala Ile Ala Thr Asn Ile Ser Ala Tyr Phe Ile
 50 55 60
 atc gtg gcc aac tcg ttt atg cag cat ccg gtg ggt gct gag tat aac 240
 Ile Val Ala Asn Ser Phe Met Gln His Pro Val Gly Ala Glu Tyr Asn
 65 70 75 80
 cct gag act ggt cgt gcg gag ctt act gat ttt tgg gct ctt ctg aca 288
 Pro Glu Thr Gly Arg Ala Glu Leu Thr Asp Phe Trp Ala Leu Leu Thr
 85 90 95
 aac tcc acc gcg ctg gct gcg ttc ccg cat gct gtt gcc ggt ggt ttt 336
 Asn Ser Thr Ala Leu Ala Ala Phe Pro His Ala Val Ala Gly Gly Phe
 100 105 110
 tta aca gct gga act ttc gtt ctc gga att tcg ggt tgg tgg att att 384
 Leu Thr Ala Gly Thr Phe Val Leu Gly Ile Ser Gly Trp Trp Ile Ile
 115 120 125
 cgt gcg cac cgt cag gcc aag aag gct gag tcg gaa atc gag tcg aag 432

Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys		
130						135					140						
cat	tcg	atg	cac	agg	ccc	gcg	ttg	tgg	gtt	ggt	tgg	tgg	acc	aca	gtt	480	
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val		
145					150					155					160		
gtc	tct	tcc	gtg	gcg	ctg	ttc	atc	act	ggc	gat	atc	cag	gcg	aag	ctc	528	
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu		
				165					170					175			
atg	ttc	gtg	caa	cag	cca	atg	aag	atg	gcg	tcg	gcg	gaa	tcc	ttg	tgt	576	
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys		
			180					185					190				
gaa	acc	gcc	aca	gat	cca	aac	ttc	tcc	att	ctg	aca	att	ggt	acg	cac	624	
Glu	Thr	Ala	Thr	Asp	Pro	Asn	Phe	Ser	Ile	Leu	Thr	Ile	Gly	Thr	His		
		195					200					205					
aac	aac	tgc	gat	acg	gta	acc	cac	ctg	atc	gat	gtt	ccg	ttt	gtg	ctt	672	
Asn	Asn	Cys	Asp	Thr	Val	Thr	His	Leu	Ile	Asp	Val	Pro	Phe	Val	Leu		
	210						215				220						
cca	ttc	ttg	gct	gaa	gga	aaa	ttc	acc	ggc	gtg	act	ttg	cag	ggt	gta	720	
Pro	Phe	Leu	Ala	Glu	Gly	Lys	Phe	Thr	Gly	Val	Thr	Leu	Gln	Gly	Val		
225					230				235						240		
aac	cag	ctc	caa	gct	gca	gcg	gag	caa	gca	tac	ggc	cct	ggc	aac	tac	768	
Asn	Gln	Leu	Gln	Ala	Ala	Ala	Glu	Gln	Ala	Tyr	Gly	Pro	Gly	Asn	Tyr		
				245					250					255			
tcc	cct	aac	ttg	ttt	gtc	acc	tac	tgg	tca	ttc	cgc	gca	atg	atc	ggc	816	
Ser	Pro	Asn	Leu	Phe	Val	Thr	Tyr	Trp	Ser	Phe	Arg	Ala	Met	Ile	Gly		
			260					265					270				
ctg	atg	ctt	ggc	tct	ttg	gct	atc	gct	gcg	att	gcg	tgg	ctg	ttg	ctg	864	
Leu	Met	Leu	Gly	Ser	Leu	Ala	Ile	Ala	Ala	Ile	Ala	Trp	Leu	Leu	Leu		
		275					280					285					
cgt	aag	aag	cgc	aca	cca	act	gga	aag	att	gct	cgt	ctg	ttc	cag	atc	912	
Arg	Lys	Lys	Arg	Thr	Pro	Thr	Gly	Lys	Ile	Ala	Arg	Leu	Phe	Gln	Ile		
	290					295					300						
ggc	agc	ctc	att	gct	atc	ccg	ttc	cca	ttc	ttg	gcc	aac	tct	gct	ggc	960	
Gly	Ser	Leu	Ile	Ala	Ile	Pro	Phe	Pro	Phe	Leu	Ala	Asn	Ser	Ala	Gly		
305					310					315					320		
tgg	atc	ttc	acc	gag	atg	ggc	cgc	cag	cct	tgg	gtg	gtg	cac	ccg	aac	1008	
Trp	Ile	Phe	Thr	Glu	Met	Gly	Arg	Gln	Pro	Trp	Val	Val	His	Pro	Asn		
				325					330					335			
cct	gaa	tct	gcc	ggc	gat	gcc	cga	aca	gag	atg	atc	cgg	atg	act	gtt	1056	
Pro	Glu	Ser	Ala	Gly	Asp	Ala	Arg	Thr	Glu	Met	Ile	Arg	Met	Thr	Val		
			340					345					350				
gat	atg	ggc	gta	tct	gat	cat	gcg	cca	tgg	caa	gtc	tgg	ctg	act	ctc	1104	
Asp	Met	Gly	Val	Ser	Asp	His	Ala	Pro	Trp	Gln	Val	Trp	Leu	Thr	Leu		
		355					360					365					
att	ggc	ttc	acg	att	ctc	tat	ctc	att	ttg	ttc	gtg	gtg	tgg	gtg	tgg	1152	
Ile	Gly	Phe	Thr	Ile	Leu	Tyr	Leu	Ile	Leu	Phe	Val	Val	Trp	Val	Trp		

370	375	380	
ctg att cgc cgc gca gtt ctg atc gga cca cca gag gaa ggc gct cca			1200
Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro			
385	390	395	400
tcc gtg gag gca aag act gga ccg gca acc ccg att ggt tca gat atg			1248
Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met			
	405	410	415
ccc atg aca ccg ctg caa ttt act gcc gct gcc cca acc aca ggt gaa			1296
Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu			
	420	425	430
aag gaa taaccatgga tctcaatacc ttt			1325
Lys Glu			

<210> 646
 <211> 434
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 646

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Ala	Leu	Glu	Gly	Leu	Ile	Ala	Phe	Phe	Leu	Glu	Ser	Val	Phe	Leu	Gly
			20					25					30		
Leu	Trp	Ile	Phe	Gly	Trp	Gly	Lys	Ile	Pro	Gly	Trp	Leu	His	Thr	Ala
		35					40					45			
Ser	Ile	Trp	Ile	Val	Ala	Ile	Ala	Thr	Asn	Ile	Ser	Ala	Tyr	Phe	Ile
	50					55					60				
Ile	Val	Ala	Asn	Ser	Phe	Met	Gln	His	Pro	Val	Gly	Ala	Glu	Tyr	Asn
65					70					75					80
Pro	Glu	Thr	Gly	Arg	Ala	Glu	Leu	Thr	Asp	Phe	Trp	Ala	Leu	Leu	Thr
				85					90					95	
Asn	Ser	Thr	Ala	Leu	Ala	Ala	Phe	Pro	His	Ala	Val	Ala	Gly	Gly	Phe
			100					105					110		
Leu	Thr	Ala	Gly	Thr	Phe	Val	Leu	Gly	Ile	Ser	Gly	Trp	Trp	Ile	Ile
		115					120					125			
Arg	Ala	His	Arg	Gln	Ala	Lys	Lys	Ala	Glu	Ser	Glu	Ile	Glu	Ser	Lys
	130					135					140				
His	Ser	Met	His	Arg	Pro	Ala	Leu	Trp	Val	Gly	Trp	Trp	Thr	Thr	Val
145					150					155					160
Val	Ser	Ser	Val	Ala	Leu	Phe	Ile	Thr	Gly	Asp	Ile	Gln	Ala	Lys	Leu
				165					170					175	
Met	Phe	Val	Gln	Gln	Pro	Met	Lys	Met	Ala	Ser	Ala	Glu	Ser	Leu	Cys
			180					185					190		

Glu Thr Ala Thr Asp Pro Asn Phe Ser Ile Leu Thr Ile Gly Thr His
 195 200 205
 Asn Asn Cys Asp Thr Val Thr His Leu Ile Asp Val Pro Phe Val Leu
 210 215 220
 Pro Phe Leu Ala Glu Gly Lys Phe Thr Gly Val Thr Leu Gln Gly Val
 225 230 235 240
 Asn Gln Leu Gln Ala Ala Ala Glu Gln Ala Tyr Gly Pro Gly Asn Tyr
 245 250 255
 Ser Pro Asn Leu Phe Val Thr Tyr Trp Ser Phe Arg Ala Met Ile Gly
 260 265 270
 Leu Met Leu Gly Ser Leu Ala Ile Ala Ala Ile Ala Trp Leu Leu Leu
 275 280 285
 Arg Lys Lys Arg Thr Pro Thr Gly Lys Ile Ala Arg Leu Phe Gln Ile
 290 295 300
 Gly Ser Leu Ile Ala Ile Pro Phe Pro Phe Leu Ala Asn Ser Ala Gly
 305 310 315 320
 Trp Ile Phe Thr Glu Met Gly Arg Gln Pro Trp Val Val His Pro Asn
 325 330 335
 Pro Glu Ser Ala Gly Asp Ala Arg Thr Glu Met Ile Arg Met Thr Val
 340 345 350
 Asp Met Gly Val Ser Asp His Ala Pro Trp Gln Val Trp Leu Thr Leu
 355 360 365
 Ile Gly Phe Thr Ile Leu Tyr Leu Ile Leu Phe Val Val Trp Val Trp
 370 375 380
 Leu Ile Arg Arg Ala Val Leu Ile Gly Pro Pro Glu Glu Gly Ala Pro
 385 390 395 400
 Ser Val Glu Ala Lys Thr Gly Pro Ala Thr Pro Ile Gly Ser Asp Met
 405 410 415
 Pro Met Thr Pro Leu Gln Phe Thr Ala Ala Ala Pro Thr Thr Gly Glu
 420 425 430

Lys Glu

<210> 647
 <211> 307
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(307)
 <223> RXA00379

<400> 647
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 Met Ser Glu Ile Val
 1 5

gta gcc caa agc atc ggc cag cag ttt gct gac gtc gca gct tcc ggg 163
 Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp Val Ala Ala Ser Gly
 10 15 20

cca ctg ttc ctt ggc atc ctt gcc gca gcg ctc gca ggt ctg gtg tct 211
 Pro Leu Phe Leu Gly Ile Leu Ala Ala Leu Ala Gly Leu Val Ser
 25 30 35

ttt gcc agc ccg tgt gtt gtg ccg ttg gtg cca gga tat att tcc tac 259
 Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro Gly Tyr Ile Ser Tyr
 40 45 50

ctc gcc ggc gtg gtc ggt ggg gaa gtg gaa tac agc gct cat gcc acc 307
 Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr Ser Ala His Ala Thr
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<210> 648

<211> 69

<212> PRT

<213> Corynebacterium glutamicum

<400> 648

Met Ser Glu Ile Val Val Ala Gln Ser Ile Gly Gln Gln Phe Ala Asp
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Val Ala Ala Ser Gly Pro Leu Phe Leu Gly Ile Leu Ala Ala Ala Leu
 20 25 30

Ala Gly Leu Val Ser Phe Ala Ser Pro Cys Val Val Pro Leu Val Pro
 35 40 45

Gly Tyr Ile Ser Tyr Leu Ala Gly Val Val Gly Gly Glu Val Glu Tyr
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Ser Ala His Ala Thr
 65

<210> 649

<211> 362

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (1)..(339)

<223> RXA00385

<400> 649

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 1 5 10 15

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 Leu Ala Ala Ile Ile Ser Ile Ser Ala Gly Thr Glu Gly Met Thr Ala

20										25										30										
gcg	cgt	ggc	gtg	atc	tta	att	gtg	ggt	tac	tgc	ctc	gga	ctg	ggg	ctg		144													
Ala	Arg	Gly	Val	Ile	Leu	Ile	Val	Gly	Tyr	Cys	Leu	Gly	Leu	Gly	Leu															
		35						40					45																	
ccg	ttc	ctg	ctg	atc	gcg	ttg	ggc	tcc	agc	aag	gca	ctc	acc	gga	gtc		192													
Pro	Phe	Leu	Leu	Ile	Ala	Leu	Gly	Ser	Ser	Lys	Ala	Leu	Thr	Gly	Val															
		50					55					60																		
gag	tgg	ttg	cgc	aag	cat	tcc	cgc	acc	ctg	caa	att	atc	ggc	ggt	gtg		240													
Glu	Trp	Leu	Arg	Lys	His	Ser	Arg	Thr	Leu	Gln	Ile	Ile	Gly	Gly	Val															
		65				70					75				80															
ttt	ttg	atc	ttg	gtc	gga	gta	gcg	ttg	ctc	tct	ggc	tca	tgg	gca	att		288													
Phe	Leu	Ile	Leu	Val	Gly	Val	Ala	Leu	Leu	Ser	Gly	Ser	Trp	Ala	Ile															
				85					90					95																
ttt	atc	aac	tgg	gtc	cgt	cag	tgg	acc	ggt	gaa	tac	ggc	gca	aca	ctg		336													
Phe	Ile	Asn	Trp	Val	Arg	Gln	Trp	Thr	Val	Glu	Tyr	Gly	Ala	Thr	Leu															
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Leu																														

<210> 650
 <211> 113
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 650															
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			20					25					30		
Ala	Arg	Gly	Val	Ile	Leu	Ile	Val	Gly	Tyr	Cys	Leu	Gly	Leu	Gly	Leu
		35					40					45			
Pro	Phe	Leu	Leu	Ile	Ala	Leu	Gly	Ser	Ser	Lys	Ala	Leu	Thr	Gly	Val
		50				55					60				
Glu	Trp	Leu	Arg	Lys	His	Ser	Arg	Thr	Leu	Gln	Ile	Ile	Gly	Gly	Val
		65			70					75					80
Phe	Leu	Ile	Leu	Val	Gly	Val	Ala	Leu	Leu	Ser	Gly	Ser	Trp	Ala	Ile
			85					90						95	
Phe	Ile	Asn	Trp	Val	Arg	Gln	Trp	Thr	Val	Glu	Tyr	Gly	Ala	Thr	Leu
			100					105					110		
Leu															

<210> 651
 <211> 901
 <212> DNA

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Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr Asp Ala Ala Lys Ala
185 190 195

gct cca gta gtc gca ctt ctt gct gcg gtg act ggt gga cct ttc gtg 739
 Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr Gly Gly Pro Phe Val
 200 205 210
 ttg tgg gct gcc atc gca tac ggc cgt tcc tgg tcc tgg atc ctc gca 787
 Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp Ser Trp Ile Leu Ala
 215 220 225
 gtg ctg atc atc gca gcg gtt ctc ggt gga gct ttc gca ctg atc aaa 835
 Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala Phe Ala Leu Ile Lys
 230 235 240 245
 gac cgc gat gga tta agc ttc ctg tcc act tcc gtc gct gtc atc ggt 883
 Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser Val Ala Val Ile Gly
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 gtc gtt gca ctg ctg ttt 901
 Val Val Ala Leu Leu Phe
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 <213> Corynebacterium glutamicum

<400> 652
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 Gly Tyr Phe Leu Leu Glu Gly Phe Asp Phe Gly Val Gly Ile Leu Ala
 20 25 30
 Pro Ile Ile Gly Lys Asp Ser Ala Ala Arg Asn Thr Val Ile Arg Thr
 35 40 45
 Ile Gly Pro Val Trp Asp Gly Asn Glu Val Trp Leu Ile Val Ala Gly
 50 55 60
 Gly Ala Leu Phe Ala Ala Phe Pro Glu Trp Tyr Ala Thr Met Phe Ser
 65 70 75 80
 Gly Met Tyr Leu Pro Leu Phe Leu Val Leu Val Ser Leu Ile Met Arg
 85 90 95
 Val Val Gly Leu Glu Trp Arg Lys Lys Val Asp Asp Pro Arg Trp Gln
 100 105 110
 Lys Trp Ser Asp Arg Ala Ile Phe Ile Gly Ser Trp Thr Pro Pro Leu
 115 120 125
 Met Trp Gly Phe Ile Phe Ala Asn Ile Leu Arg Gly Met Pro Leu Lys
 130 135 140
 Ala Asp His Thr Ile Asp Ala Ala Ala Ala Leu Pro Gly Met Val Asn
 145 150 155 160
 Val Phe Ala Ile Leu Gly Ala Leu Ala Phe Thr Ala Leu Phe Ala Leu
 165 170 175

His Gly Leu Ala Phe Ile Arg Leu Lys Thr Ala Gly Arg Val Arg Thr
 180 185 190
 Asp Ala Ala Lys Ala Ala Pro Val Val Ala Leu Leu Ala Ala Val Thr
 195 200 205
 Gly Gly Pro Phe Val Leu Trp Ala Ala Ile Ala Tyr Gly Arg Ser Trp
 210 215 220
 Ser Trp Ile Leu Ala Val Leu Ile Ile Ala Ala Val Leu Gly Gly Ala
 225 230 235 240
 Phe Ala Leu Ile Lys Asp Arg Asp Gly Leu Ser Phe Leu Ser Thr Ser
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 Val Ala Val Ile Gly Val Val Ala Leu Leu Phe
 260 265

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 <223> RXN02480

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 Met Thr Thr Thr Asp 5
 1
 cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttc 163
 His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe 20
 10 15
 ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
 Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr 35
 25 30
 cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
 Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr 50
 40 45
 atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
 Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp 65
 55 60
 ggt ttt gct aac tac gtc ctg cca ctt cag atc ggt gcg cct gac gta 355
 Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile Gly Ala Pro Asp Val 85
 70 75 80
 gct ttc cca cgt ttg aat gct ttc ggc ttc tgg atc acc acc gtc ggt 403
 Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp Ile Thr Thr Val Gly 100
 90 95
 ggt gtc gcg atg ctg acc ggc ttc ctg acc ccg ggt ggt gct gcc gac 451

Gly	Val	Ala	Met	Leu	Thr	Gly	Phe	Leu	Thr	Pro	Gly	Gly	Ala	Ala	Asp		
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Phe	Gly	Trp	Thr	Met	Tyr	Ser	Pro	Leu	Ser	Asp	Ala	Ile	His	Ser	Pro		
		120					125					130					
ggc	ctt	ggc	tct	gac	atg	tgg	att	gtc	ggt	gtc	ggt	gca	act	ggt	att	547	
Gly	Leu	Gly	Ser	Asp	Met	Trp	Ile	Val	Gly	Val	Gly	Ala	Thr	Gly	Ile		
	135					140					145						
ggc	tcc	ggt	gct	tcc	gca	att	aac	atg	ctc	acc	acc	atc	ctc	tgc	ctc	595	
Gly	Ser	Val	Ala	Ser	Ala	Ile	Asn	Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu		
150					155				160						165		
cgc	gca	cct	ggt	atg	acc	atg	ttc	cgt	atg	cct	att	ttc	acc	tgg	aat	643	
Arg	Ala	Pro	Gly	Met	Thr	Met	Phe	Arg	Met	Pro	Ile	Phe	Thr	Trp	Asn		
			170					175						180			
atc	ttc	ggt	ggt	tcc	ggt	ctt	gct	ctg	ctg	atc	ttc	cca	ctg	ctg	ctc	691	
Ile	Phe	Val	Val	Ser	Val	Leu	Ala	Leu	Leu	Ile	Phe	Pro	Leu	Leu	Leu		
		185						190					195				
gct	gct	gca	ctg	ggt	ggt	ctg	tat	gac	cgc	aag	ctt	ggt	gga	cac	ctg	739	
Ala	Ala	Ala	Leu	Gly	Val	Leu	Tyr	Asp	Arg	Lys	Leu	Gly	Gly	His	Leu		
		200					205					210					
tac	gat	cca	gct	aac	ggc	ggc	tcc	ctc	ctg	tgg	cag	cac	ctg	ttc	tgg	787	
Tyr	Asp	Pro	Ala	Asn	Gly	Gly	Ser	Leu	Leu	Trp	Gln	His	Leu	Phe	Trp		
	215					220					225						
ttc	ttc	gga	cac	cct	gag	ggt	tac	ggt	ctg	gcg	ctg	ccg	ttc	ttc	ggc	835	
Phe	Phe	Gly	His	Pro	Glu	Val	Tyr	Val	Leu	Ala	Leu	Pro	Phe	Phe	Gly		
230					235				240						245		
att	ggt	tct	gag	atc	att	cct	gtg	ttc	tcc	cgt	aag	cca	atg	ttc	ggt	883	
Ile	Val	Ser	Glu	Ile	Ile	Pro	Val	Phe	Ser	Arg	Lys	Pro	Met	Phe	Gly		
			250					255						260			
tac	gtc	ggc	ctg	atc	ttc	gca	acc	ttg	tcc	att	ggt	gca	ctg	tcc	atg	931	
Tyr	Val	Gly	Leu	Ile	Phe	Ala	Thr	Leu	Ser	Ile	Gly	Ala	Leu	Ser	Met		
			265					270					275				
gct	gtg	tgg	gct	cac	cac	atg	ttc	ggt	act	ggc	gca	ggt	ttg	ctt	ccg	979	
Ala	Val	Trp	Ala	His	His	Met	Phe	Val	Thr	Gly	Ala	Val	Leu	Leu	Pro		
		280					285					290					
ttc	ttc	tcc	ttc	atg	acg	ttc	ctg	att	tgc	ggt	cct	acc	ggc	ggt	aag	1027	
Phe	Phe	Ser	Phe	Met	Thr	Phe	Leu	Ile	Ser	Val	Pro	Thr	Gly	Val	Lys		
		295					300				305						
ttc	ttc	aac	tgg	ggt	gga	acc	atg	tgg	aag	ggt	cac	atc	act	tgg	gaa	1075	
Phe	Phe	Asn	Trp	Val	Gly	Thr	Met	Trp	Lys	Gly	His	Ile	Thr	Trp	Glu		
310					315					320					325		
acc	cca	atg	atc	tgg	tct	ggt	ggc	ttc	atg	gct	acc	ttc	ctc	ttc	ggt	1123	
Thr	Pro	Met	Ile	Trp	Ser	Val	Gly	Phe	Met	Ala	Thr	Phe	Leu	Phe	Gly		
			330					335						340			
ggt	ctg	acc	ggc	att	atg	ctg	gcg	tcc	cca	cca	ctg	gac	ttc	cac	ttg	1171	
Gly	Leu	Thr	Gly	Ile	Met	Leu	Ala	Ser	Pro	Pro	Leu	Asp	Phe	His	Leu		

345								350				355								
gct	gac	tcc	tac	ttc	ctg	atc	gcg	cac	ttc	cac	tac	acc	ctc	ttc	ggc	1219				
Ala	Asp	Ser	Tyr	Phe	Leu	Ile	Ala	His	Phe	His	Tyr	Thr	Leu	Phe	Gly					
360				365				370												
acc	gtg	gtg	ttc	gca	tcg	tgt	gca	ggc	gtt	tac	ttc	tgg	ttc	ccg	aag	1267				
Thr	Val	Val	Phe	Ala	Ser	Cys	Ala	Gly	Val	Tyr	Phe	Trp	Phe	Pro	Lys					
375				380				385												
atg	act	ggc	cgc	atg	atg	gac	gag	cgt	ctt	ggc	aag	atc	cac	ttc	tgg	1315				
Met	Thr	Gly	Arg	Met	Met	Asp	Glu	Arg	Leu	Gly	Lys	Ile	His	Phe	Trp					
390				395				400				405								
ttg	acc	ttc	gtc	ggc	ttc	cac	gga	acc	ttc	ctc	atc	cag	cac	tgg	gtg	1363				
Leu	Thr	Phe	Val	Gly	Phe	His	Gly	Thr	Phe	Leu	Ile	Gln	His	Trp	Val					
410				415				420												
ggc	aac	atg	ggc	atg	cca	cgt	cgt	tac	gct	gac	tac	ctg	gat	tct	gat	1411				
Gly	Asn	Met	Gly	Met	Pro	Arg	Arg	Tyr	Ala	Asp	Tyr	Leu	Asp	Ser	Asp					
425				430				435												
ggc	ttc	acc	atc	tac	aac	cag	atc	tcc	acc	gtg	ttc	tac	ttc	ctg	ctt	1459				
Gly	Phe	Thr	Ile	Tyr	Asn	Gln	Ile	Ser	Thr	Val	Phe	Tyr	Phe	Leu	Leu					
440				445				450												
ggc	ctg	tct	gtc	att	cca	ttc	atc	tgg	aac	gtc	ttc	aag	tcc	tgg	cgc	1507				
Gly	Leu	Ser	Val	Ile	Pro	Phe	Ile	Trp	Asn	Val	Phe	Lys	Ser	Trp	Arg					
455				460				465												
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Tyr	Gly	Glu	Leu	Val	Thr	Val	Asp	Asp	Pro	Trp	Gly	Tyr	Gly	Asn	Ser					
470				475				480				485								
ctg	gag	tgg	gca	acc	tcc	tgc	cct	cct	cct	cgc	cac	aac	ttc	gca	tcc	1603				
Leu	Glu	Trp	Ala	Thr	Ser	Cys	Pro	Pro	Pro	Arg	His	Asn	Phe	Ala	Ser					
490				495				500												
ttg	cct	cgt	atc	cgc	tcc	gag	cgc	cct	gcg	ttc	gag	ctg	cac	tac	ccg	1651				
Leu	Pro	Arg	Ile	Arg	Ser	Glu	Arg	Pro	Ala	Phe	Glu	Leu	His	Tyr	Pro					
505				510				515												
cac	atg	att	gaa	cgc	atg	cgc	gca	gag	gca	cac	act	gga	cat	cac	gat	1699				
His	Met	Ile	Glu	Arg	Met	Arg	Ala	Glu	Ala	His	Thr	Gly	His	His	Asp					
520				525				530												
gat	att	aat	gct	cca	gaa	ttg	ggc	acc	gcc	cca	gcc	ctt	gca	tct	gac	1747				
Asp	Ile	Asn	Ala	Pro	Glu	Leu	Gly	Thr	Ala	Pro	Ala	Leu	Ala	Ser	Asp					
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Ser	Ser	Arg																		
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<211> 552

<212> PRT

<213> Corynebacterium glutamicum

<400> 654

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 Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
 35 40 45
 Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
 50 55 60
 Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Gln Ile
 65 70 75 80
 Gly Ala Pro Asp Val Ala Phe Pro Arg Leu Asn Ala Phe Gly Phe Trp
 85 90 95
 Ile Thr Thr Val Gly Gly Val Ala Met Leu Thr Gly Phe Leu Thr Pro
 100 105 110
 Gly Gly Ala Ala Asp Phe Gly Trp Thr Met Tyr Ser Pro Leu Ser Asp
 115 120 125
 Ala Ile His Ser Pro Gly Leu Gly Ser Asp Met Trp Ile Val Gly Val
 130 135 140
 Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn Met Leu Thr
 145 150 155 160
 Thr Ile Leu Cys Leu Arg Ala Pro Gly Met Thr Met Phe Arg Met Pro
 165 170 175
 Ile Phe Thr Trp Asn Ile Phe Val Val Ser Val Leu Ala Leu Leu Ile
 180 185 190
 Phe Pro Leu Leu Leu Ala Ala Ala Leu Gly Val Leu Tyr Asp Arg Lys
 195 200 205
 Leu Gly Gly His Leu Tyr Asp Pro Ala Asn Gly Gly Ser Leu Leu Trp
 210 215 220
 Gln His Leu Phe Trp Phe Phe Gly His Pro Glu Val Tyr Val Leu Ala
 225 230 235 240
 Leu Pro Phe Phe Gly Ile Val Ser Glu Ile Ile Pro Val Phe Ser Arg
 245 250 255
 Lys Pro Met Phe Gly Tyr Val Gly Leu Ile Phe Ala Thr Leu Ser Ile
 260 265 270
 Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly
 275 280 285
 Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val
 290 295 300
 Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly
 305 310 315 320
 His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala

325										330					335				
Thr	Phe	Leu	Phe	Gly	Gly	Leu	Thr	Gly	Ile	Met	Leu	Ala	Ser	Pro	Pro				
			340					345					350						
Leu	Asp	Phe	His	Leu	Ala	Asp	Ser	Tyr	Phe	Leu	Ile	Ala	His	Phe	His				
		355					360					365							
Tyr	Thr	Leu	Phe	Gly	Thr	Val	Val	Phe	Ala	Ser	Cys	Ala	Gly	Val	Tyr				
	370					375					380								
Phe	Trp	Phe	Pro	Lys	Met	Thr	Gly	Arg	Met	Met	Asp	Glu	Arg	Leu	Gly				
385					390					395					400				
Lys	Ile	His	Phe	Trp	Leu	Thr	Phe	Val	Gly	Phe	His	Gly	Thr	Phe	Leu				
			405						410					415					
Ile	Gln	His	Trp	Val	Gly	Asn	Met	Gly	Met	Pro	Arg	Arg	Tyr	Ala	Asp				
			420					425					430						
Tyr	Leu	Asp	Ser	Asp	Gly	Phe	Thr	Ile	Tyr	Asn	Gln	Ile	Ser	Thr	Val				
		435					440					445							
Phe	Tyr	Phe	Leu	Leu	Gly	Leu	Ser	Val	Ile	Pro	Phe	Ile	Trp	Asn	Val				
	450					455					460								
Phe	Lys	Ser	Trp	Arg	Tyr	Gly	Glu	Leu	Val	Thr	Val	Asp	Asp	Pro	Trp				
465					470					475					480				
Gly	Tyr	Gly	Asn	Ser	Leu	Glu	Trp	Ala	Thr	Ser	Cys	Pro	Pro	Pro	Arg				
			485					490						495					
His	Asn	Phe	Ala	Ser	Leu	Pro	Arg	Ile	Arg	Ser	Glu	Arg	Pro	Ala	Phe				
			500					505					510						
Glu	Leu	His	Tyr	Pro	His	Met	Ile	Glu	Arg	Met	Arg	Ala	Glu	Ala	His				
		515					520					525							
Thr	Gly	His	His	Asp	Asp	Ile	Asn	Ala	Pro	Glu	Leu	Gly	Thr	Ala	Pro				
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Ala	Leu	Ala	Ser	Asp	Ser	Ser	Arg												
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> FRXA01919

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 <223> n = a,c,g,or t

<220>

<221> VARIANT

<222> 82

<223> Xaa = any amino acid

<400> 655

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gacaggccat gcacgcaagg gcagcaaagc atggttaatg atg acc acc acc gac 115
Met Thr Thr Thr Asp
1 5

cac aag cag ctg ggc att atg tac atc att atg tcc ttc agc ttc ttt 163
His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met Ser Phe Ser Phe Phe
10 15 20

ttc ctc ggt ggc ttg atg gcc ctg ctt atc cga gcg gag ctt ttc acc 211
Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg Ala Glu Leu Phe Thr
25 30 35

cct ggt ctg cag ttc ctg tct aat gag cag ttc aac cag ctg ttc acc 259
Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe Asn Gln Leu Phe Thr
40 45 50

atg cac gga act gtc atg ctg ctg ctg tac gga act cca att gtt tgg 307
Met His Gly Thr Val Met Leu Leu Leu Tyr Gly Thr Pro Ile Val Trp
55 60 65

ggt ttt gct aac tac gtc ctg cca ctt cca acc acc ang caa gcc ttc 355
Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr Thr Xaa Gln Ala Phe
70 75 80 85

tct aaa acc cgg gtg aac tct ccc agg gag 385
Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
90 95

<210> 656

<211> 95

<212> PRT

<213> Corynebacterium glutamicum

<220>

<221> VARIANT

<222> 82

<223> Xaa = any amino acid

<400> 656

Met Thr Thr Thr Asp His Lys Gln Leu Gly Ile Met Tyr Ile Ile Met
1 5 10 15

Ser Phe Ser Phe Phe Phe Leu Gly Gly Leu Met Ala Leu Leu Ile Arg
20 25 30

Ala Glu Leu Phe Thr Pro Gly Leu Gln Phe Leu Ser Asn Glu Gln Phe
35 40 45

Asn Gln Leu Phe Thr Met His Gly Thr Val Met Leu Leu Leu Tyr Gly
50 55 60

Thr Pro Ile Val Trp Gly Phe Ala Asn Tyr Val Leu Pro Leu Pro Thr
65 70 75 80

Thr Xaa Gln Ala Phe Ser Lys Thr Arg Val Asn Ser Pro Arg Glu
 85 90 95

<210> 657
 <211> 972
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(949)
 <223> FRXA02480

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 Leu Ser Ile Gly Ala
 1 5
 ctg tcc atg gct gtg tgg gct cac cac atg ttc gtt act ggc gca gtt 163
 Leu Ser Met Ala Val Trp Ala His His Met Phe Val Thr Gly Ala Val
 10 15 20
 ttg ctt ccg ttc ttc tcc ttc atg acg ttc ctg att tcg gtt cct acc 211
 Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu Ile Ser Val Pro Thr
 25 30 35
 ggc gtt aag ttc ttc aac tgg gtt gga acc atg tgg aag ggt cac atc 259
 Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met Trp Lys Gly His Ile
 40 45 50
 act tgg gaa acc cca atg atc tgg tct gtt ggc ttc atg gct acc ttc 307
 Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly Phe Met Ala Thr Phe
 55 60 65
 ctc ttc ggt ggt ctg acc ggc att atg ctg gcg tcc cca cca ctg gac 355
 Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala Ser Pro Pro Leu Asp
 70 75 80 85
 ttc cac ttg gct gac tcc tac ttc ctg atc gcg cac ttc cac tac acc 403
 Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala His Phe His Tyr Thr
 90 95 100
 ctc ttc ggt acc gtg gtg ttc gca tcg tgt gca ggc gtt tac ttc tgg 451
 Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala Gly Val Tyr Phe Trp
 105 110 115
 ttc ccg aag atg act ggc cgc atg atg gac gag cgt ctt ggc aag atc 499
 Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu Arg Leu Gly Lys Ile
 120 125 130
 cac ttc tgg ttg acc ttc gtc ggt ttc cac gga acc ttc ctc atc cag 547
 His Phe Trp Leu Thr Phe Val Gly Phe His Gly Thr Phe Leu Ile Gln
 135 140 145
 cac tgg gtg ggc aac atg ggt atg cca cgt cgt tac gct gac tac ctg 595
 His Trp Val Gly Asn Met Gly Met Pro Arg Arg Tyr Ala Asp Tyr Leu
 150 155 160 165

gat tct gat ggt ttc acc atc tac aac cag atc tcc acc gtg ttc tac 643
Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile Ser Thr Val Phe Tyr
170 175 180

ttc ctg ctt ggc ctg tct gtc att cca ttc atc tgg aac gtc ttc aag 691
Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile Trp Asn Val Phe Lys
185 190 195

tcc tgg cgc tac ggt gag ctc gtt acc gtt gat gat cct tgg ggt tac 739
Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp Asp Pro Trp Gly Tyr
200 205 210

ggc aac tcc ctg gag tgg gca acc tcc tgc cct cct cct cgc cac aac 787
Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro Pro Pro Arg His Asn
215 220 225

ttc gca tcc ttg cct cgt atc cgc tcc gag cgc cct gcg ttc gag ctg 835
Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg Pro Ala Phe Glu Leu
230 235 240 245

cac tac ccg cac atg att gaa cgc atg cgc gca gag gca cac act gga 883
His Tyr Pro His Met Ile Glu Arg Met Arg Ala Glu Ala His Thr Gly
250 255 260

cat cac gat gat att aat gct cca gaa ttg ggt acc gcc cca gcc ctt 931
His His Asp Asp Ile Asn Ala Pro Glu Leu Gly Thr Ala Pro Ala Leu
265 270 275

gca tct gac tcc agc cgc taaaagcgtc tgatttaagt cgg 972
Ala Ser Asp Ser Ser Arg
280

<210> 658

<211> 283

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 658

Leu Ser Ile Gly Ala Leu Ser Met Ala Val Trp Ala His His Met Phe
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Val Thr Gly Ala Val Leu Leu Pro Phe Phe Ser Phe Met Thr Phe Leu
20 25 30

Ile Ser Val Pro Thr Gly Val Lys Phe Phe Asn Trp Val Gly Thr Met
35 40 45

Trp Lys Gly His Ile Thr Trp Glu Thr Pro Met Ile Trp Ser Val Gly
50 55 60

Phe Met Ala Thr Phe Leu Phe Gly Gly Leu Thr Gly Ile Met Leu Ala
65 70 75 80

Ser Pro Pro Leu Asp Phe His Leu Ala Asp Ser Tyr Phe Leu Ile Ala
85 90 95

His Phe His Tyr Thr Leu Phe Gly Thr Val Val Phe Ala Ser Cys Ala
100 105 110

Gly Val Tyr Phe Trp Phe Pro Lys Met Thr Gly Arg Met Met Asp Glu
 115 120 125
 Arg Leu Gly Lys Ile His Phe Trp Leu Thr Phe Val Gly Phe His Gly
 130 135 140
 Thr Phe Leu Ile Gln His Trp Val Gly Asn Met Gly Met Pro Arg Arg
 145 150 155 160
 Tyr Ala Asp Tyr Leu Asp Ser Asp Gly Phe Thr Ile Tyr Asn Gln Ile
 165 170 175
 Ser Thr Val Phe Tyr Phe Leu Leu Gly Leu Ser Val Ile Pro Phe Ile
 180 185 190
 Trp Asn Val Phe Lys Ser Trp Arg Tyr Gly Glu Leu Val Thr Val Asp
 195 200 205
 Asp Pro Trp Gly Tyr Gly Asn Ser Leu Glu Trp Ala Thr Ser Cys Pro
 210 215 220
 Pro Pro Arg His Asn Phe Ala Ser Leu Pro Arg Ile Arg Ser Glu Arg
 225 230 235 240
 Pro Ala Phe Glu Leu His Tyr Pro His Met Ile Glu Arg Met Arg Ala
 245 250 255
 Glu Ala His Thr Gly His His Asp Asp Ile Asn Ala Pro Glu Leu Gly
 260 265 270
 Thr Ala Pro Ala Leu Ala Ser Asp Ser Ser Arg
 275 280

<210> 659
 <211> 735
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(712)
 <223> FRXA02481

<400> 659
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 tgctttcggc ttctgaatca ccaccgtcgg tgggtgtcgcg atg ctg acc ggc ttc 115
 Met Leu Thr Gly Phe 5
 cta acc ccg ggt ggt gct gcc gac ttg ggt gga cca tgt act ccc cac 163
 Leu Thr Pro Gly Gly Ala Ala Asp Leu Gly Gly Pro Cys Thr Pro His 20
 10 15 20
 tgt ctg acg caa ttc act ccc cag gcc ttg gtt cta aca tgt gga ttg 211
 Cys Leu Thr Gln Phe Thr Pro Gln Ala Leu Val Leu Thr Cys Gly Leu 35
 25 30 35
 tcg ggt gtc ggt gca act ggt att ggc tcc gtt gct tcc gca att aac 259
 Ser Gly Val Gly Ala Thr Gly Ile Gly Ser Val Ala Ser Ala Ile Asn

40										45										50										
atg	ctc	acc	acc	atc	ctc	tgc	ctc	cgc	gca	cct	ggt	atg	acc	atg	ttc	307														
Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu	Arg	Ala	Pro	Gly	Met	Thr	Met	Phe															
	55					60					65																			
cgt	atg	cct	att	ttc	acc	tgg	aat	atc	ttc	ggt	ggt	tcc	ggt	ctt	gct	355														
Arg	Met	Pro	Ile	Phe	Thr	Trp	Asn	Ile	Phe	Val	Val	Ser	Val	Leu	Ala															
	70				75					80					85															
ctg	ctg	atc	ttc	cca	ctg	ctg	ctc	gct	gct	gca	ctg	ggt	ggt	ctg	tat	403														
Leu	Leu	Ile	Phe	Pro	Leu	Leu	Leu	Ala	Ala	Ala	Leu	Gly	Val	Leu	Tyr															
				90					95					100																
gac	cgc	aag	ctt	ggt	gga	cac	ctg	tac	gat	cca	gct	aac	ggc	ggc	tcc	451														
Asp	Arg	Lys	Leu	Gly	Gly	His	Leu	Tyr	Asp	Pro	Ala	Asn	Gly	Gly	Ser															
			105					110					115																	
ctc	ctg	tgg	cag	cac	ctg	ttc	tgg	ttc	ttc	gga	cac	cct	gag	ggt	tac	499														
Leu	Leu	Trp	Gln	His	Leu	Phe	Trp	Phe	Phe	Gly	His	Pro	Glu	Val	Tyr															
		120					125						130																	
ggt	ctg	gcg	ctg	ccg	ttc	ttc	ggc	att	ggt	tct	gag	atc	att	cct	gtg	547														
Val	Leu	Ala	Leu	Pro	Phe	Phe	Gly	Ile	Val	Ser	Glu	Ile	Ile	Pro	Val															
	135					140					145																			
ttc	tcc	cgt	aag	cca	atg	ttc	ggg	tta	cgt	cgg	cct	gat	ctt	cgc	aac	595														
Phe	Ser	Arg	Lys	Pro	Met	Phe	Gly	Leu	Arg	Arg	Pro	Asp	Leu	Arg	Asn															
	150				155				160						165															
ctt	gtc	cat	tgg	tgc	act	gtc	cat	ggc	tgt	gtg	ggc	tca	cca	cat	ggt	643														
Leu	Val	His	Trp	Cys	Thr	Val	His	Gly	Cys	Val	Gly	Ser	Pro	His	Val															
				170				175						180																
cgt	tac	tgg	cgc	agt	ttt	gct	tcc	ggt	ctt	ctc	ctt	cat	gac	ggt	cct	691														
Arg	Tyr	Trp	Arg	Ser	Phe	Ala	Ser	Val	Leu	Leu	Leu	His	Asp	Val	Pro															
			185					190					195																	
gat	ttc	ggt	tcc	tac	cgg	cgt	taagttcttc	aactggggttg	gaa							735														
Asp	Phe	Gly	Ser	Tyr	Arg	Arg																								
		200																												

<210> 660

<211> 204

<212> PRT

<213> Corynebacterium glutamicum

<400> 660

Met	Leu	Thr	Gly	Phe	Leu	Thr	Pro	Gly	Gly	Ala	Ala	Asp	Leu	Gly	Gly	
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Pro	Cys	Thr	Pro	His	Cys	Leu	Thr	Gln	Phe	Thr	Pro	Gln	Ala	Leu	Val	
			20					25					30			
Leu	Thr	Cys	Gly	Leu	Ser	Gly	Val	Gly	Ala	Thr	Gly	Ile	Gly	Ser	Val	
		35					40					45				
Ala	Ser	Ala	Ile	Asn	Met	Leu	Thr	Thr	Ile	Leu	Cys	Leu	Arg	Ala	Pro	
	50					55					60					

Gly Met Thr Met Phe Arg Met Pro Ile Phe Thr Trp Asn Ile Phe Val
 65 70 75 80
 Val Ser Val Leu Ala Leu Leu Ile Phe Pro Leu Leu Leu Ala Ala Ala
 85 90 95
 Leu Gly Val Leu Tyr Asp Arg Lys Leu Gly Gly His Leu Tyr Asp Pro
 100 105 110
 Ala Asn Gly Gly Ser Leu Leu Trp Gln His Leu Phe Trp Phe Phe Gly
 115 120 125
 His Pro Glu Val Tyr Val Leu Ala Leu Pro Phe Phe Gly Ile Val Ser
 130 135 140
 Glu Ile Ile Pro Val Phe Ser Arg Lys Pro Met Phe Gly Leu Arg Arg
 145 150 155 160
 Pro Asp Leu Arg Asn Leu Val His Trp Cys Thr Val His Gly Cys Val
 165 170 175
 Gly Ser Pro His Val Arg Tyr Trp Arg Ser Phe Ala Ser Val Leu Leu
 180 185 190
 Leu His Asp Val Pro Asp Phe Gly Ser Tyr Arg Arg
 195 200

<210> 661
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1177)
 <223> RXA02140

<400> 661
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 aggtctcttg tttttgtgtg gacaggaagg cagaacacac gtg gaa cag caa aat 115
 Val Glu Gln Gln Asn
 1 5
 aag cgt ggt tta aag cgc aag gcc ctg ctt ggc ggt gtc ttg ggc tta 163
 Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly Gly Val Leu Gly Leu
 10 15 20
 ggt ggc ctc gcc atg gca ggc tgt gaa gtc gcc cct cct ggc ggt gtg 211
 Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala Pro Pro Gly Gly Val
 25 30 35
 ctt gga gat ttc cta cgt atg ggt tgg cct gat ggc att acc cct gaa 259
 Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp Gly Ile Thr Pro Glu
 40 45 50
 gca gtg gcc atg ggt aac ttc tgg tca tgg gtc tgg gtt gct gcc tgg 307
 Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val Trp Val Ala Ala Trp
 55 60 65

atc atc ggc atc atc atg tgg ggt cta ttc ctc acc gcc atc ttt gcc	355
Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu Thr Ala Ile Phe Ala	
70 75 80 85	
tgg ggc gca aag agg gct gaa aag cgc ggc gag ggt gaa ttc cct aag	403
Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu Gly Glu Phe Pro Lys	
90 95 100	
cag ctc cag tac aac gtt cca ctt gag ctc gtt ctg acg atc gtt ccg	451
Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val Leu Thr Ile Val Pro	
105 110 115	
atc atc att gtt atg gtg ctg ttc ttc ttc acc gtt caa act cag gac	499
Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr Val Gln Thr Gln Asp	
120 125 130	
aag gtc acc gct ctg gat aag aac cca gag gtt acc gtg gac gtc acc	547
Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val Thr Val Asp Val Thr	
135 140 145	
gct tac cag tgg aac tgg aag ttc gga tac tcc gaa att gat ggc tca	595
Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser Glu Ile Asp Gly Ser	
150 155 160 165	
ctg gca cct ggt gga cag gat tac caa gga agc gac ccg gag cgt cag	643
Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser Asp Pro Glu Arg Gln	
170 175 180	
gca gct gcc gag gct tcc aag aag gat cct tct gga gat aac cca att	691
Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser Gly Asp Asn Pro Ile	
185 190 195	
cac ggc aac tca aag tct gac gtt tct tac ctt gag ttc aac cga att	739
His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu Glu Phe Asn Arg Ile	
200 205 210	
gaa acc ctc gga acc act gat gaa atc cca gtg atg gtt ctt cct gtg	787
Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val Met Val Leu Pro Val	
215 220 225	
aac acc cca atc gag ttc aac ctc gca tct gct gac gtt gca cac tcc	835
Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala Asp Val Ala His Ser	
230 235 240 245	
ttc tgg gtt cca gag ttc ctc ttc aag cga gat gct tac gca cac cct	883
Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp Ala Tyr Ala His Pro	
250 255 260	
gag gca aac aag tcc cag cgt gtc ttc cag att gaa gag atc act gag	931
Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile Glu Glu Ile Thr Glu	
265 270 275	
gaa ggc gca ttc gtt ggt cgc tgt gca gaa atg tgc ggt act tac cac	979
Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met Cys Gly Thr Tyr His	
280 285 290	
gca atg atg aac ttc gag ctt cgt gtc gtc gat cgc gat tcc ttc gct	1027
Ala Met Met Asn Phe Glu Leu Arg Val Val Asp Arg Asp Ser Phe Ala	
295 300 305	
gag tac atc agc ttc cgt gac tcc aac cca gac gca acc aac gct cag	1075

Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp Ala Thr Asn Ala Gln
 310 315 320 325
 gca ctt gag cac att ggt caa gct cct tac gct act tcc act agc cca 1123
 Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala Thr Ser Thr Ser Pro
 330 335 340
 ttc gtt tcc gat cgc acc gca acc cgc gac ggc gaa aac act cag agc 1171
 Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly Glu Asn Thr Gln Ser
 345 350 355
 aac gct taagaaggag tggcgaaaaa atg 1200
 Asn Ala

<210> 662

<211> 359

<212> PRT

<213> Corynebacterium glutamicum

<400> 662

Val Glu Gln Gln Asn Lys Arg Gly Leu Lys Arg Lys Ala Leu Leu Gly
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 Gly Val Leu Gly Leu Gly Gly Leu Ala Met Ala Gly Cys Glu Val Ala
 20 25 30
 Pro Pro Gly Gly Val Leu Gly Asp Phe Leu Arg Met Gly Trp Pro Asp
 35 40 45
 Gly Ile Thr Pro Glu Ala Val Ala Met Gly Asn Phe Trp Ser Trp Val
 50 55 60
 Trp Val Ala Ala Trp Ile Ile Gly Ile Ile Met Trp Gly Leu Phe Leu
 65 70 75 80
 Thr Ala Ile Phe Ala Trp Gly Ala Lys Arg Ala Glu Lys Arg Gly Glu
 85 90 95
 Gly Glu Phe Pro Lys Gln Leu Gln Tyr Asn Val Pro Leu Glu Leu Val
 100 105 110
 Leu Thr Ile Val Pro Ile Ile Ile Val Met Val Leu Phe Phe Phe Thr
 115 120 125
 Val Gln Thr Gln Asp Lys Val Thr Ala Leu Asp Lys Asn Pro Glu Val
 130 135 140
 Thr Val Asp Val Thr Ala Tyr Gln Trp Asn Trp Lys Phe Gly Tyr Ser
 145 150 155 160
 Glu Ile Asp Gly Ser Leu Ala Pro Gly Gly Gln Asp Tyr Gln Gly Ser
 165 170 175
 Asp Pro Glu Arg Gln Ala Ala Ala Glu Ala Ser Lys Lys Asp Pro Ser
 180 185 190
 Gly Asp Asn Pro Ile His Gly Asn Ser Lys Ser Asp Val Ser Tyr Leu
 195 200 205

Glu Phe Asn Arg Ile Glu Thr Leu Gly Thr Thr Asp Glu Ile Pro Val
 210 215 220
 Met Val Leu Pro Val Asn Thr Pro Ile Glu Phe Asn Leu Ala Ser Ala
 225 230 235 240
 Asp Val Ala His Ser Phe Trp Val Pro Glu Phe Leu Phe Lys Arg Asp
 245 250 255
 Ala Tyr Ala His Pro Glu Ala Asn Lys Ser Gln Arg Val Phe Gln Ile
 260 265 270
 Glu Glu Ile Thr Glu Glu Gly Ala Phe Val Gly Arg Cys Ala Glu Met
 275 280 285
 Cys Gly Thr Tyr His Ala Met Met Asn Phe Glu Leu Arg Val Val Asp
 290 295 300
 Arg Asp Ser Phe Ala Glu Tyr Ile Ser Phe Arg Asp Ser Asn Pro Asp
 305 310 315 320
 Ala Thr Asn Ala Gln Ala Leu Glu His Ile Gly Gln Ala Pro Tyr Ala
 325 330 335
 Thr Ser Thr Ser Pro Phe Val Ser Asp Arg Thr Ala Thr Arg Asp Gly
 340 345 350
 Glu Asn Thr Gln Ser Asn Ala
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<210> 663
 <211> 774
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(751)
 <223> RXA02142

<400> 663
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 aagccgagtt caaactttca attgaaacgg ggggcttgaa gtg act ttg gcc aac 115
 Val Thr Leu Ala Asn
 1 5
 caa aca gcc ata cta gat agc gtg acg agc gca gtt gga aat aca ggt 163
 Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala Val Gly Asn Thr Gly
 10 15 20
 atg gca gca cca caa cgt gtt gcg gca ctg aac cgt ccg aat atg gtc 211
 Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn Arg Pro Asn Met Val
 25 30 35
 agt gtc ggc acc att gtg ttc ctg tct cag gaa tta atg ttc ttc gcc 259
 Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu Leu Met Phe Phe Ala
 40 45 50
 ggg cta ttc gcg atg tac ttc gtg tcc cgt gcg aac gga ctg gca aat 307

Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala Asn Gly Leu Ala Asn
 55 60 65
 gga tca tgg gga gag cag aca gat cac ctc aac gtg ccc tac gca ctg 355
 Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn Val Pro Tyr Ala Leu 85
 70 75 80
 ttg att acg gtc att ctg gtg tct tcc tca gtg act tgc cag ttc gga 403
 Leu Ile Thr Val Ile Leu Val Ser Ser Val Thr Cys Gln Phe Gly 100
 90 95
 gtt ttt gcg gct gaa agg ggt gac gtt tac ggc ctc cgc aag tgg ttc 451
 Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly Leu Arg Lys Trp Phe 115
 105 110
 ttg gtc acg att atc ctc gga tca atc ttc gtg atc gga cag ggc tac 499
 Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val Ile Gly Gln Gly Tyr 130
 120 125
 gag tac atc act ctc gta ggt cac gga ctt aca atc cag agc agt gtc 547
 Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr Ile Gln Ser Ser Val 145
 135 140
 tac gga tcg gca ttc ttt att aca acc ggt ttc cac gca ctg cac gtg 595
 Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe His Ala Leu His Val 165
 150 155 160
 atc gcg ggt gtt atg gcc ttc gtt gtg gtt ctt atg aga atc cat aag 643
 Ile Ala Gly Val Met Ala Phe Val Val Val Leu Met Arg Ile His Lys 180
 170 175
 tcg aag ttc act ccg gca cag gca acc gca gca atg gtt gtg tct tat 691
 Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala Met Val Val Ser Tyr 195
 185 190
 tac tgg cac ttc gtt gac gtg gtc tgg atc ggc ctc ttc atc act att 739
 Tyr Trp His Phe Val Asp Val Val Trp Ile Gly Leu Phe Ile Thr Ile 210
 200 205
 tac ttc att cag taggcagtaa ggaatcctca acg 774
 Tyr Phe Ile Gln
 215

<210> 664

<211> 217

<212> PRT

<213> Corynebacterium glutamicum

<400> 664

Val Thr Leu Ala Asn Gln Thr Ala Ile Leu Asp Ser Val Thr Ser Ala
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 Val Gly Asn Thr Gly Met Ala Ala Pro Gln Arg Val Ala Ala Leu Asn
 20 25 30
 Arg Pro Asn Met Val Ser Val Gly Thr Ile Val Phe Leu Ser Gln Glu
 35 40 45
 Leu Met Phe Phe Ala Gly Leu Phe Ala Met Tyr Phe Val Ser Arg Ala
 50 55 60

Asn Gly Leu Ala Asn Gly Ser Trp Gly Glu Gln Thr Asp His Leu Asn
 65 70 75 80
 Val Pro Tyr Ala Leu Leu Ile Thr Val Ile Leu Val Ser Ser Ser Val
 85 90 95
 Thr Cys Gln Phe Gly Val Phe Ala Ala Glu Arg Gly Asp Val Tyr Gly
 100 105 110
 Leu Arg Lys Trp Phe Leu Val Thr Ile Ile Leu Gly Ser Ile Phe Val
 115 120 125
 Ile Gly Gln Gly Tyr Glu Tyr Ile Thr Leu Val Gly His Gly Leu Thr
 130 135 140
 Ile Gln Ser Ser Val Tyr Gly Ser Ala Phe Phe Ile Thr Thr Gly Phe
 145 150 155 160
 His Ala Leu His Val Ile Ala Gly Val Met Ala Phe Val Val Val Leu
 165 170 175
 Met Arg Ile His Lys Ser Lys Phe Thr Pro Ala Gln Ala Thr Ala Ala
 180 185 190
 Met Val Val Ser Tyr Tyr Trp His Phe Val Asp Val Val Trp Ile Gly
 195 200 205
 Leu Phe Ile Thr Ile Tyr Phe Ile Gln
 210 215

<210> 665
 <211> 1347
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1324)
 <223> RXA02144

<400> 665
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 tggtcctcgt ggccgccgct atgtggattg gatcacgttc atg agt aac aac aac 115
 Met Ser Asn Asn Asn
 1 5
 gac aaa cag tac aca acc caa gaa ctc aac gcg atg agc aat gag gat 163
 Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala Met Ser Asn Glu Asp
 10 15 20
 ctt gca cga ctt ggt aca gag ctg gac gac gtt acc att gca tac cgc 211
 Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val Thr Ile Ala Tyr Arg
 25 30 35
 aag gaa cgt ttc cca atc gct aat gac cca gct gag aag cgc gct gca 259
 Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala Glu Lys Arg Ala Ala
 40 45 50

cgt gca gtt act ttc tgg cta gtc ctc ggc atc att ggt gga ctt ggg	307
Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile Ile Gly Gly Leu Gly	
55 60 65	
ttc ctg gct acc tac att ttc tgg cct tgg gag tac aag gca cac gga	355
Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu Tyr Lys Ala His Gly	
70 75 80 85	
gat gaa ggt ctc ctg gcg tac acc ttg tac acc cca atg ctg ggt att	403
Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr Pro Met Leu Gly Ile	
90 95 100	
act tcc ggt ctt tgc atc ctg tcc ctg gga ttt gca gtt gtc ctt tat	451
Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe Ala Val Val Leu Tyr	
105 110 115	
gtc aag aag ttc att cca gag gaa atc gca gta cag cgt cgc cac gac	499
Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val Gln Arg Arg His Asp	
120 125 130	
ggt cct tct gaa gaa gtt gac cgc cgc acc atc gtt gca ctt ctc aat	547
Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile Val Ala Leu Leu Asn	
135 140 145	
gac tct tgg cag acc tct act ctt ggt cgt cgc aag ctg atc atg gga	595
Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg Lys Leu Ile Met Gly	
150 155 160 165	
ctt gca ggt ggc gga gca gta ctg gcc ggc ctg acc atc atc gct cca	643
Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu Thr Ile Ile Ala Pro	
170 175 180	
atg ggc ggt atg atc aag aac cct tgg aat cct aag gaa ggc cca atg	691
Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro Lys Glu Gly Pro Met	
185 190 195	
gac gtt cag ggt gac ggc acc ctg tgg act tcc ggt tgg act ctc gtt	739
Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser Gly Trp Thr Leu Val	
200 205 210	
gag aac gac gtc aag gtt tac ctc ggc cgc gac act gca gca att gcg	787
Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp Thr Ala Ala Ile Ala	
215 220 225	
gag tcc cac acc gat gca acc ggt gag cac tgg tca acc act ggt gtt	835
Glu Ser His Thr Asp Ala Thr Gly Glu His Trp Ser Thr Thr Gly Val	
230 235 240 245	
tcc cgc ctg gtt cgt atg cgc cca gaa gat ctg gca gca gca tcc atg	883
Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu Ala Ala Ala Ser Met	
250 255 260	
gaa act gtc ttc cca ctt cca gct gaa atg gtg aac gac ggt gct gaa	931
Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val Asn Asp Gly Ala Glu	
265 270 275	
tac gat cct gcg aag gac gtc tac gag cac caa atg cac tcg gtg cac	979
Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln Met His Ser Val His	
280 285 290	
ggc cca cgc aac gca gtt atg ttg atc cgt ctc cgt acc gct gac gct	1027

Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu Arg Thr Ala Asp Ala
 295 300 305
 gaa aag gtt atc gaa cgc gaa ggc cag gag tcc ttc cac tac ggt gac 1075
 Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser Phe His Tyr Gly Asp 325
 310 315 320
 tac tac gct tac tcc aag att tgt aca cac att ggt tgc cca acc tca 1123
 Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile Gly Cys Pro Thr Ser 340
 330 335
 ctg tac gag gct cag acc aat cgt att ctg tgc cca tgt cac cag tcg 1171
 Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys Pro Cys His Gln Ser 355
 345 350
 cag ttt gac gca ttg cac tac gga aag cca gtc ttt gga cct gct gcc 1219
 Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val Phe Gly Pro Ala Ala 370
 360 365
 cgt gca ctg cca cag ctg cca att acc gtt gat gaa gag ggc tac ctc 1267
 Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp Glu Glu Gly Tyr Leu 385
 375 380
 atc gcc gct ggt aac ttc att gag cca ctc ggc cct gca ttc tgg gag 1315
 Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly Pro Ala Phe Trp Glu 405
 390 395 400
 cgt aag tca tgagtctagc taccgtggga aac 1347
 Arg Lys Ser

<210> 666

<211> 408

<212> PRT

<213> Corynebacterium glutamicum

<400> 666

Met Ser Asn Asn Asn Asp Lys Gln Tyr Thr Thr Gln Glu Leu Asn Ala
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 Met Ser Asn Glu Asp Leu Ala Arg Leu Gly Thr Glu Leu Asp Asp Val
 20 25 30
 Thr Ile Ala Tyr Arg Lys Glu Arg Phe Pro Ile Ala Asn Asp Pro Ala
 35 40 45
 Glu Lys Arg Ala Ala Arg Ala Val Thr Phe Trp Leu Val Leu Gly Ile
 50 55 60
 Ile Gly Gly Leu Gly Phe Leu Ala Thr Tyr Ile Phe Trp Pro Trp Glu
 65 70 75 80
 Tyr Lys Ala His Gly Asp Glu Gly Leu Leu Ala Tyr Thr Leu Tyr Thr
 85 90 95
 Pro Met Leu Gly Ile Thr Ser Gly Leu Cys Ile Leu Ser Leu Gly Phe
 100 105 110
 Ala Val Val Leu Tyr Val Lys Lys Phe Ile Pro Glu Glu Ile Ala Val
 115 120 125

Gln Arg Arg His Asp Gly Pro Ser Glu Glu Val Asp Arg Arg Thr Ile
 130 135 140
 Val Ala Leu Leu Asn Asp Ser Trp Gln Thr Ser Thr Leu Gly Arg Arg
 145 150 155 160
 Lys Leu Ile Met Gly Leu Ala Gly Gly Gly Ala Val Leu Ala Gly Leu
 165 170 175
 Thr Ile Ile Ala Pro Met Gly Gly Met Ile Lys Asn Pro Trp Asn Pro
 180 185 190
 Lys Glu Gly Pro Met Asp Val Gln Gly Asp Gly Thr Leu Trp Thr Ser
 195 200 205
 Gly Trp Thr Leu Val Glu Asn Asp Val Lys Val Tyr Leu Gly Arg Asp
 210 215 220
 Thr Ala Ala Ile Ala Glu Ser His Thr Asp Ala Thr Gly Glu His Trp
 225 230 235 240
 Ser Thr Thr Gly Val Ser Arg Leu Val Arg Met Arg Pro Glu Asp Leu
 245 250 255
 Ala Ala Ala Ser Met Glu Thr Val Phe Pro Leu Pro Ala Glu Met Val
 260 265 270
 Asn Asp Gly Ala Glu Tyr Asp Pro Ala Lys Asp Val Tyr Glu His Gln
 275 280 285
 Met His Ser Val His Gly Pro Arg Asn Ala Val Met Leu Ile Arg Leu
 290 295 300
 Arg Thr Ala Asp Ala Glu Lys Val Ile Glu Arg Glu Gly Gln Glu Ser
 305 310 315 320
 Phe His Tyr Gly Asp Tyr Tyr Ala Tyr Ser Lys Ile Cys Thr His Ile
 325 330 335
 Gly Cys Pro Thr Ser Leu Tyr Glu Ala Gln Thr Asn Arg Ile Leu Cys
 340 345 350
 Pro Cys His Gln Ser Gln Phe Asp Ala Leu His Tyr Gly Lys Pro Val
 355 360 365
 Phe Gly Pro Ala Ala Arg Ala Leu Pro Gln Leu Pro Ile Thr Val Asp
 370 375 380
 Glu Glu Gly Tyr Leu Ile Ala Ala Gly Asn Phe Ile Glu Pro Leu Gly
 385 390 395 400
 Pro Ala Phe Trp Glu Arg Lys Ser
 405

<210> 667

<211> 1053

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1030)

<223> RXA02740

<400> 667

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                                   Leu Asp Thr Ile Lys
                                   1 5

gcc tat att gcg cta acg aag ccc agg gtt att gaa ctc ctc ctt gtc 163
Ala Tyr Ile Ala Leu Thr Lys Pro Arg Val Ile Glu Leu Leu Leu Val
              10              15              20

gcc aca atc ccc aca atg ctt cag gct gaa cgc ggt gag aac aac att 211
Ala Thr Ile Pro Thr Met Leu Gln Ala Glu Arg Gly Glu Asn Asn Ile
              25              30              35

gtg ctc atc ttg ctg act gtg ttc ggt ggc tgg atg ggt gcg gcc gcc 259
Val Leu Ile Leu Leu Thr Val Phe Gly Gly Trp Met Gly Ala Ala Ala
              40              45              50

gcc aac acc ttc aac atg gtg gca gac tcc gat att gat cag cgc atg 307
Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp Ile Asp Gln Arg Met
              55              60              65

gga cgc act agg gct cgc cct ttg gtg cgc cac acc gtg agt aat cgc 355
Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His Thr Val Ser Asn Arg
              70              75              80              85

gac gcc tcc att ttt gcg tgg gtc ctg aca gtg gcc agc ttc ttg tgg 403
Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val Ala Ser Phe Leu Trp
              90              95              100

ctg tgg ctg ctg tgc gat tgc atg ctc gcc ggc atc ttc gtg ttg atc 451
Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly Ile Phe Val Leu Ile
              105              110              115

acg att ttc ttc tac att ttt gtc tac acc aag tgg ctg aag cgc cgc 499
Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys Trp Leu Lys Arg Arg
              120              125              130

acg cac atg aat atc gtg tgg ggc gga gcc gca ggt tgt atg cca gtg 547
Thr His Met Asn Ile Val Trp Gly Gly Ala Ala Gly Cys Met Pro Val
              135              140              145

ctc gtc ggc tgg gca gtg atc gtt gat cag ttt gag cca ggc gtt cca 595
Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe Glu Pro Gly Val Pro
              150              155              160              165

cag cag tgg tgg cag gca att gtc ctg ttc atg gtg att ttc ttc tgg 643
Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met Val Ile Phe Phe Trp
              170              175              180

acc cca cct cac acc tgg gct ctg gcc atg aag tac cgc gaa gac tac 691
Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys Tyr Arg Glu Asp Tyr
              185              190              195

aag gcg gct ggc gtc cca atg ctt cct gtc gtg cgc acc cca gtc cag 739

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Lys Ala Ala Gly Val Pro Met Leu Pro Val Val Arg Thr Pro Val Gln
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 gtc acc gca caa atc gtg tgg tac tcc gtg gca act gtg ctg acc acc 787
 Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala Thr Val Leu Thr Thr
 215 220 225
 ttc ttg ctc atc cca gca act ggt tgg atc tac gca gcg atc gcc gtc 835
 Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr Ala Ala Ile Ala Val
 230 235 240 245
 att tcc ggc gtc acc ttc ttg ttc atg gcc atc aag ctg cac ctc ggc 883
 Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile Lys Leu His Leu Gly
 250 255 260
 atc aaa aac ggt ggc aag gtc aag cct ctg aag ctg ttt att ttg tcc 931
 Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys Leu Phe Ile Leu Ser
 265 270 275
 aac aac tac ttg gca gtc ctc ttc gtg gca ttg tcc gtc gac gcg gtc 979
 Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu Ser Val Asp Ala Val
 280 285 290
 ctc ggc ctt gag acc atc ggc gag atg ctc ggc tgg acc acc acc ttc 1027
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 Phe
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<210> 668

<211> 310

<212> PRT

<213> Corynebacterium glutamicum

<400> 668

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 35 40 45
 Met Gly Ala Ala Ala Ala Asn Thr Phe Asn Met Val Ala Asp Ser Asp
 50 55 60
 Ile Asp Gln Arg Met Gly Arg Thr Arg Ala Arg Pro Leu Val Arg His
 65 70 75 80
 Thr Val Ser Asn Arg Asp Ala Ser Ile Phe Ala Trp Val Leu Thr Val
 85 90 95
 Ala Ser Phe Leu Trp Leu Trp Leu Leu Cys Asp Ser Met Leu Ala Gly
 100 105 110
 Ile Phe Val Leu Ile Thr Ile Phe Phe Tyr Ile Phe Val Tyr Thr Lys
 115 120 125

Trp Leu Lys Arg Arg Thr His Met Asn Ile Val Trp Gly Gly Ala Ala
 130 135 140
 Gly Cys Met Pro Val Leu Val Gly Trp Ala Val Ile Val Asp Gln Phe
 145 150 155 160
 Glu Pro Gly Val Pro Gln Gln Trp Trp Gln Ala Ile Val Leu Phe Met
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 Val Ile Phe Phe Trp Thr Pro Pro His Thr Trp Ala Leu Ala Met Lys
 180 185 190
 Tyr Arg Glu Asp Tyr Lys Ala Ala Gly Val Pro Met Leu Pro Val Val
 195 200 205
 Arg Thr Pro Val Gln Val Thr Ala Gln Ile Val Trp Tyr Ser Val Ala
 210 215 220
 Thr Val Leu Thr Thr Phe Leu Leu Ile Pro Ala Thr Gly Trp Ile Tyr
 225 230 235 240
 Ala Ala Ile Ala Val Ile Ser Gly Val Thr Phe Leu Phe Met Ala Ile
 245 250 255
 Lys Leu His Leu Gly Ile Lys Asn Gly Gly Lys Val Lys Pro Leu Lys
 260 265 270
 Leu Phe Ile Leu Ser Asn Asn Tyr Leu Ala Val Leu Phe Val Ala Leu
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 <212> DNA
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 <222> (101)..(1138)
 <223> RXA02743

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 Val Ser Thr Ser Asp
 1 5
 gct ccc tca aat aat cca gtt gag ttg aag ccc att act ttc tgg gca 163
 Ala Pro Ser Asn Asn Pro Val Glu Leu Lys Pro Ile Thr Phe Trp Ala
 10 15 20
 ccg acc atc aaa gtg cag cgc att ctc gcg ctc cta ctg ttg att ttc 211
 Pro Thr Ile Lys Val Gln Arg Ile Leu Ala Leu Leu Leu Ile Phe

25						30						35						
cag	gga	ggc	atc	acc	gtt	acg	ggc	tct	atc	gtc	cgt	gtc	aca	ggc	tcc	259		
Gln	Gly	Gly	Ile	Thr	Val	Thr	Gly	Ser	Ile	Val	Arg	Val	Thr	Gly	Ser			
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ggc	ctc	ggg	tgt	gat	acc	tgg	cca	cta	tgc	cac	gaa	ggg	tca	cta	gtc	307		
Gly	Leu	Gly	Cys	Asp	Thr	Trp	Pro	Leu	Cys	His	Glu	Gly	Ser	Leu	Val			
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cca	gtc	gca	ggc	gca	gca	cca	tgg	atc	cac	cag	gca	gtg	gaa	ttt	ggg	355		
Pro	Val	Ala	Gly	Ala	Ala	Pro	Trp	Ile	His	Gln	Ala	Val	Glu	Phe	Gly			
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aac	cgc	atg	ctc	act	ttc	gtg	ctt	gct	gcc	gca	gcg	ctt	gcg	ttg	ttc	403		
Asn	Arg	Met	Leu	Thr	Phe	Val	Leu	Ala	Ala	Ala	Ala	Leu	Ala	Leu	Phe			
90						95						100						
att	gca	gtt	ctt	ggc	gca	aaa	cgc	cgc	cgc	gag	atc	ctg	gtc	cat	tcc	451		
Ile	Ala	Val	Leu	Gly	Ala	Lys	Arg	Arg	Arg	Glu	Ile	Leu	Val	His	Ser			
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ttc	atc	cag	ggg	ttg	ggc	atc	atc	ttg	cag	gct	gtc	atc	ggg	ggc	atc	499		
Phe	Ile	Gln	Gly	Leu	Gly	Ile	Ile	Leu	Gln	Ala	Val	Ile	Gly	Gly	Ile			
120						125						130						
acc	gtg	ctg	gtt	gat	ttg	cac	tgg	tac	gcc	gtt	gct	ttg	cac	ttc	ctg	547		
Thr	Val	Leu	Val	Asp	Leu	His	Trp	Tyr	Ala	Val	Ala	Leu	His	Phe	Leu			
135						140						145						
cca	tcc	atg	atc	ctt	gtt	ttc	atg	gcc	gcg	att	ttg	tac	acc	cgc	atc	595		
Pro	Ser	Met	Ile	Leu	Val	Phe	Met	Ala	Ala	Ile	Leu	Tyr	Thr	Arg	Ile			
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Gly	Glu	Pro	Asp	Asp	Gly	Glu	Ile	Thr	Thr	Thr	Phe	Pro	Thr	Trp	Ile			
170						175						180						
cgc	aat	gta	gct	gtc	att	ggg	gca	gta	gcg	ctc	tcc	gta	gta	ctg	atc	691		
Arg	Asn	Val	Ala	Val	Ile	Gly	Ala	Val	Ala	Leu	Ser	Val	Val	Leu	Ile			
185						190						195						
acc	ggc	acc	atg	acc	acc	ggc	gct	ggc	gtt	cac	tct	ggc	gat	gca	tca	739		
Thr	Gly	Thr	Met	Thr	Thr	Gly	Ala	Gly	Val	His	Ser	Gly	Asp	Ala	Ser			
200						205						210						
atc	acc	atg	gat	gat	cgc	ctc	gat	gtc	agc	atc	gac	ttg	atg	gcc	cac	787		
Ile	Thr	Met	Asp	Asp	Arg	Leu	Asp	Val	Ser	Ile	Asp	Leu	Met	Ala	His			
215						220						225						
atc	cac	ggc	tac	agc	atg	tac	atc	tac	ctc	ttc	ttc	acc	ctc	atc	gtg	835		
Ile	His	Gly	Tyr	Ser	Met	Tyr	Ile	Tyr	Leu	Phe	Phe	Thr	Leu	Ile	Val			
230						235						240						245
gtc	gcc	ggg	ctg	tac	aag	gca	aaa	acc	acc	aag	cac	aac	aag	cag	ctt	883		
Val	Ala	Gly	Leu	Tyr	Lys	Ala	Lys	Thr	Thr	Lys	His	Asn	Lys	Gln	Leu			
250						255						260						
ggc	ctc	atg	ctg	att	ctg	ttc	att	ctg	att	cag	gca	ggg	atc	ggc	atc	931		
Gly	Leu	Met	Leu	Ile	Leu	Phe	Ile	Leu	Ile	Gln	Ala	Gly	Ile	Gly	Ile			
265						270						275						

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 280 285 290

 gca atg tct tct gtc gtt gtt gcc ttc act tcc ctt ctg tgg gcg cag 1027
 Ala Met Ser Ser Val Val Val Ala Phe Thr Ser Leu Leu Trp Ala Gln
 295 300 305

 ggt cgt ata cgc gtc ggc ggt aaa gcc acc gtt act ggt tct gtt gat 1075
 Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val Thr Gly Ser Val Asp
 310 315 320 325

 ggc gat att aag aac gag atc att acg aac ccc ttt gag aag aaa tca 1123
 Gly Asp Ile Lys Asn Glu Ile Ile Thr Asn Pro Phe Glu Lys Lys Ser
 330 335 340

 aag cag cct gtt aaa taacacgcaa ctgtatcggg aaa 1161
 Lys Gln Pro Val Lys
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<210> 670

<211> 346

<212> PRT

<213> Corynebacterium glutamicum

<400> 670

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 35 40 45

 Arg Val Thr Gly Ser Gly Leu Gly Cys Asp Thr Trp Pro Leu Cys His
 50 55 60

 Glu Gly Ser Leu Val Pro Val Ala Gly Ala Ala Pro Trp Ile His Gln
 65 70 75 80

 Ala Val Glu Phe Gly Asn Arg Met Leu Thr Phe Val Leu Ala Ala Ala
 85 90 95

 Ala Leu Ala Leu Phe Ile Ala Val Leu Gly Ala Lys Arg Arg Arg Glu
 100 105 110

 Ile Leu Val His Ser Phe Ile Gln Gly Leu Gly Ile Ile Leu Gln Ala
 115 120 125

 Val Ile Gly Gly Ile Thr Val Leu Val Asp Leu His Trp Tyr Ala Val
 130 135 140

 Ala Leu His Phe Leu Pro Ser Met Ile Leu Val Phe Met Ala Ala Ile
 145 150 155 160

 Leu Tyr Thr Arg Ile Gly Glu Pro Asp Asp Gly Glu Ile Thr Thr Thr
 165 170 175

Phe Pro Thr Trp Ile Arg Asn Val Ala Val Ile Gly Ala Val Ala Leu
 180 185 190
 Ser Val Val Leu Ile Thr Gly Thr Met Thr Thr Gly Ala Gly Val His
 195 200 205
 Ser Gly Asp Ala Ser Ile Thr Met Asp Asp Arg Leu Asp Val Ser Ile
 210 215 220
 Asp Leu Met Ala His Ile His Gly Tyr Ser Met Tyr Ile Tyr Leu Phe
 225 230 235 240
 Phe Thr Leu Ile Val Val Ala Gly Leu Tyr Lys Ala Lys Thr Thr Lys
 245 250 255
 His Asn Lys Gln Leu Gly Leu Met Leu Ile Leu Phe Ile Leu Ile Gln
 260 265 270
 Ala Gly Ile Gly Ile Leu Gln Tyr Arg Met Gly Val Pro Arg Trp Ser
 275 280 285
 Ile Pro Phe His Ile Ala Met Ser Ser Val Val Val Ala Phe Thr Ser
 290 295 300
 Leu Leu Trp Ala Gln Gly Arg Ile Arg Val Gly Gly Lys Ala Thr Val
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 340 345

<210> 671
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 <212> DNA
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 <222> (101)..(421)
 <223> RXA01227

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 Met Thr Tyr Thr Ile
 1 5
 gcc cag ccc tgc gtt gat gtc ctg gat cga gcc tgc gtc gag gaa tgt 163
 Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys
 10 15 20
 ccc gtg gac tgc atc tac gag ggc aaa cgg atg ctc tac atc cac ccc 211
 Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro
 25 30 35
 gat gag tgc gtc gac tgc ggt gcc tgc gag ccc gtc tgc ccg gtt gaa 259
 Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Val Cys Pro Val Glu

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          40          45          50
gcc atc ttc tac gaa gat gat gtt ccc cac gaa tgg tgg gac tac acc 307
Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu Trp Trp Asp Tyr Thr
   55          60          65

ggc gct aac gcc gcc ttt ttc gac gac ctc ggt tcg cca ggc ggt gcc 355
Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala
   70          75          80          85

gcc agc ctg ggt ccg cag gac ttc gac gcc cag ctc gtc gcg gtg ctg 403
Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln Leu Val Ala Val Leu
          90          95          100

ccg cca cag aac cag aac taggacctga tatcggccct aaa 444
Pro Pro Gln Asn Gln Asn
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<210> 672
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 <212> PRT
 <213> Corynebacterium glutamicum

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Cys Val Glu Glu Cys Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met
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Leu Tyr Ile His Pro Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro
   35          40          45

Val Cys Pro Val Glu Ala Ile Phe Tyr Glu Asp Asp Val Pro His Glu
   50          55          60

Trp Trp Asp Tyr Thr Gly Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly
   65          70          75          80

Ser Pro Gly Gly Ala Ala Ser Leu Gly Pro Gln Asp Phe Asp Ala Gln
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Leu Val Ala Val Leu Pro Pro Gln Asn Gln Asn
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<210> 673
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 <222> (101)..(415)
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Ala Gln Pro Cys Val Asp Val Leu Asp Arg Ala Cys Val Glu Glu Cys						
cca gta gat tgc atc tac gaa ggt aag cgc atg ctg tac atc cac ccg						211
Pro Val Asp Cys Ile Tyr Glu Gly Lys Arg Met Leu Tyr Ile His Pro						
gat gag tgc gtt gac tgt ggt gca tgt gag cct gct tgc cca gtt gag						259
Asp Glu Cys Val Asp Cys Gly Ala Cys Glu Pro Ala Cys Pro Val Glu						
gca atc ttc tac gag gac gat gtc cca gac gaa tgg ctt gac tac aac						307
Ala Ile Phe Tyr Glu Asp Asp Val Pro Asp Glu Trp Leu Asp Tyr Asn						
gat gcc aac gct gca ttc ttc gat gat ctg ggc tcc cca ggt ggt gcg						355
Asp Ala Asn Ala Ala Phe Phe Asp Asp Leu Gly Ser Pro Gly Gly Ala						
gct aag ctt gga cca caa gat ttt gat cac cca atg atc gct gcg ctg						403
Ala Lys Leu Gly Pro Gln Asp Phe Asp His Pro Met Ile Ala Ala Leu						
ccg cct cag gca taatctaacg catgacctct cgc						438
Pro Pro Gln Ala						

<210> 674

<211> 105

<212> PRT

<213> Corynebacterium glutamicum

<400> 674

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		20						25					30		
Leu	Tyr	Ile	His	Pro	Asp	Glu	Cys	Val	Asp	Cys	Gly	Ala	Cys	Glu	Pro
		35					40					45			
Ala	Cys	Pro	Val	Glu	Ala	Ile	Phe	Tyr	Glu	Asp	Asp	Val	Pro	Asp	Glu
		50				55					60				
Trp	Leu	Asp	Tyr	Asn	Asp	Ala	Asn	Ala	Ala	Phe	Phe	Asp	Asp	Leu	Gly
		65			70					75				80	
Ser	Pro	Gly	Gly	Ala	Ala	Lys	Leu	Gly	Pro	Gln	Asp	Phe	Asp	His	Pro
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Met	Ile	Ala	Ala	Leu	Pro	Pro	Gln	Ala							
		100					105								

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<211> 441
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(418)
 <223> RXA00680

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 Met Ser Thr Ile His
 1 5
 ttc att gat cat gct ggc aaa acc cgc acc atc gag gcg act gtt ggt 163
 Phe Ile Asp His Ala Gly Lys Thr Arg Thr Ile Glu Ala Thr Val Gly
 10 15 20
 gat tca gta atg gag acc gca gtc cga aac gga gtg cct gga att gtt 211
 Asp Ser Val Met Glu Thr Ala Val Arg Asn Gly Val Pro Gly Ile Val
 25 30 35
 gct gaa tgc ggc ggt tcc tta tcg tgt gca acc tgc cat gtg ttt gtt 259
 Ala Glu Cys Gly Gly Ser Leu Ser Cys Ala Thr Cys His Val Phe Val
 40 45 50
 gac cct gca cag tat gat gcg ctt ccc cca atg gag gag atg gaa gat 307
 Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met Glu Glu Met Glu Asp
 55 60 65
 gaa atg ctg tgg ggt gct gcc gtg gac cgt gag gat tgc tcc cgt ttg 355
 Glu Met Leu Trp Gly Ala Ala Val Asp Arg Glu Asp Cys Ser Arg Leu
 70 75 80 85
 tct tgc caa atc aag gtc acc gaa ggc atg gat ctt tcg ttg acc acg 403
 Ser Cys Gln Ile Lys Val Thr Glu Gly Met Asp Leu Ser Leu Thr Thr
 90 95 100
 cca gaa acg caa gtg tgaggttgaa tcatgaatac ttc 441
 Pro Glu Thr Gln Val
 105

<210> 676
 <211> 106
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 676
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 35 40 45
 Cys His Val Phe Val Asp Pro Ala Gln Tyr Asp Ala Leu Pro Pro Met

<400> 677															
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ttcgttgacc acgccagaaa cgcaagtgtg aggttgaatc atg aat act tca gct 115															
Met Asn Thr Ser Ala 5															
gaa act gga atc ttg atc atc ggt gca aac caa tcg ggt gtg cag ctg 163															
Glu Thr Gly Ile Leu Ile Ile Gly Ala Asn Gln Ser Gly Val Gln Leu 20															
gcg att tcc ctg cgg gcc acg ggt ttc acc gaa tcg atc acg ctt cta 211															
Ala Ile Ser Leu Arg Ala Thr Gly Phe Thr Glu Ser Ile Thr Leu Leu 35															
ggc gag gag gat cac cgc ccc tac cag cgt ccc gcc ttg tcc aag gag 259															
Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro Ala Leu Ser Lys Glu 50															
ttc ctc cag gac aag atc gac aaa gag cgt ctg att ttc cgt tcc aat 307															
Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu Ile Phe Arg Ser Asn 65															
gag tat tgg gaa gaa aat aat att cgc ctg gtc aag ggc gtg cgc atc 355															
Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val Lys Gly Val Arg Ile 85															
gaa cgc att gaa aag aac gac gac gga tca ggg gtc gcc tac ggc gcc 403															
Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly Val Ala Tyr Gly Ala 100															
gga caa gaa ttc gct ttt cga cgt ctc gct cta gcg gtt ggt gcc cgc 451															
Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu Ala Val Gly Ala Arg 115															
cct cgc cac ctc gac ctc ccg ggc gcc acc ttg gag ggt gtc acc tac 499															
Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu Glu Gly Val Thr Tyr 120															

ctg	cgc	aac	gcg	gac	gac	gcc	ttg	gcg	ctc	aaa	gcg	atg	att	ggg	tct	547
Leu	Arg	Asn	Ala	Asp	Asp	Ala	Leu	Ala	Leu	Lys	Ala	Met	Ile	Gly	Ser	
135						140					145					
gtc	acc	gat	gcc	gtt	gta	gtc	ggg	ggg	ggg	ttc	atc	gga	ttg	gaa	gct	595
Val	Thr	Asp	Ala	Val	Val	Val	Gly	Gly	Gly	Phe	Ile	Gly	Leu	Glu	Ala	
150					155					160					165	
gcg	tgt	tcg	ctt	cat	gac	ctc	ggc	aaa	aat	gtc	acc	gtc	ctg	gaa	tat	643
Ala	Cys	Ser	Leu	His	Asp	Leu	Gly	Lys	Asn	Val	Thr	Val	Leu	Glu	Tyr	
				170					175					180		
ggg	ccg	cgt	ctg	att	ggc	cga	gcg	gtg	ggg	gaa	gaa	acc	gca	gca	ttc	691
Gly	Pro	Arg	Leu	Ile	Gly	Arg	Ala	Val	Gly	Glu	Glu	Thr	Ala	Ala	Phe	
			185					190					195			
ttc	ctc	gaa	caa	cac	cgt	tcc	cgt	ggc	gta	aat	atc	gtg	ctt	gat	gcc	739
Phe	Leu	Glu	Gln	His	Arg	Ser	Arg	Gly	Val	Asn	Ile	Val	Leu	Asp	Ala	
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Arg	Met	Lys	Gln	Phe	Val	Gly	Lys	Asp	Gly	Lys	Leu	Ser	Gly	Ile	Glu	
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cta	gaa	gat	ggc	aca	gta	att	cct	gcc	caa	cta	gtc	att	gtg	ggc	atc	835
Leu	Glu	Asp	Gly	Thr	Val	Ile	Pro	Ala	Gln	Leu	Val	Ile	Val	Gly	Ile	
230					235					240					245	
ggg	gtc	att	ccg	aac	aca	gaa	ctt	gcc	gct	gtt	ctg	ggc	tta	gac	atc	883
Gly	Val	Ile	Pro	Asn	Thr	Glu	Leu	Ala	Ala	Val	Leu	Gly	Leu	Asp	Ile	
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aac	aac	ggc	atc	gtg	gtg	gat	aaa	cat	gcc	gtc	gcg	tca	gat	ggc	acc	931
Asn	Asn	Gly	Ile	Val	Val	Asp	Lys	His	Ala	Val	Ala	Ser	Asp	Gly	Thr	
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Thr	Ile	Ala	Ile	Gly	Asp	Val	Ala	Asn	Ile	Pro	Asn	Pro	Ile	Pro	Gly	
		280					285					290				
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Ser	Pro	Ala	Asp	Glu	Arg	Ile	Arg	Leu	Glu	Ser	Val	Asn	Asn	Ala	Ile	
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gag	cac	gca	aag	atc	gct	gca	tac	tca	ctc	gtc	ggc	cag	ccc	gaa	gcc	1075
Glu	His	Ala	Lys	Ile	Ala	Ala	Tyr	Ser	Leu	Val	Gly	Gln	Pro	Glu	Ala	
310					315					320					325	
tac	gcc	gga	atc	ccc	tgg	ttc	tgg	tcc	aac	caa	ggc	gat	ctc	aaa	cta	1123
Tyr	Ala	Gly	Ile	Pro	Trp	Phe	Trp	Ser	Asn	Gln	Gly	Asp	Leu	Lys	Leu	
				330					335					340		
caa	att	gca	gga	ctt	acc	ctt	ggg	tat	gac	agc	aca	gta	atc	cga	cag	1171
Gln	Ile	Ala	Gly	Leu	Thr	Leu	Gly	Tyr	Asp	Ser	Thr	Val	Ile	Arg	Gln	
			345					350					355			
gat	ccc	gag	aaa	aag	aag	ttc	tct	gtc	ctt	tat	tac	cgt	ggc	gac	aac	1219
Asp	Pro	Glu	Lys	Lys	Lys	Phe	Ser	Val	Leu	Tyr	Tyr	Arg	Gly	Asp	Asn	
		360				365						370				
atc	atc	gcc	gcc	gat	tgt	gtc	aac	gct	cca	ctg	gat	ttc	atg	gct	gtg	1267

Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu Asp Phe Met Ala Val
 375 380 385
 cgc agt gca ctt tcc agg aac caa aat atc ccc gcc gac ctt gct gca 1315
 Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro Ala Asp Leu Ala Ala
 390 395 400 405
 gat att tcg cag ccg ctg aaa aaa cta gcc gtt gac ctg gag gtt acc 1363
 Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val Asp Leu Glu Val Thr
 410 415 420
 cga tgactcgcag taatttaccc gct 1389
 Arg

<210> 678
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 678
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 Ser Ile Thr Leu Leu Gly Glu Glu Asp His Arg Pro Tyr Gln Arg Pro
 35 40 45
 Ala Leu Ser Lys Glu Phe Leu Gln Asp Lys Ile Asp Lys Glu Arg Leu
 50 55 60
 Ile Phe Arg Ser Asn Glu Tyr Trp Glu Glu Asn Asn Ile Arg Leu Val
 65 70 75 80
 Lys Gly Val Arg Ile Glu Arg Ile Glu Lys Asn Asp Asp Gly Ser Gly
 85 90 95
 Val Ala Tyr Gly Ala Gly Gln Glu Phe Ala Phe Arg Arg Leu Ala Leu
 100 105 110
 Ala Val Gly Ala Arg Pro Arg His Leu Asp Leu Pro Gly Ala Thr Leu
 115 120 125
 Glu Gly Val Thr Tyr Leu Arg Asn Ala Asp Asp Ala Leu Ala Leu Lys
 130 135 140
 Ala Met Ile Gly Ser Val Thr Asp Ala Val Val Val Gly Gly Gly Phe
 145 150 155 160
 Ile Gly Leu Glu Ala Ala Cys Ser Leu His Asp Leu Gly Lys Asn Val
 165 170 175
 Thr Val Leu Glu Tyr Gly Pro Arg Leu Ile Gly Arg Ala Val Gly Glu
 180 185 190
 Glu Thr Ala Ala Phe Phe Leu Glu Gln His Arg Ser Arg Gly Val Asn
 195 200 205

Ile Val Leu Asp Ala Arg Met Lys Gln Phe Val Gly Lys Asp Gly Lys
 210 215 220
 Leu Ser Gly Ile Glu Leu Glu Asp Gly Thr Val Ile Pro Ala Gln Leu
 225 230 235 240
 Val Ile Val Gly Ile Gly Val Ile Pro Asn Thr Glu Leu Ala Ala Val
 245 250 255
 Leu Gly Leu Asp Ile Asn Asn Gly Ile Val Val Asp Lys His Ala Val
 260 265 270
 Ala Ser Asp Gly Thr Thr Ile Ala Ile Gly Asp Val Ala Asn Ile Pro
 275 280 285
 Asn Pro Ile Pro Gly Ser Pro Ala Asp Glu Arg Ile Arg Leu Glu Ser
 290 295 300
 Val Asn Asn Ala Ile Glu His Ala Lys Ile Ala Ala Tyr Ser Leu Val
 305 310 315 320
 Gly Gln Pro Glu Ala Tyr Ala Gly Ile Pro Trp Phe Trp Ser Asn Gln
 325 330 335
 Gly Asp Leu Lys Leu Gln Ile Ala Gly Leu Thr Leu Gly Tyr Asp Ser
 340 345 350
 Thr Val Ile Arg Gln Asp Pro Glu Lys Lys Lys Phe Ser Val Leu Tyr
 355 360 365
 Tyr Arg Gly Asp Asn Ile Ile Ala Ala Asp Cys Val Asn Ala Pro Leu
 370 375 380
 Asp Phe Met Ala Val Arg Ser Ala Leu Ser Arg Asn Gln Asn Ile Pro
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 Ala Asp Leu Ala Ala Asp Ile Ser Gln Pro Leu Lys Lys Leu Ala Val
 405 410 415
 Asp Leu Glu Val Thr Arg
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1051)
 <223> RXA00224

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 Met Ser Ile Ser Tyr
 1 5
 gtg ctg gtt gag cag cta gat ggc cgc cca gaa cca gtt acc ctt gaa 163

Val	Leu.	Val	Glu	Gln	Leu	Asp	Gly	Arg	Pro	Glu	Pro	Val	Thr	Leu	Glu	
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ttg	atc	act	gct	gct	cgc	gca	ctc	ggc	gac	gtc	gtt	gcc	gtt	gtc	gtt	211
Leu	Ile	Thr	Ala	Ala	Arg	Ala	Leu	Gly	Asp	Val	Val	Ala	Val	Val	Val	
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ggc	gag	cca	ggc	gcc	ggc	gta	aac	ctt	gct	gct	gag	ctc	ggc	aat	tgg	259
Gly	Glu	Pro	Gly	Ala	Gly	Val	Asn	Leu	Ala	Ala	Glu	Leu	Gly	Asn	Trp	
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ggc	gca	gca	cag	gtt	gtt	tcc	gct	gaa	atc	tct	ggc	gct	tcc	aac	cgt	307
Gly	Ala	Ala	Gln	Val	Val	Ser	Ala	Glu	Ile	Ser	Gly	Ala	Ser	Asn	Arg	
	55					60					65					
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Leu	Ile	Leu	Pro	Ala	Val	Asp	Ala	Leu	His	Ile	Leu	Ala	Ala	Asn	Asn	
	70				75				80						85	
cca	ggc	cca	att	gtt	atc	gct	gca	act	gca	agc	ggc	aat	gag	atc	gct	403
Pro	Gly	Pro	Ile	Val	Ile	Ala	Ala	Thr	Ala	Ser	Gly	Asn	Glu	Ile	Ala	
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ggc	cgt	ttg	gct	gcc	cgt	ttg	gct	tct	ggc	gtg	ctc	acc	gat	gtc	gtc	451
Gly	Arg	Leu	Ala	Ala	Arg	Leu	Ala	Ser	Gly	Val	Leu	Thr	Asp	Val	Val	
			105				110					115				
gga	atc	aat	gcc	gac	cgc	acc	gca	cag	cag	tcc	att	ttc	ggc	gac	acc	499
Gly	Ile	Asn	Ala	Asp	Arg	Thr	Ala	Gln	Gln	Ser	Ile	Phe	Gly	Asp	Thr	
		120					125					130				
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Ile	Gln	Val	Ser	Ala	Ala	Val	Gly	Gly	Ala	Ser	Pro	Leu	Tyr	Thr	Leu	
		135				140					145					
cgt	cca	ggc	gcc	ctt	gat	ggc	gtg	gcc	gtt	cct	gca	acc	ggc	gaa	ttg	595
Arg	Pro	Gly	Ala	Leu	Asp	Gly	Val	Ala	Val	Pro	Ala	Thr	Gly	Glu	Leu	
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gca	acc	att	gag	atc	cca	ggc	gca	acc	gcc	aag	gat	gtc	acc	atc	acc	643
Ala	Thr	Ile	Glu	Ile	Pro	Gly	Ala	Thr	Ala	Lys	Asp	Val	Thr	Ile	Thr	
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tcc	ttc	acg	cca	agc	acc	cag	agc	gat	cgc	cct	gag	ctg	cca	cag	gca	691
Ser	Phe	Thr	Pro	Ser	Thr	Gln	Ser	Asp	Arg	Pro	Glu	Leu	Pro	Gln	Ala	
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Lys	Val	Val	Ile	Ala	Gly	Gly	Arg	Gly	Val	Gly	Ser	Glu	Glu	Asn	Phe	
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Arg	Ser	Ile	Val	Glu	Pro	Leu	Ala	Asp	Ala	Leu	Gly	Gly	Ala	Val	Gly	
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gca	acc	cgc	gac	gcc	gtt	gat	ctg	ggc	tac	tac	cca	ggc	gag	tac	cag	835
Ala	Thr	Arg	Asp	Ala	Val	Asp	Leu	Gly	Tyr	Tyr	Pro	Gly	Glu	Tyr	Gln	
		230			235				240						245	
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Val	Gly	Gln	Thr	Gly	Val	Thr	Val	Ser	Pro	Asp	Leu	Tyr	Ile	Gly	Leu	

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Gly	Ile	Ser	Gly	Ala	Ile	Gln	His	Thr	Ser	Gly	Met	Gln	Thr	Ala	Lys					
265										270					275					
aag	gtt	att	gtg	atc	aac	aac	gat	gag	gac	gcg	ccg	atc	ttc	cag	att	979				
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280										285					290					
gcg	gac	ctc	ggt	gtc	gtt	ggc	gac	ctc	ttt	gac	atc	gcc	cct	gcg	ctc	1027				
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295										300					305					
atc	gaa	gag	atc	aac	aag	cg	aag	taggagtttt	gaacactttt	tat						1074				
Ile	Glu	Glu	Ile	Asn	Lys	Arg	Lys													
310										315										

<210> 680

<211> 317

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 680

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Val	Ala	Val	Val	Val	Gly	Glu	Pro	Gly	Ala	Gly	Val	Asn	Leu	Ala	Ala
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Gly	Ala	Ser	Asn	Arg	Leu	Ile	Leu	Pro	Ala	Val	Asp	Ala	Leu	His	Ile
65					70				75					80	
Leu	Ala	Ala	Asn	Asn	Pro	Gly	Pro	Ile	Val	Ile	Ala	Ala	Thr	Ala	Ser
			85					90					95		
Gly	Asn	Glu	Ile	Ala	Gly	Arg	Leu	Ala	Ala	Arg	Leu	Ala	Ser	Gly	Val
	100						105					110			
Leu	Thr	Asp	Val	Val	Gly	Ile	Asn	Ala	Asp	Arg	Thr	Ala	Gln	Gln	Ser
	115						120					125			
Ile	Phe	Gly	Asp	Thr	Ile	Gln	Val	Ser	Ala	Ala	Val	Gly	Gly	Ala	Ser
130						135					140				
Pro	Leu	Tyr	Thr	Leu	Arg	Pro	Gly	Ala	Leu	Asp	Gly	Val	Ala	Val	Pro
145					150					155					160
Ala	Thr	Gly	Glu	Leu	Ala	Thr	Ile	Glu	Ile	Pro	Gly	Ala	Thr	Ala	Lys
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Asp	Val	Thr	Ile	Thr	Ser	Phe	Thr	Pro	Ser	Thr	Gln	Ser	Asp	Arg	Pro
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Glu Leu Pro Gln Ala Lys Val Val Ile Ala Gly Gly Arg Gly Val Gly
 195 200 205
 Ser Glu Glu Asn Phe Arg Ser Ile Val Glu Pro Leu Ala Asp Ala Leu
 210 215 220
 Gly Gly Ala Val Gly Ala Thr Arg Asp Ala Val Asp Leu Gly Tyr Tyr
 225 230 235 240
 Pro Gly Glu Tyr Gln Val Gly Gln Thr Gly Val Thr Val Ser Pro Asp
 245 250 255
 Leu Tyr Ile Gly Leu Gly Ile Ser Gly Ala Ile Gln His Thr Ser Gly
 260 265 270
 Met Gln Thr Ala Lys Lys Val Ile Val Ile Asn Asn Asp Glu Asp Ala
 275 280 285
 Pro Ile Phe Gln Ile Ala Asp Leu Gly Val Val Gly Asp Leu Phe Asp
 290 295 300
 Ile Ala Pro Ala Leu Ile Glu Glu Ile Asn Lys Arg Lys
 305 310 315

<210> 681
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 <212> DNA
 <213> Corynebacterium glutamicum

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 <223> RXA00225

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 Met Ser Thr Ile Val 5
 gtt ctg gtt aaa aat gtt cca gac acc tgg tct aag agg act ctg gaa 163
 Val Leu Val Lys Asn Val Pro Asp Thr Trp Ser Lys Arg Thr Leu Glu 20
 gct gat ttc acc ctt gac cgt gag ggt gta gat cga gtc ttg gat gag 211
 Ala Asp Phe Thr Leu Asp Arg Glu Gly Val Asp Arg Val Leu Asp Glu 35
 atc aat gag ttt gct ctg gag cag gca ctg cgc ttg cgg gag tcc aac 259
 Ile Asn Glu Phe Ala Leu Glu Gln Ala Leu Arg Leu Arg Glu Ser Asn 50
 ccg gat gct ggt tac cgc gtt gtt gcg ctg agc gcc ggc cct gcc ggt 307
 Pro Asp Ala Gly Tyr Arg Val Val Ala Leu Ser Ala Gly Pro Ala Gly 65
 ggg gaa gag gcg ctg cgt aag gcg ctg tcc atg ggt gct gat gaa gca 355
 Gly Glu Glu Ala Leu Arg Lys Ala Leu Ser Met Gly Ala Asp Glu Ala 80

atc cag ctc agt gat gat gcc ttg gct ggt tct gat ctt ttg gga acc 403
 Ile Gln Leu Ser Asp Asp Ala Leu Ala Gly Ser Asp Leu Leu Gly Thr
 90 95 100

gct tgg gcg ctg aac aac gct atc aac acc atc gcg ggt gtt gct ctc 451
 Ala Trp Ala Leu Asn Asn Ala Ile Asn Thr Ile Ala Gly Val Ala Leu
 105 110 115

atc gtg acg ggt tcg gct tct tcc gat ggt tcc atg ggt gcg ctt cct 499
 Ile Val Thr Gly Ser Ala Ser Ser Asp Gly Ser Met Gly Ala Leu Pro
 120 125 130

ggc gtg tta gct gag tac cgc cag gtc cca gcg ttg act aac ttg tct 547
 Gly Val Leu Ala Glu Tyr Arg Gln Val Pro Ala Leu Thr Asn Leu Ser
 135 140 145

gcg ctg aag gtc gag ggt gca tct att act gcc act cgc att gat aac 595
 Ala Leu Lys Val Glu Gly Ala Ser Ile Thr Ala Thr Arg Ile Asp Asn
 150 155 160 165

cac ggc acc tat gag ttg cag gct gca ctt cct gcg gtt gtg tcg att 643
 His Gly Thr Tyr Glu Leu Gln Ala Ala Leu Pro Ala Val Val Ser Ile
 170 175 180

tcc gat aag gct gac aag cca cgt ttc cct aac ttc aag ggc atc atg 691
 Ser Asp Lys Ala Asp Lys Pro Arg Phe Pro Asn Phe Lys Gly Ile Met
 185 190 195

gct gct aag aag gct gag atc aag aag ctt tcc ttg gct gaa atc ggc 739
 Ala Ala Lys Lys Ala Glu Ile Lys Lys Leu Ser Leu Ala Glu Ile Gly
 200 205 210

gtg gct cca gag cag gtt ggt ctg tct cac gcg gca act gct gtt act 787
 Val Ala Pro Glu Gln Val Gly Leu Ser His Ala Ala Thr Ala Val Thr
 215 220 225

gct gca gct gat cgt cct gag cgc tcc caa ggt gat gtc att ggt gca 835
 Ala Ala Ala Asp Arg Pro Glu Arg Ser Gln Gly Asp Val Ile Gly Ala
 230 235 240 245

tcg ggt gct gct gaa aag att gct gag tac ctc gct tca gag aac ctc 883
 Ser Gly Ala Ala Glu Lys Ile Ala Glu Tyr Leu Ala Ser Glu Asn Leu
 250 255 260

atc tagccactat cttcacaaag gag 909
 Ile

<210> 682

<211> 262

<212> PRT

<213> Corynebacterium glutamicum

<400> 682

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<212> DNA
<213> Corynebacterium glutamicum
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Ala	Met	Ser	Ala	Phe	Thr	Lys	Ser	Ala	Gln	Phe	Pro	Phe	His	Phe	Trp		
				15					20					25			
ctg	cct	gag	gcg	atg	gct	gcg	gcc	acc	cca	gtg	tcg	gcg	ttc	ctg	cac		207
Leu	Pro	Glu	Ala	Met	Ala	Ala	Ala	Thr	Pro	Val	Ser	Ala	Phe	Leu	His		
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Ile	Val	Phe	His	Asp	Val	Ala	Val	Trp	Asn	Trp	Leu	Leu	Ile	Ile	Val		
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Gly	Met	Gly	Thr	Ala	Ile	Met	Ser	Ala	Tyr	Phe	Ala	Val	Gln	Lys	Thr		
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Asp	Leu	Lys	Lys	Leu	Thr	Ala	Tyr	Ser	Thr	Val	Ser	His	Leu	Gly	Trp		
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Ile	Val	Ala	Thr	Ile	Gly	Val	Gly	Thr	Pro	Phe	Ala	Leu	Gly	Ala	Ala		
			110					115					120				
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Ile	Val	His	Thr	Leu	Ser	His	Ala	Leu	Phe	Lys	Ser	Ser	Leu	Phe	Met		
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ctc	att	ggc	gtg	att	gat	cac	cag	act	ggc	acg	cgc	gat	att	cgt	cgc		543
Leu	Ile	Gly	Val	Ile	Asp	His	Gln	Thr	Gly	Thr	Arg	Asp	Ile	Arg	Arg		
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Leu	Gly	Phe	Leu	Val	Lys	Lys	Met	Pro	Phe	Thr	Phe	Val	Ser	Val	Leu		
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tcc	aaa	gaa	ggc	atg	atc	aca	gcg	ttc	atg	gac	gcc	ccc	atc	ggc	aac		687
Ser	Lys	Glu	Gly	Met	Ile	Thr	Ala	Phe	Met	Asp	Ala	Pro	Ile	Gly	Asn		
			190					195					200				
tcc	tat	gtt	gta	tta	ctg	ctg	gtc	ggc	gca	gca	atc	ggc	gcg	gtc	cta		735
Ser	Tyr	Val	Val	Leu	Leu	Leu	Val	Gly	Ala	Ala	Ile	Gly	Ala	Val	Leu		
		205					210					215					
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Thr	Phe	Thr	Tyr	Ser	Ala	Lys	Leu	Val	Leu	Gly	Ala	Phe	Val	Asp	Gly		
	220					225				230							
cca	cgc	gac	atg	tca	cac	gtc	aag	gaa	gcc	ccc	gtc	tcc	ctc	tgg	ctt		831
Pro	Arg	Asp	Met	Ser	His	Val	Lys	Glu	Ala	Pro	Val	Ser	Leu	Trp	Leu		

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Pro Ala Ala Leu Pro Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu				
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Ser Leu Phe Asp Ala Pro Val Ser Ala Ala Thr Ser Ala Ala Gly				
270	275	280		
gaa gcg gcg cac atg cac ctg gca ttg tgg cac ggc atc aac acc cca	975			
Glu Ala Ala His Met His Leu Ala Leu Trp His Gly Ile Asn Thr Pro				
285	290	295		
ctg ttg att tcc ttg ggt gtg ctg gtg gcc gga atc ctt ggt gtg ctg	1023			
Leu Leu Ile Ser Leu Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu				
300	305	310		
ttc cgc aaa gag ctg tgg aaa atc gcc gag acc agc cct ttc ccc atc	1071			
Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile				
315	320	325	330	
gcc aca ggc aac gac atc cta tcg atg ctg gtt tac cga gcc aac ttg	1119			
Ala Thr Gly Asn Asp Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu				
335	340	345		
ctg ggt aaa ttc ttc ggt cgc atg gct gat tcg atg agc cca cgc agg	1167			
Leu Gly Lys Phe Phe Gly Arg Met Ala Asp Ser Met Ser Pro Arg Arg				
350	355	360		
cac ttg gtc agc ctc atc gtg ctg ctc tgg gcg ctg gct gct ttt gcc	1215			
His Leu Val Ser Leu Ile Val Leu Leu Trp Ala Leu Ala Ala Phe Ala				
365	370	375		
acc att cac ccc tcg gtt cag ctt gca cca aag caa ccg gga att gat	1263			
Thr Ile His Pro Ser Val Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp				
380	385	390		
cgt tgg atc gac ctc att ccg ctt gcc atc atc gcg cta tct gtc ttc	1311			
Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile Ile Ala Leu Ser Val Phe				
395	400	405	410	
ggc ctg ctc acc acc cga aac cgc ctc agc gca gcc gtg ctt gtg ggt	1359			
Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser Ala Ala Val Leu Val Gly				
415	420	425		
acc gtt ggt gtg ggt gtt tcc ttc cag atg cta ctt ctg ggc gct ccc	1407			
Thr Val Gly Val Gly Val Ser Phe Gln Met Leu Leu Leu Gly Ala Pro				
430	435	440		
gat gtt gca ctt acc cag ttc ctg gta gaa ggc ctc gtc gtg gta atc	1455			
Asp Val Ala Leu Thr Gln Phe Leu Val Glu Gly Leu Val Val Val Ile				
445	450	455		
atc atg atg gtt gtc cgg cac cag cct gcc aac ttc aag cgc atc aag	1503			
Ile Met Met Val Val Arg His Gln Pro Ala Asn Phe Lys Arg Ile Lys				
460	465	470		
ccc agc aga agg cgc agc acc gtt ctt gtc gcc gtc ctt gct gcc ttc	1551			
Pro Ser Arg Arg Arg Ser Thr Val Leu Val Ala Val Leu Ala Ala Phe				
475	480	485	490	

gcc gca ttc atg gcg gtg tgg gga ttg ctt ggc cgt cac gaa cgt tct	1599
Ala Ala Phe Met Ala Val Trp Gly Leu Leu Gly Arg His Glu Arg Ser	
495 500 505	
gag ctg gcc atg tgg tac ctc aac caa ggt cca gag atc acc tct ggc	1647
Glu Leu Ala Met Trp Tyr Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly	
510 515 520	
gcc aac gtg gtg aac acc atc ctc gtg gaa ttc cgt gca ctg gat acg	1695
Ala Asn Val Val Asn Thr Ile Leu Val Glu Phe Arg Ala Leu Asp Thr	
525 530 535	
ttg ggc gag ctc tcc gtg ctt ggc atg gca gct gtc gtc atc ggt gcg	1743
Leu Gly Glu Leu Ser Val Leu Gly Met Ala Ala Val Val Ile Gly Ala	
540 545 550	
atg gtg gct tcc atg cct cgt cat ccg ttt gcc aag ggc acc cac cct	1791
Met Val Ala Ser Met Pro Arg His Pro Phe Ala Lys Gly Thr His Pro	
555 560 565 570	
cgc ccc ttt ggc caa tca cag ttg aac tcc att ccg ctg cgc atg ctg	1839
Arg Pro Phe Gly Gln Ser Gln Leu Asn Ser Ile Pro Leu Arg Met Leu	
575 580 585	
ctt aag gtg ctg gtt cca gcg cta tgc ttc ttg agc ttc atg gtg ttc	1887
Leu Lys Val Leu Val Pro Ala Leu Cys Phe Leu Ser Phe Met Val Phe	
590 595 600	
atg cgt gga cac aat gat ccg gga ggc ggt ttc atc gca gcc cta att	1935
Met Arg Gly His Asn Asp Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile	
605 610 615	
gcc ggt ggc gcg ctg atg ctc ctg tac ctg tcc aag gcc aaa gat ggc	1983
Ala Gly Gly Ala Leu Met Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly	
620 625 630	
cgc att ttc cgc ccg aat gtt cct ttc att ctc act ggt gcg ggc atc	2031
Arg Ile Phe Arg Pro Asn Val Pro Phe Ile Leu Thr Gly Ala Gly Ile	
635 640 645 650	
ttg atg gca gtg ttc tcg ggc gta ctg gga ctc acc cac ggt tct ttc	2079
Leu Met Ala Val Phe Ser Gly Val Leu Gly Leu Thr His Gly Ser Phe	
655 660 665	
ctg tac gcc atc cac ttc aac ttc gta ggc cag cac tgg acc acc tcg	2127
Leu Tyr Ala Ile His Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser	
670 675 680	
atg atc ttc gac ctc ggc gtg tac ctg gcc gtg ttg ggc atg gtg tcc	2175
Met Ile Phe Asp Leu Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser	
685 690 695	
atg gca atc aac ggc ctg ggc gga tac ctg cgc cca ggt acc gac aat	2223
Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn	
700 705 710	
gca gat ctg gac tac gcc cgc cga agt ggc cca ctg cca gca acg cca	2271
Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro	
715 720 725 730	

acg gtt gaa ccc gaa cca gaa ggc gat gaa gac tgg ccc gaa ccc atc 2319
 Thr Val Glu Pro Glu Pro Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile
 735 740 745

aac ccc gca ggc gat aac aaa gag gag gca aac cga tgattctcgc 2365
 Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala Asn Arg
 750 755

actgacagtc gcg 2378

<210> 684
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 <213> Corynebacterium glutamicum

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 Lys Ser Ala Gln Phe Pro Phe His Phe Trp Leu Pro Glu Ala Met Ala
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 35 40 45
 Ala Gly Ile Tyr Leu Leu Leu Arg Phe Ser Ile Val Phe His Asp Val
 50 55 60
 Ala Val Trp Asn Trp Leu Leu Ile Ile Val Gly Met Gly Thr Ala Ile
 65 70 75 80
 Met Ser Ala Tyr Phe Ala Val Gln Lys Thr Asp Leu Lys Lys Leu Thr
 85 90 95
 Ala Tyr Ser Thr Val Ser His Leu Gly Trp Ile Val Ala Thr Ile Gly
 100 105 110
 Val Gly Thr Pro Phe Ala Leu Gly Ala Ala Ile Val His Thr Leu Ser
 115 120 125
 His Ala Leu Phe Lys Ser Ser Leu Phe Met Leu Ile Gly Val Ile Asp
 130 135 140
 His Gln Thr Gly Thr Arg Asp Ile Arg Arg Leu Gly Phe Leu Val Lys
 145 150 155 160
 Lys Met Pro Phe Thr Phe Val Ser Val Leu Ile Gly Ala Leu Ser Met
 165 170 175
 Ala Ser Val Pro Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile
 180 185 190
 Thr Ala Phe Met Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu
 195 200 205
 Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala
 210 215 220
 Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His
 225 230 235 240

Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly
 245 250 255
 Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro
 260 265 270
 Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His
 275 280 285
 Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly
 290 295 300
 Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp
 305 310 315 320
 Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile
 325 330 335
 Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly
 340 345 350
 Arg Met Ala Asp Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile
 355 360 365
 Val Leu Leu Trp Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val
 370 375 380
 Gln Leu Ala Pro Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile
 385 390 395 400
 Pro Leu Ala Ile Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg
 405 410 415
 Asn Arg Leu Ser Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val
 420 425 430
 Ser Phe Gln Met Leu Leu Leu Gly Ala Pro Asp Val Ala Leu Thr Gln
 435 440 445
 Phe Leu Val Glu Gly Leu Val Val Val Ile Ile Met Met Val Val Arg
 450 455 460
 His Gln Pro Ala Asn Phe Lys Arg Ile Lys Pro Ser Arg Arg Arg Ser
 465 470 475 480
 Thr Val Leu Val Ala Val Leu Ala Ala Phe Ala Ala Phe Met Ala Val
 485 490 495
 Trp Gly Leu Leu Gly Arg His Glu Arg Ser Glu Leu Ala Met Trp Tyr
 500 505 510
 Leu Asn Gln Gly Pro Glu Ile Thr Ser Gly Ala Asn Val Val Asn Thr
 515 520 525
 Ile Leu Val Glu Phe Arg Ala Leu Asp Thr Leu Gly Glu Leu Ser Val
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 Leu Gly Met Ala Ala Val Val Ile Gly Ala Met Val Ala Ser Met Pro
 545 550 555 560

Arg His Pro Phe Ala Lys Gly Thr His Pro Arg Pro Phe Gly Gln Ser
 565 570 575
 Gln Leu Asn Ser Ile Pro Leu Arg Met Leu Leu Lys Val Leu Val Pro
 580 585 590
 Ala Leu Cys Phe Leu Ser Phe Met Val Phe Met Arg Gly His Asn Asp
 595 600 605
 Pro Gly Gly Gly Phe Ile Ala Ala Leu Ile Ala Gly Gly Ala Leu Met
 610 615 620
 Leu Leu Tyr Leu Ser Lys Ala Lys Asp Gly Arg Ile Phe Arg Pro Asn
 625 630 635 640
 Val Pro Phe Ile Leu Thr Gly Ala Gly Ile Leu Met Ala Val Phe Ser
 645 650 655
 Gly Val Leu Gly Leu Thr His Gly Ser Phe Leu Tyr Ala Ile His Phe
 660 665 670
 Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu Gly
 675 680 685
 Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu
 690 695 700
 Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala
 705 710 715 720
 Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro
 725 730 735
 Glu Gly Asp Glu Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn
 740 745 750
 Lys Glu Glu Ala Asn Arg
 755

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 <212> DNA
 <213> Corynebacterium glutamicum

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 <222> (101)..(1849)
 <223> FRXA00606

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 Met Ala Ser Val Pro
 1 5
 ccg ttg ctc ggc ttc gtg tcc aaa gaa ggc atg atc aca gcg ttc atg 163
 Pro Leu Leu Gly Phe Val Ser Lys Glu Gly Met Ile Thr Ala Phe Met
 10 15 20

gac gcc ccc atc ggc aac tcc tat gtt gta tta ctg ctg gtc ggc gca	211
Asp Ala Pro Ile Gly Asn Ser Tyr Val Val Leu Leu Val Gly Ala	
25 30 35	
gca atc ggc gcg gtc cta acc ttc aca tac tcc gcg aaa ctc gtg ctc	259
Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser Ala Lys Leu Val Leu	
40 45 50	
ggc gca ttc gtc gac ggc cca cgc gac atg tca cac gtc aag gaa gcc	307
Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser His Val Lys Glu Ala	
55 60 65	
ccc gtc tcc ctc tgg ctt ccg gcc gcc ctg cct gga ctt atg tct ctg	355
Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro Gly Leu Met Ser Leu	
70 75 80 85	
cca cta gtc cta gta ctt tcg ctt ttc gac gcc ccc gtc tcc gcc gca	403
Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala Pro Val Ser Ala Ala	
90 95 100	
gcc acc tcc gcc gcg ggg gaa gcg gcg cac atg cac ctg gca ttg tgg	451
Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met His Leu Ala Leu Trp	
105 110 115	
cac ggc atc aac acc cca ctg ttg att tcc ttg ggt gtg ctg gtg gcc	499
His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu Gly Val Leu Val Ala	
120 125 130	
gga atc ctt ggt gtg ctg ttc cgc aaa gag ctg tgg aaa atc gcc gag	547
Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu Trp Lys Ile Ala Glu	
135 140 145	
acc agc cct ttc ccc atc gcc aca ggc aac gac atc cta tcg atg ctg	595
Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp Ile Leu Ser Met Leu	
150 155 160 165	
gtt tac cga gcc aac ttg ctg ggt aaa ttc ttc ggt cgc atg gct gat	643
Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe Gly Arg Met Ala Asp	
170 175 180	
tcg atg agc cca cgc agg cac ttg gtc agc ctc atc gtg ctg ctc tgg	691
Ser Met Ser Pro Arg Arg His Leu Val Ser Leu Ile Val Leu Leu Trp	
185 190 195	
gcg ctg gct gct ttt gcc acc att cac ccc tcg gtt cag ctt gca cca	739
Ala Leu Ala Ala Phe Ala Thr Ile His Pro Ser Val Gln Leu Ala Pro	
200 205 210	
aag caa ccg gga att gat cgt tgg atc gac ctc att ccg ctt gcc atc	787
Lys Gln Pro Gly Ile Asp Arg Trp Ile Asp Leu Ile Pro Leu Ala Ile	
215 220 225	
atc gcg cta tct gtc ttc ggc ctg ctc acc acc cga aac cgc ctc agc	835
Ile Ala Leu Ser Val Phe Gly Leu Leu Thr Thr Arg Asn Arg Leu Ser	
230 235 240 245	
gca gcc gtg ctt gtg ggt acc gtt ggt gtg ggt gtt tcc ttc cag atg	883
Ala Ala Val Leu Val Gly Thr Val Gly Val Gly Val Ser Phe Gln Met	
250 255 260	
cta ctt ctg ggc gct ccc gat gtt gca ctt acc cag ttc ctg gta gaa	931

Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	Gln	Phe	Leu	Val	Glu	
			265					270					275			
ggc	ctc	gtc	gtg	gta	atc	atc	atg	atg	gtt	gtc	cgg	cac	cag	cct	gcc	979
Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	Arg	His	Gln	Pro	Ala	
		280					285					290				
aac	ttc	aag	cgc	atc	aag	ccc	agc	aga	agg	cgc	agc	acc	gtt	ctt	gtc	1027
Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	Ser	Thr	Val	Leu	Val	
	295					300					305					
gcc	gtc	ctt	gct	gcc	ttc	gcc	gca	ttc	atg	gcg	gtg	tgg	gga	ttg	ctt	1075
Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	Val	Trp	Gly	Leu	Leu	
310					315					320					325	
ggc	cgt	cac	gaa	cgt	tct	gag	ctg	gcc	atg	tgg	tac	ctc	aac	caa	ggc	1123
Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp	Tyr	Leu	Asn	Gln	Gly	
				330					335					340		
cca	gag	atc	acc	tct	ggc	gcc	aac	gtg	gtg	aac	acc	atc	ctc	gtg	gaa	1171
Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn	Thr	Ile	Leu	Val	Glu	
			345					350					355			
ttc	cgt	gca	ctg	gat	acg	ttg	ggc	gag	ctc	tcc	gtg	ctt	ggc	atg	gca	1219
Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser	Val	Leu	Gly	Met	Ala	
		360					365					370				
gct	gtc	gtc	atc	ggc	gcg	atg	gtg	gct	tcc	atg	cct	cgt	cat	ccg	ttt	1267
Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met	Pro	Arg	His	Pro	Phe	
	375					380					385					
gcc	aag	ggc	acc	cac	cct	cgc	ccc	ttt	ggc	caa	tca	cag	ttg	aac	tcc	1315
Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln	Ser	Gln	Leu	Asn	Ser	
390					395					400					405	
att	ccg	ctg	cgc	atg	ctg	ctt	aag	gtg	ctg	gtt	cca	gcg	cta	tgc	ttc	1363
Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	Pro	Ala	Leu	Cys	Phe	
				410					415					420		
ttg	agc	ttc	atg	gtg	ttc	atg	cgt	gga	cac	aat	gat	ccg	gga	ggc	ggc	1411
Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	Asp	Pro	Gly	Gly	Gly	
			425					430					435			
ttc	atc	gca	gcc	cta	att	gcc	ggc	ggc	gcg	ctg	atg	ctc	ctg	tac	ctg	1459
Phe	Ile	Ala	Ala	Leu	Ile	Ala	Gly	Gly	Ala	Leu	Met	Leu	Leu	Tyr	Leu	
		440					445					450				
tcc	aag	gcc	aaa	gat	ggc	cgc	att	ttc	cgc	ccg	aat	gtt	cct	ttc	att	1507
Ser	Lys	Ala	Lys	Asp	Gly	Arg	Ile	Phe	Arg	Pro	Asn	Val	Pro	Phe	Ile	
	455					460					465					
ctc	act	ggc	gcg	ggc	atc	ttg	atg	gca	gtg	ttc	tcg	ggc	gta	ctg	gga	1555
Leu	Thr	Gly	Ala	Gly	Ile	Leu	Met	Ala	Val	Phe	Ser	Gly	Val	Leu	Gly	
470					475					480					485	
ctc	acc	cac	ggc	tct	ttc	ctg	tac	gcc	atc	cac	ttc	aac	ttc	gta	ggc	1603
Leu	Thr	His	Gly	Ser	Phe	Leu	Tyr	Ala	Ile	His	Phe	Asn	Phe	Val	Gly	
				490				495						500		
cag	cac	tgg	acc	acc	tcg	atg	atc	ttc	gac	ctc	ggc	gtg	tac	ctg	gcc	1651
Gln	His	Trp	Thr	Thr	Ser	Met	Ile	Phe	Asp	Leu	Gly	Val	Tyr	Leu	Ala	

505	510	515	
gtg ttg ggc atg gtg tcc atg gca atc aac ggc ctg ggc gga tac ctg Val Leu Gly Met Val Ser Met Ala Ile Asn Gly Leu Gly Gly Tyr Leu 520 525 530			1699
cgc cca ggt acc gac aat gca gat ctg gac tac gcc cgc cga agt ggc Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr Ala Arg Arg Ser Gly 535 540 545			1747
cca ctg cca gca acg cca acg gtt gaa ccc gaa cca gaa ggc gat gaa Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu Pro Glu Gly Asp Glu 550 555 560			1795
gac tgg ccc gaa ccc atc aac ccc gca ggc gat aac aaa gag gag gca Asp Trp Pro Glu Pro Ile Asn Pro Ala Gly Asp Asn Lys Glu Glu Ala 570 575 580			1843
aac cga tgattctcgc actgacagtc gcg Asn Arg			1872

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 <213> Corynebacterium glutamicum

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 Leu Leu Val Gly Ala Ala Ile Gly Ala Val Leu Thr Phe Thr Tyr Ser
 35 40 45
 Ala Lys Leu Val Leu Gly Ala Phe Val Asp Gly Pro Arg Asp Met Ser
 50 55 60
 His Val Lys Glu Ala Pro Val Ser Leu Trp Leu Pro Ala Ala Leu Pro
 65 70 75 80
 Gly Leu Met Ser Leu Pro Leu Val Leu Val Leu Ser Leu Phe Asp Ala
 85 90 95
 Pro Val Ser Ala Ala Ala Thr Ser Ala Ala Gly Glu Ala Ala His Met
 100 105 110
 His Leu Ala Leu Trp His Gly Ile Asn Thr Pro Leu Leu Ile Ser Leu
 115 120 125
 Gly Val Leu Val Ala Gly Ile Leu Gly Val Leu Phe Arg Lys Glu Leu
 130 135 140
 Trp Lys Ile Ala Glu Thr Ser Pro Phe Pro Ile Ala Thr Gly Asn Asp
 145 150 155 160
 Ile Leu Ser Met Leu Val Tyr Arg Ala Asn Leu Leu Gly Lys Phe Phe
 165 170 175

Gly	Arg	Met	Ala	Asp	Ser	Met	Ser	Pro	Arg	Arg	His	Leu	Val	Ser	Leu	180	185	190	
Ile	Val	Leu	Leu	Trp	Ala	Leu	Ala	Ala	Phe	Ala	Thr	Ile	His	Pro	Ser	195	200	205	
Val	Gln	Leu	Ala	Pro	Lys	Gln	Pro	Gly	Ile	Asp	Arg	Trp	Ile	Asp	Leu	210	215	220	
Ile	Pro	Leu	Ala	Ile	Ile	Ala	Leu	Ser	Val	Phe	Gly	Leu	Leu	Thr	Thr	225	230	235	240
Arg	Asn	Arg	Leu	Ser	Ala	Ala	Val	Leu	Val	Gly	Thr	Val	Gly	Val	Gly	245	250	255	
Val	Ser	Phe	Gln	Met	Leu	Leu	Leu	Gly	Ala	Pro	Asp	Val	Ala	Leu	Thr	260	265	270	
Gln	Phe	Leu	Val	Glu	Gly	Leu	Val	Val	Val	Ile	Ile	Met	Met	Val	Val	275	280	285	
Arg	His	Gln	Pro	Ala	Asn	Phe	Lys	Arg	Ile	Lys	Pro	Ser	Arg	Arg	Arg	290	295	300	
Ser	Thr	Val	Leu	Val	Ala	Val	Leu	Ala	Ala	Phe	Ala	Ala	Phe	Met	Ala	305	310	315	320
Val	Trp	Gly	Leu	Leu	Gly	Arg	His	Glu	Arg	Ser	Glu	Leu	Ala	Met	Trp	325	330	335	
Tyr	Leu	Asn	Gln	Gly	Pro	Glu	Ile	Thr	Ser	Gly	Ala	Asn	Val	Val	Asn	340	345	350	
Thr	Ile	Leu	Val	Glu	Phe	Arg	Ala	Leu	Asp	Thr	Leu	Gly	Glu	Leu	Ser	355	360	365	
Val	Leu	Gly	Met	Ala	Ala	Val	Val	Ile	Gly	Ala	Met	Val	Ala	Ser	Met	370	375	380	
Pro	Arg	His	Pro	Phe	Ala	Lys	Gly	Thr	His	Pro	Arg	Pro	Phe	Gly	Gln	385	390	395	400
Ser	Gln	Leu	Asn	Ser	Ile	Pro	Leu	Arg	Met	Leu	Leu	Lys	Val	Leu	Val	405	410	415	
Pro	Ala	Leu	Cys	Phe	Leu	Ser	Phe	Met	Val	Phe	Met	Arg	Gly	His	Asn	420	425	430	
Asp	Pro	Gly	Gly	Gly	Phe	Ile	Ala	Ala	Leu	Ile	Ala	Gly	Gly	Ala	Leu	435	440	445	
Met	Leu	Leu	Tyr	Leu	Ser	Lys	Ala	Lys	Asp	Gly	Arg	Ile	Phe	Arg	Pro	450	455	460	
Asn	Val	Pro	Phe	Ile	Leu	Thr	Gly	Ala	Gly	Ile	Leu	Met	Ala	Val	Phe	465	470	475	480
Ser	Gly	Val	Leu	Gly	Leu	Thr	His	Gly	Ser	Phe	Leu	Tyr	Ala	Ile	His	485	490	495	

Phe Asn Phe Val Gly Gln His Trp Thr Thr Ser Met Ile Phe Asp Leu
 500 505 510
 Gly Val Tyr Leu Ala Val Leu Gly Met Val Ser Met Ala Ile Asn Gly
 515 520 525
 Leu Gly Gly Tyr Leu Arg Pro Gly Thr Asp Asn Ala Asp Leu Asp Tyr
 530 535 540
 Ala Arg Arg Ser Gly Pro Leu Pro Ala Thr Pro Thr Val Glu Pro Glu
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 565 570 575
 Asn Lys Glu Glu Ala Asn Arg
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 <212> DNA
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 <222> (101)..(1630)
 <223> RXN00595

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 Met Ala Met Asp Val
 1 5
 ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163
 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
 10 15 20
 gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
 25 30 35
 cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
 40 45 50
 gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg 307
 Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val
 55 60 65
 gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc 355
 Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr
 70 75 80 85
 acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt 403
 Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly
 90 95 100
 gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg 451

Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr	105	110	115	
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg	499			
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val	120	125	130	
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc	547			
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr	135	140	145	
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat	595			
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn	150	155	160	165
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt	643			
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly	170	175	180	
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc	691			
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly	185	190	195	
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg	739			
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala	200	205	210	
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat	787			
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr	215	220	225	
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc	835			
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr	230	235	240	245
aaa gtc gcg gta tac atg ctc tat cgc att tgg gtc cac att ttt aac	883			
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp Val His Ile Phe Asn	250	255	260	
atg gat ccc acg tgg aat tgg ctg att gtc gca ttc atg gtg ata tcc	931			
Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala Phe Met Val Ile Ser	265	270	275	
atg ctg gtc ggt ggc ttc gct gga ctt gct gaa aac tcc atc cgt cgc	979			
Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu Asn Ser Ile Arg Arg	280	285	290	
gtc ctt gcc tac caa atg gtc aac ggc atg cca ttt att ctc atc atg	1027			
Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro Phe Ile Leu Ile Met	295	300	305	
atg gcg ttt acc tct gac gat cca cag cgc gca ctt gcc gct ggt ctg	1075			
Met Ala Phe Thr Ser Asp Pro Gln Arg Ala Leu Ala Ala Gly Leu	310	315	320	325
ttg tac acc ctg cac cac atg atc acc atc gcc gca ttg gtg ctc act	1123			
Leu Tyr Thr Leu His His Met Ile Thr Ile Ala Ala Leu Val Leu Thr	330	335	340	
tcc ggc gca atc gaa gaa acc tac ggc acc ggt atg ttg tcc aag ctg	1171			
Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly Met Leu Ser Lys Leu				

345										350					355					
tct	ggc	ctt	gca	cgc	cgc	gaa	ccc	gtc	gtc	gca	gca	gtg	ttc	gct	gca	1219				
Ser	Gly	Leu	Ala	Arg	Arg	Glu	Pro	Val	Val	Ala	Ala	Val	Phe	Ala	Ala					
360						365					370									
ggt	gcc	ttc	tct	gtt	gtc	ggt	ttc	cca	ccg	ttt	tcc	ggt	atg	tgg	ggc	1267				
Gly	Ala	Phe	Ser	Val	Val	Gly	Phe	Pro	Pro	Phe	Ser	Gly	Met	Trp	Gly					
375						380					385									
aaa	gcg	ctc	atc	ctg	ctc	gag	atc	gcc	cgc	gtc	ggc	aat	att	gca	gca	1315				
Lys	Ala	Leu	Ile	Leu	Leu	Glu	Ile	Ala	Arg	Val	Gly	Asn	Ile	Ala	Ala					
390						395					400				405					
tgg	atc	gca	atc	gcc	gcc	atc	atc	atc	gcc	agc	ctg	ggc	gca	ctg	ctc	1363				
Trp	Ile	Ala	Ile	Ala	Ala	Ile	Ile	Ile	Ala	Ser	Leu	Gly	Ala	Leu	Leu					
410						415					420									
tcg	atg	atc	cgc	gtg	tgg	cgt	gaa	gtc	ttc	tgg	ggt	ggc	gca	atg	cac	1411				
Ser	Met	Ile	Arg	Val	Trp	Arg	Glu	Val	Phe	Trp	Gly	Gly	Ala	Met	His					
425						430					435									
cag	cgc	ggc	gtc	tcg	ccg	cag	ctg	cgc	atc	agc	cca	gca	aaa	atc	gcc	1459				
Gln	Arg	Gly	Val	Ser	Pro	Gln	Leu	Arg	Ile	Ser	Pro	Ala	Lys	Ile	Ala					
440						445					450									
cca	gcg	ctc	agc	ctg	atc	att	tta	tcg	gta	ggc	atg	ttc	atc	ttc	gcg	1507				
Pro	Ala	Leu	Ser	Leu	Ile	Ile	Leu	Ser	Val	Gly	Met	Phe	Ile	Phe	Ala					
455						460					465									
ggc	ccg	ctt	atc	gac	gcg	acc	ctc	acc	gcc	acc	gac	ggc	ctc	ttg	aac	1555				
Gly	Pro	Leu	Ile	Asp	Ala	Thr	Leu	Thr	Ala	Thr	Asp	Gly	Leu	Leu	Asn					
470						475					480				485					
acc	gat	gca	tac	caa	cag	gct	gtg	ctc	ggt	gaa	aat	gcc	atc	gga	gtg	1603				
Thr	Asp	Ala	Tyr	Gln	Gln	Ala	Val	Leu	Gly	Glu	Asn	Ala	Ile	Gly	Val					
490						495					500									
cca	agc	cct	agc	tac	cag	gga	gga	aac	taatgcttaa	cgccctgaaa						1650				
Pro	Ser	Pro	Ser	Tyr	Gln	Gly	Gly	Asn												
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ttc																1653				

<210> 688

<211> 510

<212> PRT

<213> Corynebacterium glutamicum

<400> 688

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Ala	Ser	Ala	Ile	Ala	Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile
			20					25					30		

Leu	His	Ile	Ile	Val	Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu
		35					40					45			

Phe	Ala	His	Thr	Ala	Glu	His	Gly	Pro	Ile	Ala	His	Asn	Val	Gly	Leu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50	55	60
Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala		
65	70	75
Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe		
	85	90
Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr		
	100	105
Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu		
	115	120
Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly		
	130	135
Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile		
145	150	155
Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val		
	165	170
Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln		
	180	185
Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val		
	195	200
Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp		
	210	215
Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe		
225	230	235
Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile Trp		
	245	250
Val His Ile Phe Asn Met Asp Pro Thr Trp Asn Trp Leu Ile Val Ala		
	260	265
Phe Met Val Ile Ser Met Leu Val Gly Gly Phe Ala Gly Leu Ala Glu		
	275	280
Asn Ser Ile Arg Arg Val Leu Ala Tyr Gln Met Val Asn Gly Met Pro		
	290	295
Phe Ile Leu Ile Met Met Ala Phe Thr Ser Asp Asp Pro Gln Arg Ala		
305	310	315
Leu Ala Ala Gly Leu Leu Tyr Thr Leu His His Met Ile Thr Ile Ala		
	325	330
Ala Leu Val Leu Thr Ser Gly Ala Ile Glu Glu Thr Tyr Gly Thr Gly		
	340	345
Met Leu Ser Lys Leu Ser Gly Leu Ala Arg Arg Glu Pro Val Val Ala		
	355	360
Ala Val Phe Ala Ala Gly Ala Phe Ser Val Val Gly Phe Pro Pro Phe		
	370	375
		380

Ser Gly Met Trp Gly Lys Ala Leu Ile Leu Leu Glu Ile Ala Arg Val
 385 390 395 400

Gly Asn Ile Ala Ala Trp Ile Ala Ile Ala Ala Ile Ile Ile Ala Ser
 405 410 415

Leu Gly Ala Leu Leu Ser Met Ile Arg Val Trp Arg Glu Val Phe Trp
 420 425 430

Gly Gly Ala Met His Gln Arg Gly Val Ser Pro Gln Leu Arg Ile Ser
 435 440 445

Pro Ala Lys Ile Ala Pro Ala Leu Ser Leu Ile Ile Leu Ser Val Gly
 450 455 460

Met Phe Ile Phe Ala Gly Pro Leu Ile Asp Ala Thr Leu Thr Ala Thr
 465 470 475 480

Asp Gly Leu Leu Asn Thr Asp Ala Tyr Gln Gln Ala Val Leu Gly Glu
 485 490 495

Asn Ala Ile Gly Val Pro Ser Pro Ser Tyr Gln Gly Gly Asn
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 <223> FRXA00608

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 Met Ala Met Asp Val
 1 5

ctc ctt cct att ttc gtt gca gtt ccc ctt gct gcc tct gcc att gcg 163
 Leu Leu Pro Ile Phe Val Ala Val Pro Leu Ala Ala Ser Ala Ile Ala
 10 15 20

gtg ctt ctg ccg tgg cgt ctc atc cgc gat att ttg cac atc atc gtg 211
 Val Leu Leu Pro Trp Arg Leu Ile Arg Asp Ile Leu His Ile Ile Val
 25 30 35

cct ttc gcg ggt att ttt gct ggc atc tgg ttg ttt gca cac acc gct 259
 Pro Phe Ala Gly Ile Phe Ala Gly Ile Trp Leu Phe Ala His Thr Ala
 40 45 50

gaa cac ggc ccg att gct cac aac gtg ggc ctt tat gtc ggt ggc gtg 307
 Glu His Gly Pro Ile Ala His Asn Val Gly Leu Tyr Val Gly Gly Val
 55 60 65

gca atc ccc ttt gct gcc gat acg ttc agc gcc atc atg ttg atc acc 355
 Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala Ile Met Leu Ile Thr

70	75	80	85	
acc tcg atc gtt gcg gtg gct gcc aac tgg ttt gcc acc atc gtc ggt				403
Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe Ala Thr Ile Val Gly				
	90	95	100	
gaa acc cgc gcg cgt ttc tat cca gcg ctc aca ttg atg ctg atc acg				451
Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr Leu Met Leu Ile Thr				
	105	110	115	
ggc gtc aac ggt gct ctg ctg act gcc gat ctg ttc aac ttc ttt gtg				499
Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu Phe Asn Phe Phe Val				
	120	125	130	
ttc atc gaa gtg atg ctg ctg cct tcc tat ggt ttg atc gcc atg acc				547
Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly Leu Ile Ala Met Thr				
	135	140	145	
gga acg tgg gcg cgc cta gcc tct gga cga atc ttc gta cta gtc aat				595
Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile Phe Val Leu Val Asn				
	150	155	160	165
ctc tct gcc tcc aca ttg ctg gtt gca ggt gtg gga atc gtc tac ggt				643
Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val Gly Ile Val Tyr Gly				
	170	175	180	
gtc ata ggc tca gtc aac atc gca gct ctg caa gat gtc gta gag ggc				691
Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln Asp Val Val Glu Gly				
	185	190	195	
aac ccc ctg gtt gcc agc gca atg ggc atc gtg gtt att gcc atc gcg				739
Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val Val Ile Ala Ile Ala				
	200	205	210	
gtt aaa gcc ggt gta ttc cca gtg cac aca tgg ctg cca cgc acc tat				787
Val Lys Ala Gly Val Phe Pro Val His Thr Trp Leu Pro Arg Thr Tyr				
	215	220	225	
cct ggt aca tca gca gct gtg atg ggg ttg ttc tcc ggt ttg cac acc				835
Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe Ser Gly Leu His Thr				
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aaa gtc gcg gta tac atg ctc tat cgc att				865
Lys Val Ala Val Tyr Met Leu Tyr Arg Ile				
	250	255		

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<211> 255

<212> PRT

<213> Corynebacterium glutamicum

<400> 690

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Ala	Ser	Ala	Ile	Ala	Val	Leu	Leu	Pro	Trp	Arg	Leu	Ile	Arg	Asp	Ile
			20					25					30		

Leu	His	Ile	Ile	Val	Pro	Phe	Ala	Gly	Ile	Phe	Ala	Gly	Ile	Trp	Leu
		35					40					45			

Phe Ala His Thr Ala Glu His Gly Pro Ile Ala His Asn Val Gly Leu
 50 55 60
 Tyr Val Gly Gly Val Ala Ile Pro Phe Ala Ala Asp Thr Phe Ser Ala
 65 70 75 80
 Ile Met Leu Ile Thr Thr Ser Ile Val Ala Val Ala Ala Asn Trp Phe
 85 90 95
 Ala Thr Ile Val Gly Glu Thr Arg Ala Arg Phe Tyr Pro Ala Leu Thr
 100 105 110
 Leu Met Leu Ile Thr Gly Val Asn Gly Ala Leu Leu Thr Ala Asp Leu
 115 120 125
 Phe Asn Phe Phe Val Phe Ile Glu Val Met Leu Leu Pro Ser Tyr Gly
 130 135 140
 Leu Ile Ala Met Thr Gly Thr Trp Ala Arg Leu Ala Ser Gly Arg Ile
 145 150 155 160
 Phe Val Leu Val Asn Leu Ser Ala Ser Thr Leu Leu Val Ala Gly Val
 165 170 175
 Gly Ile Val Tyr Gly Val Ile Gly Ser Val Asn Ile Ala Ala Leu Gln
 180 185 190
 Asp Val Val Glu Gly Asn Pro Leu Val Ala Ser Ala Met Gly Ile Val
 195 200 205
 Val Ile Ala Ile Ala Val Lys Ala Gly Val Phe Pro Val His Thr Trp
 210 215 220
 Leu Pro Arg Thr Tyr Pro Gly Thr Ser Ala Ala Val Met Gly Leu Phe
 225 230 235 240
 Ser Gly Leu His Thr Lys Val Ala Val Tyr Met Leu Tyr Arg Ile
 245 250 255

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 <223> RXA00913

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 Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
 20 25 30
 aca gtt ggt gcc att gac cac acc acc gga act cgt gat att cgt aaa 144

Thr	Val	Gly	Ala	Ile	Asp	His	Thr	Thr	Gly	Thr	Arg	Asp	Ile	Arg	Lys	
		35					40					45				
ctc	tcc	ggt	ctg	tgg	cgt	aaa	caa	ccg	atc	ctg	ttc	gcc	gtt	gct	gct	192
Leu	Ser	Gly	Leu	Trp	Arg	Lys	Gln	Pro	Ile	Leu	Phe	Ala	Val	Ala	Ala	
	50					55					60					
gtt	tcg	gcg	gcg	tcc	atg	gct	ggt	att	ccg	cca	ctg	ttt	ggt	ttt	atc	240
Val	Ser	Ala	Ala	Ser	Met	Ala	Gly	Ile	Pro	Pro	Leu	Phe	Gly	Phe	Ile	
	65				70					75					80	
gcc	aag	gaa	aca	gcg	ctg	gat	acc	gtg	ttg	aat	gag	cag	atg	ttg	cat	288
Ala	Lys	Glu	Thr	Ala	Leu	Asp	Thr	Val	Leu	Asn	Glu	Gln	Met	Leu	His	
			85						90					95		
ggc	atg	cca	ggt	cga	ttg	atg	ctg	gct	ggc	atc	gtt	ttg	ggt	tcc	atc	336
Gly	Met	Pro	Gly	Arg	Leu	Met	Leu	Ala	Gly	Ile	Val	Leu	Gly	Ser	Ile	
			100					105					110			
ttc	acc	atg	gca	tat	tcc	tgc	tac	ttc	ctg	tac	gaa	gcc	ttt	gcc	acg	384
Phe	Thr	Met	Ala	Tyr	Ser	Cys	Tyr	Phe	Leu	Tyr	Glu	Ala	Phe	Ala	Thr	
		115					120					125				
aag	cac	tcc	aaa	ttc	cca	gag	gcc	aac	ggt	gtc	tca	cct	gca	gtg	gag	432
Lys	His	Ser	Lys	Phe	Pro	Glu	Ala	Asn	Gly	Val	Ser	Pro	Ala	Val	Glu	
	130					135					140					
gca	atg	cat	ccg	gtg	aag	ttt	aag	ctg	tgg	atc	gca	cct	gtc	atc	ctg	480
Ala	Met	His	Pro	Val	Lys	Phe	Lys	Leu	Trp	Ile	Ala	Pro	Val	Ile	Leu	
	145				150					155					160	
gct	att	ttg	acc	gta	gtg	ttt	ggt	gtt	ttc	ccc	aag	cca	gtg	tcg	gaa	528
Ala	Ile	Leu	Thr	Val	Val	Phe	Gly	Val	Phe	Pro	Lys	Pro	Val	Ser	Glu	
				165					170					175		
gca	att	gtc	acg	cat	ctt	gat	aac	gtc	acg	cca	tcg	ctt	gat	gat	gtc	576
Ala	Ile	Val	Thr	His	Leu	Asp	Asn	Val	Thr	Pro	Ser	Leu	Asp	Asp	Val	
			180					185					190			
cac	acc	aaa	ctg	gcc	ttg	tgg	cat	ggt	ctg	aat	cta	ccg	ctg	ctg	ctg	624
His	Thr	Lys	Leu	Ala	Leu	Trp	His	Gly	Leu	Asn	Leu	Pro	Leu	Leu	Leu	
		195					200					205				
tct	gtg	gtg	atc	atc	att	tcc	gga	ttc	atc	atc	ttc	tgg	gag	cga	gac	672
Ser	Val	Val	Ile	Ile	Ile	Ser	Gly	Phe	Ile	Ile	Phe	Trp	Glu	Arg	Asp	
	210					215					220					
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Thr	Val	Glu	Arg	Leu	Arg	Pro	Asn	Thr	Ala	Ala	Phe	Gly	Ser	Ala	Asp	
	225				230					235				240		
acc	gcc	tac	gac	gcc	att	ctt	gat	gca	ctg	cgt	gtg	ctc	tcc	cac	cgc	768
Thr	Ala	Tyr	Asp	Ala	Ile	Leu	Asp	Ala	Leu	Arg	Val	Leu	Ser	His	Arg	
				245					250					255		
ctg	act	gca	tcc	acc	cag	cgt	ggt	tct	ttg	acc	ctg	aac	gtc	ggt	gtg	816
Leu	Thr	Ala	Ser	Thr	Gln	Arg	Gly	Ser	Leu	Thr	Leu	Asn	Val	Gly	Val	
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atc	ttc	ttc	gtc	ctc	acg	att	gtt	ccg	ctg	atc	gct	ttg	atc	act	ggc	864
Ile	Phe	Phe	Val	Leu	Thr	Ile	Val	Pro	Leu	Ile	Ala	Leu	Ile	Thr	Gly	

275					280					285										
gaa	caa	agc	gat	gtc	cgc	atg	gag	ctg	tgg	gat	agc	cct	att	cag	ggc	912				
Glu	Gln	Ser	Asp	Val	Arg	Met	Glu	Leu	Trp	Asp	Ser	Pro	Ile	Gln	Gly					
290					295					300										
ttc	atc	gcg	gcc	atc	att	atc	gtc	gtt	gcg	att	gtg	gca	acc	acc	atg	960				
Phe	Ile	Ala	Ala	Ile	Ile	Ile	Val	Val	Ala	Ile	Val	Ala	Thr	Thr	Met					
305					310					315					320					
gat	aac	cgt	ttg	tct	gcg	ctg	att	ttg	gtg	ggc	gtg	aca	ggt	tat	ggc	1008				
Asp	Asn	Arg	Leu	Ser	Ala	Leu	Ile	Leu	Val	Gly	Val	Thr	Gly	Tyr	Gly					
325					330					335										
att	gcc	gtt	atc	ttc	gcg	cta	cat	ggc	gca	ccg	gac	ttg	gcg	cta	acc	1056				
Ile	Ala	Val	Ile	Phe	Ala	Leu	His	Gly	Ala	Pro	Asp	Leu	Ala	Leu	Thr					
340					345					350										
cag	gtg	ctg	gtg	gag	acc	atc	gtc	atg	gtg	gta	ttc	atg	ctg	gtg	ctg	1104				
Gln	Val	Leu	Val	Glu	Thr	Ile	Val	Met	Val	Val	Phe	Met	Leu	Val	Leu					
355					360					365										
cgt	aaa	atg	ccg	aca	gaa	gtt	gcg	tgg	aag	gca	gaa	cct	aaa	cag	tct	1152				
Arg	Lys	Met	Pro	Thr	Glu	Val	Ala	Trp	Lys	Ala	Glu	Pro	Lys	Gln	Ser					
370					375					380										
cgc	gtg	cga	gcg	tgg	ctt	gct	ggc	gcc	acc	gga	ttg	tcc	gtt	gtt	att	1200				
Arg	Val	Arg	Ala	Trp	Leu	Ala	Gly	Ala	Thr	Gly	Leu	Ser	Val	Val	Ile					
385					390					395					400					
gtc	acc	att	ttt	gcc	atg	aat	gct	cgc	acc	act	gaa	ccg	atc	tct	gta	1248				
Val	Thr	Ile	Phe	Ala	Met	Asn	Ala	Arg	Thr	Thr	Glu	Pro	Ile	Ser	Val					
405					410					415										
tac	atg	cag	gat	ctg	gcc	tat	gag	atc	gga	cat	ggc	gca	aac	acc	gtc	1296				
Tyr	Met	Gln	Asp	Leu	Ala	Tyr	Glu	Ile	Gly	His	Gly	Ala	Asn	Thr	Val					
420					425					430										
aac	gta	ctg	ctc	gta	gac	ctg	cgt	ggc	ttt	gat	acc	ttc	ggt	gaa	att	1344				
Asn	Val	Leu	Leu	Val	Asp	Leu	Arg	Gly	Phe	Asp	Thr	Phe	Gly	Glu	Ile					
435					440					445										
tcc	gtc	ctt	gtg	atc	gcg	gca	acc	ggc	atc	gcc	tcc	ctg	gtc	tac	cga	1392				
Ser	Val	Leu	Val	Ile	Ala	Ala	Thr	Gly	Ile	Ala	Ser	Leu	Val	Tyr	Arg					
450					455					460										
aac	cgc	agc	ttc	cgc	aag	gat	tct	cgc	aga	cca	acc	ctg	gct	acc	act	1440				
Asn	Arg	Ser	Phe	Arg	Lys	Asp	Ser	Arg	Arg	Pro	Thr	Leu	Ala	Thr	Thr					
465					470					475					480					
ggc	cgc	cgt	tgg	ttg	gct	gct	gct	gtt	gat	acc	gaa	agg	gcg	cag	aac	1488				
Gly	Arg	Arg	Trp	Leu	Ala	Ala	Ala	Val	Asp	Thr	Glu	Arg	Ala	Gln	Asn					
485					490					495										
cgc	tcg	ctg	atg	gtt	gat	gtg	gca	acg	cgc	atc	ctc	ttc	cct	gcc	atg	1536				
Arg	Ser	Leu	Met	Val	Asp	Val	Ala	Thr	Arg	Ile	Leu	Phe	Pro	Ala	Met					
500					505					510										
atc	atg	ttg	tct	gtg	tac	ttc	ttc	ttc	gcc	gga	cac	aac	gcg	ccg	ggc	1584				
Ile	Met	Leu	Ser	Val	Tyr	Phe	Phe	Phe	Ala	Gly	His	Asn	Ala	Pro	Gly					
515					520					525										


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ggc gga ttc gcc ggc ggc ctt gtt gcc tcc ttg gcg ttc gcc ttg cgc 1632
Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
530 535 540

tac ctt gcc ggt gga cgt gaa gaa ctt gaa gaa gcg ttg cct atc gac 1680
Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
545 550 555 560

gcc ggc cgt atc ttg gga act gga cta ttt gtt tct gca act gca gtg 1728
Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
565 570 575

ctg tgg ccc atg gtt ctt ctt ggt gaa cca ccg ctg acc tcc cat att 1776
Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
580 585 590

tgg gat ctc aca ctg cca ctt atc ggt gag att cac att gca tcc gcg 1824
Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
595 600 605

ctg ctc ttt gac ctt ggt gtc tac ctg atc gtc atc ggt ttg acc atg 1872
Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
610 615 620

cac att ctc aac agt ttg ggc ggc cag ctc gac cgc gat gag gaa atg 1920
His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
625 630 635 640

cgt aag cag cgt gcg cgc gac cga gct cga cgc ttg gcg cgc aac cag 1968
Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
645 650 655

cgt cga gaa gca gca acc gtc ggc gca cgc agg tcg aac gag aaa tcg 2016
Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
660 665 670

aca cgc caa atg ccg acg att cgg cct cca ggg gca gac aca gaa tcg 2064
Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser
675 680 685

gtg gag cag aac ggt gag aac cag acg tcg ata agc aca aag cgt tta 2112
Val Glu Gln Asn Gly Glu Asn Gln Thr Ser Ile Ser Thr Lys Arg Leu
690 695 700

aag cag 2118
Lys Gln
705

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<210> 692

<211> 706

<212> PRT

<213> Corynebacterium glutamicum

<400> 692

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Ile Ile Ser Val Val Gly Ile Gly Thr Arg Glu Ala Leu Leu Ala Gly
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Leu Ala Leu Thr Val Ala His Ser Leu Phe Lys Ala Thr Leu Phe Met
20 25 30

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Thr Val Gly Ala Ile Asp His Thr Thr Gly Thr Arg Asp Ile Arg Lys
 35 40 45
 Leu Ser Gly Leu Trp Arg Lys Gln Pro Ile Leu Phe Ala Val Ala Ala
 50 55 60
 Val Ser Ala Ala Ser Met Ala Gly Ile Pro Pro Leu Phe Gly Phe Ile
 65 70 75 80
 Ala Lys Glu Thr Ala Leu Asp Thr Val Leu Asn Glu Gln Met Leu His
 85 90 95
 Gly Met Pro Gly Arg Leu Met Leu Ala Gly Ile Val Leu Gly Ser Ile
 100 105 110
 Phe Thr Met Ala Tyr Ser Cys Tyr Phe Leu Tyr Glu Ala Phe Ala Thr
 115 120 125
 Lys His Ser Lys Phe Pro Glu Ala Asn Gly Val Ser Pro Ala Val Glu
 130 135 140
 Ala Met His Pro Val Lys Phe Lys Leu Trp Ile Ala Pro Val Ile Leu
 145 150 155 160
 Ala Ile Leu Thr Val Val Phe Gly Val Phe Pro Lys Pro Val Ser Glu
 165 170 175
 Ala Ile Val Thr His Leu Asp Asn Val Thr Pro Ser Leu Asp Asp Val
 180 185 190
 His Thr Lys Leu Ala Leu Trp His Gly Leu Asn Leu Pro Leu Leu Leu
 195 200 205
 Ser Val Val Ile Ile Ile Ser Gly Phe Ile Ile Phe Trp Glu Arg Asp
 210 215 220
 Thr Val Glu Arg Leu Arg Pro Asn Thr Ala Ala Phe Gly Ser Ala Asp
 225 230 235 240
 Thr Ala Tyr Asp Ala Ile Leu Asp Ala Leu Arg Val Leu Ser His Arg
 245 250 255
 Leu Thr Ala Ser Thr Gln Arg Gly Ser Leu Thr Leu Asn Val Gly Val
 260 265 270
 Ile Phe Phe Val Leu Thr Ile Val Pro Leu Ile Ala Leu Ile Thr Gly
 275 280 285
 Glu Gln Ser Asp Val Arg Met Glu Leu Trp Asp Ser Pro Ile Gln Gly
 290 295 300
 Phe Ile Ala Ala Ile Ile Ile Val Val Ala Ile Val Ala Thr Thr Met
 305 310 315 320
 Asp Asn Arg Leu Ser Ala Leu Ile Leu Val Gly Val Thr Gly Tyr Gly
 325 330 335
 Ile Ala Val Ile Phe Ala Leu His Gly Ala Pro Asp Leu Ala Leu Thr
 340 345 350

Gln Val Leu Val Glu Thr Ile Val Met Val Val Phe Met Leu Val Leu
 355 360 365
 Arg Lys Met Pro Thr Glu Val Ala Trp Lys Ala Glu Pro Lys Gln Ser
 370 375 380
 Arg Val Arg Ala Trp Leu Ala Gly Ala Thr Gly Leu Ser Val Val Ile
 385 390 395 400
 Val Thr Ile Phe Ala Met Asn Ala Arg Thr Thr Glu Pro Ile Ser Val
 405 410 415
 Tyr Met Gln Asp Leu Ala Tyr Glu Ile Gly His Gly Ala Asn Thr Val
 420 425 430
 Asn Val Leu Leu Val Asp Leu Arg Gly Phe Asp Thr Phe Gly Glu Ile
 435 440 445
 Ser Val Leu Val Ile Ala Ala Thr Gly Ile Ala Ser Leu Val Tyr Arg
 450 455 460
 Asn Arg Ser Phe Arg Lys Asp Ser Arg Arg Pro Thr Leu Ala Thr Thr
 465 470 475 480
 Gly Arg Arg Trp Leu Ala Ala Ala Val Asp Thr Glu Arg Ala Gln Asn
 485 490 495
 Arg Ser Leu Met Val Asp Val Ala Thr Arg Ile Leu Phe Pro Ala Met
 500 505 510
 Ile Met Leu Ser Val Tyr Phe Phe Phe Ala Gly His Asn Ala Pro Gly
 515 520 525
 Gly Gly Phe Ala Gly Gly Leu Val Ala Ser Leu Ala Phe Ala Leu Arg
 530 535 540
 Tyr Leu Ala Gly Gly Arg Glu Glu Leu Glu Glu Ala Leu Pro Ile Asp
 545 550 555 560
 Ala Gly Arg Ile Leu Gly Thr Gly Leu Phe Val Ser Ala Thr Ala Val
 565 570 575
 Leu Trp Pro Met Val Leu Leu Gly Glu Pro Pro Leu Thr Ser His Ile
 580 585 590
 Trp Asp Leu Thr Leu Pro Leu Ile Gly Glu Ile His Ile Ala Ser Ala
 595 600 605
 Leu Leu Phe Asp Leu Gly Val Tyr Leu Ile Val Ile Gly Leu Thr Met
 610 615 620
 His Ile Leu Asn Ser Leu Gly Gly Gln Leu Asp Arg Asp Glu Glu Met
 625 630 635 640
 Arg Lys Gln Arg Ala Arg Asp Arg Ala Arg Arg Leu Ala Arg Asn Gln
 645 650 655
 Arg Arg Glu Ala Ala Thr Val Gly Ala Arg Arg Ser Asn Glu Lys Ser
 660 665 670
 Thr Arg Gln Met Pro Thr Ile Arg Pro Pro Gly Ala Asp Thr Glu Ser

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Lys Gln
705

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<211> 955
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(955)
<223> RXA00909

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              Val Leu Ile Leu Phe
              1                5

ctc gcg ctc act gca gcc gca gta gtc gcc ccc atc ctg atc cga act 163
Leu Ala Leu Thr Ala Ala Val Val Ala Pro Ile Leu Ile Arg Thr
              10                15                20

ctc ggt cga cca gct ttt ggt ctg ctg gcg ctt gta cct ggc att ggt 211
Leu Gly Arg Pro Ala Phe Gly Leu Leu Ala Leu Val Pro Gly Ile Gly
              25                30                35

ttt ttc tgg gtg ctt tcg gag ttc atc aaa ggc act ttc aag gat gga 259
Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly Thr Phe Lys Asp Gly
              40                45                50

ggg gaa ctc ctc ctc cac tat gcc tgg atg cct tcg gct cac ctc aat 307
Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro Ser Ala His Leu Asn
              55                60                65

atc gat ttc cgt atg gat tcc ctc gcg gcg ctg ttc tca ctc atc gtc 355
Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu Phe Ser Leu Ile Val
              70                75                80                85

tta ggc gtg ggc gcc cta gtg ctg ctg tac tgc tgg gga tat ttt gat 403
Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys Trp Gly Tyr Phe Asp
              90                95                100

tcc aac gcg ggt cgc ctc agt gcc ttt ggt gct gaa ctg gtg gcc ttc 451
Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala Glu Leu Val Ala Phe
              105                110                115

gcc atg gcg atg ttt ggt ctt gtc att tca gac aac atc ctg ctg atg 499
Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp Asn Ile Leu Leu Met
              120                125                130

tac gtc ttc tgg gaa atc acc tcc gtt tta tcc ttc ctc ctg gtt ggt 547
Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser Phe Leu Leu Val Gly
              135                140                145

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tat tac ggc gaa cgc gca tct tca cgt cgc tct gca ggt caa gcc ttg 595
 Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser Ala Gly Gln Ala Leu
 150 155 160 165

 atg gtg acc acc ctg ggt gga ttg gcc atg ctg gtg ggc atc att ttg 643
 Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu Val Gly Ile Ile Leu
 170 175 180

 atg ggt acc caa act ggc gtg tgg cga ttc tct gag atc cct gcc tac 691
 Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser Glu Ile Pro Ala Tyr
 185 190 195

 tca agc tcc tgg gca gat gtg ccg tat att tcc gct gct gct gcc ctt 739
 Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser Ala Ala Ala Leu
 200 205 210

 atc ttg gct ggc gca cta tcc aaa tcg gct atc gca cca acc cac ttc 787
 Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile Ala Pro Thr His Phe
 215 220 225

 tgg ctt ccc ggc gcg atg gcc gca cca acg ccg gtg tct gct tac ctg 835
 Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro Val Ser Ala Tyr Leu
 230 235 240 245

 cac tcc gca gcg atg gtg aag gcg ggt att tac ctt gtg gct cgc ctc 883
 His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr Leu Val Ala Arg Leu
 250 255 260

 tct cca gac ctc aac gta gtt ggt tcg tgg tac ctg atc atc atc ccg 931
 Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr Leu Ile Ile Ile Pro
 265 270 275

 ttg ggc atg ttg acc atg ctc atg 955
 Leu Gly Met Leu Thr Met Leu Met
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<210> 694
 <211> 285
 <212> PRT
 <213> *Corynebacterium glutamicum*

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 Val Pro Gly Ile Gly Phe Phe Trp Val Leu Ser Glu Phe Ile Lys Gly
 35 40 45

 Thr Phe Lys Asp Gly Gly Glu Leu Leu Leu His Tyr Ala Trp Met Pro
 50 55 60

 Ser Ala His Leu Asn Ile Asp Phe Arg Met Asp Ser Leu Ala Ala Leu
 65 70 75 80

 Phe Ser Leu Ile Val Leu Gly Val Gly Ala Leu Val Leu Leu Tyr Cys
 85 90 95

Trp Gly Tyr Phe Asp Ser Asn Ala Gly Arg Leu Ser Ala Phe Gly Ala
 100 105 110
 Glu Leu Val Ala Phe Ala Met Ala Met Phe Gly Leu Val Ile Ser Asp
 115 120 125
 Asn Ile Leu Leu Met Tyr Val Phe Trp Glu Ile Thr Ser Val Leu Ser
 130 135 140
 Phe Leu Leu Val Gly Tyr Tyr Gly Glu Arg Ala Ser Ser Arg Arg Ser
 145 150 155 160
 Ala Gly Gln Ala Leu Met Val Thr Thr Leu Gly Gly Leu Ala Met Leu
 165 170 175
 Val Gly Ile Ile Leu Met Gly Thr Gln Thr Gly Val Trp Arg Phe Ser
 180 185 190
 Glu Ile Pro Ala Tyr Ser Ser Ser Trp Ala Asp Val Pro Tyr Ile Ser
 195 200 205
 Ala Ala Ala Ala Leu Ile Leu Ala Gly Ala Leu Ser Lys Ser Ala Ile
 210 215 220
 Ala Pro Thr His Phe Trp Leu Pro Gly Ala Met Ala Ala Pro Thr Pro
 225 230 235 240
 Val Ser Ala Tyr Leu His Ser Ala Ala Met Val Lys Ala Gly Ile Tyr
 245 250 255
 Leu Val Ala Arg Leu Ser Pro Asp Leu Asn Val Val Gly Ser Trp Tyr
 260 265 270
 Leu Ile Ile Ile Pro Leu Gly Met Leu Thr Met Leu Met
 275 280 285

<210> 695

<211> 927

<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(904)

<223> RXA00700

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 Met Ile Asn Ala Ile
 1 5

aca ctc aag ccc aaa acc ttc ctc acc tta agc ttc ctt gcg gtt ttg 163
 Thr Leu Lys Pro Lys Thr Phe Leu Thr Leu Ser Phe Leu Ala Val Leu
 10 15 20

agc atc gtg att ttc ttc tgg ccg ctg atc gtc aac ccg gaa tcc ttc 211
 Ser Ile Val Ile Phe Phe Trp Pro Leu Ile Val Asn Pro Glu Ser Phe

				25				30				35								
ctg	tcc	gac	aaa	gcc	caa	gcg	ccc	ctc	tac	atc	gcg	atc	gtc	att	ccc		259			
Leu	Ser	Asp	Lys	Ala	Gln	Ala	Pro	Leu	Tyr	Ile	Ala	Ile	Val	Ile	Pro					
			40				45				50									
ctc	gtg	ctg	gcc	gct	gtc	atc	gcc	gaa	atc	agt	gaa	aac	gga	ttc	gac		307			
Leu	Val	Leu	Ala	Ala	Val	Ile	Ala	Glu	Ile	Ser	Glu	Asn	Gly	Phe	Asp					
		55				60				65										
gtt	aaa	gcc	gta	gcc	atg	ctc	ggc	gtc	ctc	acc	gcc	atg	gtt	gcc	gta		355			
Val	Lys	Ala	Val	Ala	Met	Leu	Gly	Val	Leu	Thr	Ala	Met	Val	Ala	Val					
		70				75				80			85							
gtc	cga	cca	ttc	ggg	gcc	ggc	gca	gca	ggc	ttt	gaa	gca	gtc	ttc	ttt		403			
Val	Arg	Pro	Phe	Gly	Ala	Gly	Ala	Ala	Gly	Phe	Glu	Ala	Val	Phe	Phe					
				90				95			100									
gtc	ctc	atc	ctc	ggc	gga	cga	gcc	ttc	gga	ccc	ggc	ttc	gga	ttc	atc		451			
Val	Leu	Ile	Leu	Gly	Gly	Arg	Ala	Phe	Gly	Pro	Gly	Phe	Gly	Phe	Ile					
			105				110			115										
ctc	ggc	aac	acc	gga	ctg	ttc	gca	tcc	gcg	ctg	ctc	acc	gca	gga	atc		499			
Leu	Gly	Asn	Thr	Gly	Leu	Phe	Ala	Ser	Ala	Leu	Leu	Thr	Ala	Gly	Ile					
			120				125			130										
gga	ccg	tgg	ctc	ccc	tac	caa	atg	ctc	gca	gcc	gcc	tgg	gtc	agc	ttc		547			
Gly	Pro	Trp	Leu	Pro	Tyr	Gln	Met	Leu	Ala	Ala	Ala	Trp	Val	Ser	Phe					
		135				140			145											
ggc	gcc	ggc	cta	ctc	ccc	caa	gta	cgc	ggc	aaa	aag	gaa	atg	ctc	atc		595			
Gly	Ala	Gly	Leu	Leu	Pro	Gln	Val	Arg	Gly	Lys	Lys	Glu	Met	Leu	Ile					
			150	155			160			165										
atc	gtc	cta	tac	gcc	atc	gtc	tct	tca	ctc	ggc	tac	gga	acc	atg	atg		643			
Ile	Val	Leu	Tyr	Ala	Ile	Val	Ser	Ser	Leu	Gly	Tyr	Gly	Thr	Met	Met					
				170				175			180									
aac	atg	agc	ttc	tgg	ccc	tac	gcc	atc	ggg	gtc	acc	agc	ggg	ctt	tcc		691			
Asn	Met	Ser	Phe	Trp	Pro	Tyr	Ala	Ile	Gly	Val	Thr	Ser	Gly	Leu	Ser					
			185				190			195										
ttc	aca	ccc	ggc	gcg	ccc	gtc	ctg	gaa	aac	ctc	cac	acc	ttc	atg	ctg		739			
Phe	Thr	Pro	Gly	Ala	Pro	Val	Leu	Glu	Asn	Leu	His	Thr	Phe	Met	Leu					
		200				205			210											
ttc	tgc	ctc	acc	aca	tcc	atg	ggg	tgg	gat	ctc	ggc	cgc	gcc	ttc	ttc		787			
Phe	Cys	Leu	Thr	Thr	Ser	Met	Gly	Trp	Asp	Leu	Gly	Arg	Ala	Phe	Phe					
			215	220			225													
acc	tca	gtg	cta	tta	ctg	ctc	aca	gcc	aaa	ccc	gtt	tta	ggg	gct	tta		835			
Thr	Ser	Val	Leu	Leu	Leu	Leu	Thr	Ala	Lys	Pro	Val	Leu	Gly	Ala	Leu					
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 696
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 20 25 30
 Asn Pro Glu Ser Phe Leu Ser Asp Lys Ala Gln Ala Pro Leu Tyr Ile
 35 40 45
 Ala Ile Val Ile Pro Leu Val Leu Ala Ala Val Ile Ala Glu Ile Ser
 50 55 60
 Glu Asn Gly Phe Asp Val Lys Ala Val Ala Met Leu Gly Val Leu Thr
 65 70 75 80
 Ala Met Val Ala Val Val Arg Pro Phe Gly Ala Gly Ala Ala Gly Phe
 85 90 95
 Glu Ala Val Phe Phe Val Leu Ile Leu Gly Gly Arg Ala Phe Gly Pro
 100 105 110
 Gly Phe Gly Phe Ile Leu Gly Asn Thr Gly Leu Phe Ala Ser Ala Leu
 115 120 125
 Leu Thr Ala Gly Ile Gly Pro Trp Leu Pro Tyr Gln Met Leu Ala Ala
 130 135 140
 Ala Trp Val Ser Phe Gly Ala Gly Leu Leu Pro Gln Val Arg Gly Lys
 145 150 155 160
 Lys Glu Met Leu Ile Ile Val Leu Tyr Ala Ile Val Ser Ser Leu Gly
 165 170 175
 Tyr Gly Thr Met Met Asn Met Ser Phe Trp Pro Tyr Ala Ile Gly Val
 180 185 190
 Thr Ser Gly Leu Ser Phe Thr Pro Gly Ala Pro Val Leu Glu Asn Leu
 195 200 205
 His Thr Phe Met Leu Phe Cys Leu Thr Thr Ser Met Gly Trp Asp Leu
 210 215 220
 Gly Arg Ala Phe Phe Thr Ser Val Leu Leu Leu Leu Thr Ala Lys Pro
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 Val Leu Gly Ala Leu Arg Arg Ala Ser Arg Arg Ala Ala Phe Gly Val
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 Glu Arg Asp Phe Gly Glu Ala Gly Val Pro Arg Val
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<210> 697

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> RXN00483

<400> 697

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                               Val Leu Val Thr Gly
                               1 5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
              10              15              20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
              25              30              35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
              40              45              50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
              55              60              65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
              70              75              80              85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
              90              95              100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
              105              110              115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
              120              125              130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile
              135              140              145

att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag 595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu
              150              155              160              165

cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag 643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu
              170              175              180

cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat 691

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Leu	Lys	Asp	Pro	Val	Asn	Arg	Ser	Cys	Asp	Ile	Gly	Cys	Gly	Lys	Ser		
		200					205					210					
tat	gaa	ttt	gcg	gat	cta	ttg	cgt	atc	tat	gcc	gat	gtt	cgg	gga	ctg	787	
Tyr	Glu	Phe	Ala	Asp	Leu	Leu	Arg	Ile	Tyr	Ala	Asp	Val	Arg	Gly	Leu		
	215					220					225						
aaa	cgt	cat	gta	aat	tcc	gta	cct	ctc	aat	ttg	ccc	atg	gac	aag	cta	835	
Lys	Arg	His	Val	Asn	Ser	Val	Pro	Leu	Asn	Leu	Pro	Met	Asp	Lys	Leu		
230					235					240					245		
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Ser	Gly	Leu	Trp	Ile	Ser	Leu	Val	Thr	Pro	Val	Pro	Phe	Gln	Leu	Ser		
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ttc	cct	tta	gct	caa	tca	atg	gct	gag	gat	gcc	gtc	act	gaa	gag	cac	931	
Phe	Pro	Leu	Ala	Gln	Ser	Met	Ala	Glu	Asp	Ala	Val	Thr	Glu	Glu	His		
			265					270					275				
agc	att	aaa	gat	att	att	tca	gat	cca	ccc	gat	ggg	ttt	att	gag	tat	979	
Ser	Ile	Lys	Asp	Ile	Ile	Ser	Asp	Pro	Pro	Asp	Gly	Phe	Ile	Glu	Tyr		
		280					285					290					
cgg	gaa	gca	gtg	gag	ctg	gca	tta	gct	gca	gaa	ttt	gat	cgt	gga	gtt	1027	
Arg	Glu	Ala	Val	Glu	Leu	Ala	Leu	Ala	Ala	Glu	Phe	Asp	Arg	Gly	Val		
	295					300					305						
cca	acg	tca	tgg	gat	cga	agc	tgg	act	gta	caa	caa	ccg	tgg	gct	ggc	1075	
Pro	Thr	Ser	Trp	Asp	Arg	Ser	Trp	Thr	Val	Gln	Gln	Pro	Trp	Ala	Gly		
310					315					320					325		
cag	cct	acc	gat	cca	gag	tgg	gcg	ggc	aaa	gct	gta	tat	gaa	gac	gtc	1123	
Gln	Pro	Thr	Asp	Pro	Glu	Trp	Ala	Gly	Lys	Ala	Val	Tyr	Glu	Asp	Val		
				330					335					340			
cgc	aca	gaa	gat	act	gat	ctc	cga	gca	gcg	cag	gtc	tgg	ccg	atc	att	1171	
Arg	Thr	Glu	Asp	Thr	Asp	Leu	Arg	Ala	Ala	Gln	Val	Trp	Pro	Ile	Ile		
			345				350						355				
gaa	ggg	ttg	ggg	ggc	gtg	aac	ggc	tgg	tat	tct	gca	cca	ctg	cta	tgg	1219	
Glu	Gly	Leu	Gly	Gly	Val	Asn	Gly	Trp	Tyr	Ser	Ala	Pro	Leu	Leu	Trp		
		360					365					370					
cga	ttg	cgg	ggg	atc	gct	gac	aga	ctc	atc	ggc	ggg	cca	ggg	ttg	ggc	1267	
Arg	Leu	Arg	Gly	Ile	Ala	Asp	Arg	Leu	Ile	Gly	Gly	Pro	Gly	Leu	Gly		
	375					380					385						
gga	cgg	cgg	gat	ccc	cgt	cat	ttg	aaa	ctt	ggg	gat	cgc	att	gat	tgg	1315	
Gly	Arg	Arg	Asp	Pro	Arg	His	Leu	Lys	Leu	Gly	Asp	Arg	Ile	Asp	Trp		
390					395					400					405		
tgg	cgg	gtt	act	gag	atc	gat	cca	cca	cat	aga	tta	gtg	ctc	acc	gca	1363	
Trp	Arg	Val	Thr	Glu	Ile	Asp	Pro	Pro	His	Arg	Leu	Val	Leu	Thr	Ala		
				410					415					420			
gag	atg	aaa	gta	gat	ggg	ggc	gct	tgg	ctg	atc	ctg	gaa	gtt	gcg	gac	1411	
Glu	Met	Lys	Val	Asp	Gly	Gly	Ala	Trp	Leu	Ile	Leu	Glu	Val	Ala	Asp		

425	430	435	
aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg			1459
Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro			
440	445	450	
aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat			1507
Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Ser Pro Phe His			
455	460	465	
gcg att att ttt cct tat atg cgt tcg aat att tta aaa gct gcg cgt			1555
Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg			
470	475	485	
aaa ctc act taatcgcaga gtaggcgtct aaa			1587
Lys Leu Thr			

<210> 698
 <211> 488
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 698
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 Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
 35 40 45
 Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
 50 55 60
 Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
 65 70 75 80
 Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
 85 90 95
 Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
 100 105 110
 Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
 115 120 125
 Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
 130 135 140
 Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
 145 150 155 160
 Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
 165 170 175
 Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
 180 185 190

Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
 195 200 205
 Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
 210 215 220
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
 225 230 235 240
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
 245 250 255
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
 260 265 270
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
 275 280 285
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
 290 295 300
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
 305 310 315 320
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
 325 330 335
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
 340 345 350
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
 355 360 365
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
 370 375 380
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
 385 390 395 400
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
 405 410 415
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
 420 425 430
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
 435 440 445
 Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
 450 455 460
 Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480
 Leu Lys Ala Ala Arg Lys Leu Thr
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<210> 699

<211> 1587

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1564)

<223> FRXA00483

<400> 699

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tcccactttg cattatcaag ctcaaaaccc gcaccggcga  gtg ctg gtc acc ggt 115
              Val Leu Val Thr Gly
              1                      5

gcg aca ggc tac att ggc ggc agg ttg att act gag tta ctt gct gcc 163
Ala Thr Gly Tyr Ile Gly Gly Arg Leu Ile Thr Glu Leu Leu Ala Ala
              10                      15                      20

ggt ttc caa gtt cgg gcc acc tcg agg aaa aaa aca agt ctt cag cgc 211
Gly Phe Gln Val Arg Ala Thr Ser Arg Lys Lys Thr Ser Leu Gln Arg
              25                      30                      35

ttt gac tgg tac gag gac gtc gag gca gtg gaa gcg gat ctg act gac 259
Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu Ala Asp Leu Thr Asp
              40                      45                      50

gcg act gag tta gat acg tta ttt aag gat gta gac gtt gtt tac tat 307
Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val Asp Val Val Tyr Tyr
              55                      60                      65

cta gtg cat tcc atg gga ggt aag aat gtt gat ttt gaa gag caa gag 355
Leu Val His Ser Met Gly Gly Lys Asn Val Asp Phe Glu Glu Gln Glu
              70                      75                      80                      85

caa cgc act gct gaa aat gta att caa gct gct gat caa gcc ggg ata 403
Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala Asp Gln Ala Gly Ile
              90                      95                      100

aaa cag att gtc tac ctt tcc ggc tta cac ccg cgt aat cga aaa ata 451
Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro Arg Asn Arg Lys Ile
              105                      110                      115

gaa gaa cta tct aag cac atg cgc tca cgg gaa aag gtc gcc cag att 499
Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu Lys Val Ala Gln Ile
              120                      125                      130

ttg ctg gca ggc cag aca cca gct tta att tta agg gct gcc aca att 547
Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu Arg Ala Ala Thr Ile
              135                      140                      145

att ggt tcc ggc tct gca tca ttt gaa ata atc cgt cat ctc acg gag 595
Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile Arg His Leu Thr Glu
              150                      155                      160                      165

cgt ttg cct aga atg ata gcg cct cag tgg att act aat cag att gag 643
Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile Thr Asn Gln Ile Glu
              170                      175                      180

cct tta gca ata cgg gat gtt ttg cat tac cta atc tcg gcg gct gat 691
Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu Ile Ser Ala Ala Asp
              185                      190                      195

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tta aag gat cca gtc aac cgc tcc tgc gat att ggg tgt gga aag tcg	739
Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile Gly Cys Gly Lys Ser	
200 205 210	
tat gaa ttt gcg gat cta ttg cgt atc tat gcc gat gtt cgg gga ctg	787
Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala Asp Val Arg Gly Leu	
215 220 225	
aaa cgt cat gta aat tcc gta cct ctc aat ttg ccc atg gac aag cta	835
Lys Arg His Val Asn Ser Val Pro Leu Asn Leu Pro Met Asp Lys Leu	
230 235 240 245	
tcc ggt ctt tgg att agt cta gtg aca cct gtt cca ttt caa ttg tct	883
Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val Pro Phe Gln Leu Ser	
250 255 260	
ttc cct tta gct caa tca atg gct gag gat gcc gtc act gaa gag cac	931
Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala Val Thr Glu Glu His	
265 270 275	
agc att aaa gat att att tca gat cca ccc gat ggt ttt att gag tat	979
Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp Gly Phe Ile Glu Tyr	
280 285 290	
cgg gaa gca gtg gag ctg gca tta gct gca gaa ttt gat cgt gga gtt	1027
Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu Phe Asp Arg Gly Val	
295 300 305	
cca acg tca tgg gat cga agc tgg act gta caa caa ccg tgg gct ggc	1075
Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln Gln Pro Trp Ala Gly	
310 315 320 325	
cag cct acc gat cca gag tgg gcg ggc aaa gct gta tat gaa gac gtc	1123
Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala Val Tyr Glu Asp Val	
330 335 340	
cgc aca gaa gat act gat ctc cga gca gcg cag gtc tgg ccg atc att	1171
Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln Val Trp Pro Ile Ile	
345 350 355	
gaa ggt ttg ggt ggc gtg aac ggc tgg tat tct gca cca ctg cta tgg	1219
Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser Ala Pro Leu Leu Trp	
360 365 370	
cga ttg cgg ggt atc gct gac aga ctc atc ggc ggt cca ggt ttg ggc	1267
Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly Gly Pro Gly Leu Gly	
375 380 385	
gga cgg cgg gat ccc cgt cat ttg aaa ctt ggg gat cgc att gat tgg	1315
Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly Asp Arg Ile Asp Trp	
390 395 400 405	
tgg cgg gtt act gag atc gat cca cca cat aga tta gtg ctc acc gca	1363
Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg Leu Val Leu Thr Ala	
410 415 420	
gag atg aaa gta gat ggt ggc gct tgg ctg atc ctg gaa gtt gcg gac	1411
Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile Leu Glu Val Ala Asp	
425 430 435	

aag gaa aat ggc gga tgt act tat acc cag cgc gca ata ttt gag ccg 1459
Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg Ala Ile Phe Glu Pro
440 445 450

aag ggt ttg ccc ggt tat ctc tat tgg tgg gtt gtt tca ccg ttc cat 1507
Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val Val Ser Pro Phe His
455 460 465

gcg att att ttt cct tat atg cgt tgc aat att tta aaa gct gcg cgt 1555
Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile Leu Lys Ala Ala Arg
470 475 480 485

aaa ctc act taatcgcaga gtaggcgtct aaa 1587
Lys Leu Thr

<210> 700

<211> 488

<212> PRT

<213> Corynebacterium glutamicum

<400> 700

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20 25 30

Thr Ser Leu Gln Arg Phe Asp Trp Tyr Glu Asp Val Glu Ala Val Glu
35 40 45

Ala Asp Leu Thr Asp Ala Thr Glu Leu Asp Thr Leu Phe Lys Asp Val
50 55 60

Asp Val Val Tyr Tyr Leu Val His Ser Met Gly Gly Lys Asn Val Asp
65 70 75 80

Phe Glu Glu Gln Glu Gln Arg Thr Ala Glu Asn Val Ile Gln Ala Ala
85 90 95

Asp Gln Ala Gly Ile Lys Gln Ile Val Tyr Leu Ser Gly Leu His Pro
100 105 110

Arg Asn Arg Lys Ile Glu Glu Leu Ser Lys His Met Arg Ser Arg Glu
115 120 125

Lys Val Ala Gln Ile Leu Leu Ala Gly Gln Thr Pro Ala Leu Ile Leu
130 135 140

Arg Ala Ala Thr Ile Ile Gly Ser Gly Ser Ala Ser Phe Glu Ile Ile
145 150 155 160

Arg His Leu Thr Glu Arg Leu Pro Arg Met Ile Ala Pro Gln Trp Ile
165 170 175

Thr Asn Gln Ile Glu Pro Leu Ala Ile Arg Asp Val Leu His Tyr Leu
180 185 190

Ile Ser Ala Ala Asp Leu Lys Asp Pro Val Asn Arg Ser Cys Asp Ile
195 200 205

Gly Cys Gly Lys Ser Tyr Glu Phe Ala Asp Leu Leu Arg Ile Tyr Ala
 210 215 220
 Asp Val Arg Gly Leu Lys Arg His Val Asn Ser Val Pro Leu Asn Leu
 225 230 235 240
 Pro Met Asp Lys Leu Ser Gly Leu Trp Ile Ser Leu Val Thr Pro Val
 245 250 255
 Pro Phe Gln Leu Ser Phe Pro Leu Ala Gln Ser Met Ala Glu Asp Ala
 260 265 270
 Val Thr Glu Glu His Ser Ile Lys Asp Ile Ile Ser Asp Pro Pro Asp
 275 280 285
 Gly Phe Ile Glu Tyr Arg Glu Ala Val Glu Leu Ala Leu Ala Ala Glu
 290 295 300
 Phe Asp Arg Gly Val Pro Thr Ser Trp Asp Arg Ser Trp Thr Val Gln
 305 310 315 320
 Gln Pro Trp Ala Gly Gln Pro Thr Asp Pro Glu Trp Ala Gly Lys Ala
 325 330 335
 Val Tyr Glu Asp Val Arg Thr Glu Asp Thr Asp Leu Arg Ala Ala Gln
 340 345 350
 Val Trp Pro Ile Ile Glu Gly Leu Gly Gly Val Asn Gly Trp Tyr Ser
 355 360 365
 Ala Pro Leu Leu Trp Arg Leu Arg Gly Ile Ala Asp Arg Leu Ile Gly
 370 375 380
 Gly Pro Gly Leu Gly Gly Arg Arg Asp Pro Arg His Leu Lys Leu Gly
 385 390 395 400
 Asp Arg Ile Asp Trp Trp Arg Val Thr Glu Ile Asp Pro Pro His Arg
 405 410 415
 Leu Val Leu Thr Ala Glu Met Lys Val Asp Gly Gly Ala Trp Leu Ile
 420 425 430
 Leu Glu Val Ala Asp Lys Glu Asn Gly Gly Cys Thr Tyr Thr Gln Arg
 435 440 445
 Ala Ile Phe Glu Pro Lys Gly Leu Pro Gly Tyr Leu Tyr Trp Trp Val
 450 455 460
 Val Ser Pro Phe His Ala Ile Ile Phe Pro Tyr Met Arg Ser Asn Ile
 465 470 475 480
 Leu Lys Ala Ala Arg Lys Leu Thr
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<210> 701

<211> 612

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(589)

<223> RXA01534

<400> 701

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                                         Met Thr Ser Ala Ile
                                         1 5
acc acc gca act gat ctt cgc tcc gta ctg cga aac gta cca acc cca 163
Thr Thr Ala Thr Asp Leu Arg Ser Val Leu Arg Asn Val Pro Thr Pro
                        10                        15                        20
att agc ttc att gca acc cac acc gat cag cct ctg ggc atg atc gtt 211
Ile Ser Phe Ile Ala Thr His Thr Asp Gln Pro Leu Gly Met Ile Val
                        25                        30                        35
ggg tca ttc gtc agc att agc gcc gaa cca cca ttg gta ggc atc ttc 259
Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro Leu Val Gly Ile Phe
                        40                        45                        50
ttg cag aag agc tct tct tca tgg cca gct atc gag cag gca tta gtt 307
Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile Glu Gln Ala Leu Val
                        55                        60                        65
acc ggc caa gag cta ggc att tct atc ctc ggc ggg gca cac gca gac 355
Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly Gly Ala His Ala Asp
70                        75                        80                        85
cat gtg cgt aag ctt tct ggc cca tcc gac cag cgc ttt gaa aac ctt 403
His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln Arg Phe Glu Asn Leu
                        90                        95                        100
ggg tgg gca tcc acc gaa aac ggt gcg att cac ctt gaa ggc gct gat 451
Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His Leu Glu Gly Ala Asp
                        105                        110                        115
gca caa cta acc acg aaa ctt cat gat ctc cag gaa atc ggc gat cac 499
Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln Glu Ile Gly Asp His
120                        125                        130
ttc ttt gca gtt cta gaa gtt att gac gct tcc gct gac caa gac ttc 547
Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser Ala Asp Gln Asp Phe
135                        140                        145
agc tca gcg ctg gtg tac cac cgc tca cag gtg tcc tcg ctg 589
Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val Ser Ser Leu
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<211> 163

<212> PRT

<213> Corynebacterium glutamicum

<400> 702

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 20 25 30
 Leu Gly Met Ile Val Gly Ser Phe Val Ser Ile Ser Ala Glu Pro Pro
 35 40 45
 Leu Val Gly Ile Phe Leu Gln Lys Ser Ser Ser Ser Trp Pro Ala Ile
 50 55 60
 Glu Gln Ala Leu Val Thr Gly Gln Glu Leu Gly Ile Ser Ile Leu Gly
 65 70 75 80
 Gly Ala His Ala Asp His Val Arg Lys Leu Ser Gly Pro Ser Asp Gln
 85 90 95
 Arg Phe Glu Asn Leu Gly Trp Ala Ser Thr Glu Asn Gly Ala Ile His
 100 105 110
 Leu Glu Gly Ala Asp Ala Gln Leu Thr Thr Lys Leu His Asp Leu Gln
 115 120 125
 Glu Ile Gly Asp His Phe Phe Ala Val Leu Glu Val Ile Asp Ala Ser
 130 135 140
 Ala Asp Gln Asp Phe Ser Ser Ala Leu Val Tyr His Arg Ser Gln Val
 145 150 155 160
 Ser Ser Leu

<210> 703
 <211> 1134
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1111)
 <223> RXA00288

<400> 703
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 Met Ser Ala Gln Met
 1 5
 gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc 163
 Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile
 10 15 20
 cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca 211
 Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro
 25 30 35
 act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att 259
 Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile

40	45	50	
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tcg cag gtc acg ctc ttc aat gtt ggt gac aaa gtg ttc tac gca gga Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly 90 95 100			403
tcc aat cag cgt cca gga agt aac gca gag tac cag gtg gtg gat gaa Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr Gln Val Val Asp Glu 105 110 115			451
cgg ctg gtg ggt cac gca cca caa agc ttg ggg gca cac gac gcc gct Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly Ala His Asp Ala Ala 120 125 130			499
gct ctc cca ctt gtc gcg ctc act gca tgg gag tca ctt ttt gac cga Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu Ser Leu Phe Asp Arg 135 140 145			547
ttg gga gta act cag tca act act gga aca ctg ttg gtc ttg ggc ggt Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu Leu Val Leu Gly Gly 150 155 160 165			595
tca gga ggt gtg cct tca gct ctt att caa ctt gct cga gct ctc act Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr 170 175 180			643
ggg ctg aaa gta gtg gca aca gct tct cgc cct gaa tca caa gaa tgg Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp 185 190 195			691
gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu 200 205 210			739
agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr 215 220 225			787
ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu 230 235 240 245			835
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln 250 255 260			883
aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe 265 270 275			931
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			20					25					30			
Glu	Val	Asp	Arg	Pro	Thr	Pro	Gly	Pro	His	Asp	Leu	Leu	Val	His	Ile	
		35					40					45				
Glu	Ala	Val	Ser	Ile	Asn	Pro	Val	Asp	Thr	Lys	Val	Arg	Met	Arg	Ala	
	50					55					60					
Gly	Lys	Gln	Lys	His	Pro	Lys	Ile	Leu	Gly	Phe	Asp	Ala	Ala	Gly	Glu	
65					70					75					80	
Val	Val	Ala	Val	Gly	Ser	Gln	Val	Thr	Leu	Phe	Asn	Val	Gly	Asp	Lys	
				85					90					95		
Val	Phe	Tyr	Ala	Gly	Ser	Asn	Gln	Arg	Pro	Gly	Ser	Asn	Ala	Glu	Tyr	
			100					105					110			
Gln	Val	Val	Asp	Glu	Arg	Leu	Val	Gly	His	Ala	Pro	Gln	Ser	Leu	Gly	
		115					120					125				
Ala	His	Asp	Ala	Ala	Ala	Leu	Pro	Leu	Val	Ala	Leu	Thr	Ala	Trp	Glu	
	130					135					140					
Ser	Leu	Phe	Asp	Arg	Leu	Gly	Val	Thr	Gln	Ser	Thr	Thr	Gly	Thr	Leu	
145				150						155					160	
Leu	Val	Leu	Gly	Gly	Ser	Gly	Gly	Val	Pro	Ser	Ala	Leu	Ile	Gln	Leu	
				165					170					175		
Ala	Arg	Ala	Leu	Thr	Gly	Leu	Lys	Val	Val	Ala	Thr	Ala	Ser	Arg	Pro	
			180					185					190			
Glu	Ser	Gln	Glu	Trp	Val	Thr	Lys	Leu	Gly	Ala	His	Glu	Val	Ile	Asp	
		195					200					205				

His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
 210 215 220
 Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
 225 230 235 240
 Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
 245 250 255
 Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
 260 265 270
 Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
 275 280 285
 Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
 290 295 300
 Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
 305 310 315 320
 His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
 325 330 335
 Val

<210> 705
 <211> 1089
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1066)
 <223> RXA02741

<400> 705
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 ttcccaacct tgtctttcag tcatggtag tgtgggaacc atg aag gca atc tta 115
 Met Lys Ala Ile Leu
 1 5
 gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac 163
 Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
 10 15 20
 gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct 211
 Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala
 25 30 35
 ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct 259
 Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala
 40 45 50
 cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag 307
 Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu
 55 60 65

gat	ccg	cag	ggg	ttg	att	gcg	gcg	ggt	acc	aag	gtg	gcg	tgg	tgt	gat	355
Asp	Pro	Gln	Gly	Leu	Ile	Ala	Ala	Gly	Thr	Lys	Val	Ala	Trp	Cys	Asp	
70					75					80					85	
gcc	atg	ggt	tcg	tat	gct	cag	cag	gtg	tgt	gtg	ccg	cgg	gat	cgc	ttg	403
Ala	Met	Gly	Ser	Tyr	Ala	Gln	Gln	Val	Cys	Val	Pro	Arg	Asp	Arg	Leu	
				90					95						100	
gtg	gcg	gtt	ccc	gag	ggc	gtg	agt	tgc	gaa	gtg	gct	gcg	tgc	atg	ttg	451
Val	Ala	Val	Pro	Glu	Gly	Val	Ser	Ser	Glu	Val	Ala	Ala	Ser	Met	Leu	
			105					110							115	
atg	cag	gga	atc	act	gcg	cat	tat	cta	acc	aat	ggt	gtg	tat	gag	ctt	499
Met	Gln	Gly	Ile	Thr	Ala	His	Tyr	Leu	Thr	Asn	Gly	Val	Tyr	Glu	Leu	
			120				125								130	
gaa	gag	ggc	gat	tct	tgc	ctc	atc	act	gct	ggc	gcg	ggt	ggt	gtt	gga	547
Glu	Glu	Gly	Asp	Ser	Cys	Leu	Ile	Thr	Ala	Gly	Ala	Gly	Gly	Val	Gly	
			135				140								145	
ttg	ttg	gct	acg	cag	atg	gcg	gcg	gcc	aag	gga	gtg	cgc	gtg	tac	agc	595
Leu	Leu	Ala	Thr	Gln	Met	Ala	Ala	Ala	Lys	Gly	Val	Arg	Val	Tyr	Ser	
					155					160					165	
gtg	gtg	tcc	acg	gat	gaa	aaa	gct	gag	ctt	gct	ttg	gat	gcc	ggt	gct	643
Val	Val	Ser	Thr	Asp	Glu	Lys	Ala	Glu	Leu	Ala	Leu	Asp	Ala	Gly	Ala	
				170					175						180	
tat	gag	gtg	ttt	cgt	tat	tcc	gat	aat	ttg	gcg	gag	cag	gtt	cgt	cgg	691
Tyr	Glu	Val	Phe	Arg	Tyr	Ser	Asp	Asn	Leu	Ala	Glu	Gln	Val	Arg	Arg	
			185					190							195	
cac	aac	ggg	ggt	cgc	gga	gtt	gat	gtg	gtg	tat	gac	ggt	gtc	ggc	cag	739
His	Asn	Gly	Gly	Arg	Gly	Val	Asp	Val	Val	Tyr	Asp	Gly	Val	Gly	Gln	
			200				205								210	
tcc	acg	ttc	aat	gag	tcc	tta	gag	gct	gtt	cgt	ccg	cgc	ggc	act	gtg	787
Ser	Thr	Phe	Asn	Glu	Ser	Leu	Glu	Ala	Val	Arg	Pro	Arg	Gly	Thr	Val	
			215				220								225	
tgt	ttg	ttt	ggt	gcg	gcg	tgc	ggt	cct	gtg	gag	cct	ttt	gat	ccg	cag	835
Cys	Leu	Phe	Gly	Ala	Ala	Ser	Gly	Pro	Val	Glu	Pro	Phe	Asp	Pro	Gln	
					235					240					245	
ctg	ttg	aac	act	cac	ggt	tgc	atc	ttc	ttg	acc	cgc	cca	agc	att	ggc	883
Leu	Leu	Asn	Thr	His	Gly	Ser	Ile	Phe	Leu	Thr	Arg	Pro	Ser	Ile	Gly	
				250					255						260	
gcg	tgg	acg	tct	gag	gag	ggc	gaa	ttt	gcc	aag	cgt	gca	cag	gcg	gtc	931
Ala	Trp	Thr	Ser	Glu	Glu	Gly	Glu	Phe	Ala	Lys	Arg	Ala	Gln	Ala	Val	
			265					270							275	
acg	cag	gcc	atc	gtc	gaa	ggc	acc	ttg	cgg	gtt	cgc	gtt	act	ggc	aca	979
Thr	Gln	Ala	Ile	Val	Glu	Gly	Thr	Leu	Arg	Val	Arg	Val	Thr	Gly	Thr	
			280				285								290	
tat	tgc	ctt	gcc	gac	gcc	tac	atc	gcc	cac	cgc	gac	ctt	cag	gcg	cgt	1027
Tyr	Ser	Leu	Ala	Asp	Ala	Tyr	Ile	Ala	His	Arg	Asp	Leu	Gln	Ala	Arg	
			295				300				305					
agc	acg	agc	ggt	tct	ttg	gtc	ttg	gaa	atc	ccg	aag	gac	taa	acacgca		1076

Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
 310 315 320

taaaaagatc ctg

1089

<210> 706

<211> 322

<212> PRT

<213> Corynebacterium glutamicum

<400> 706

Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
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Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
 20 25 30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
 35 40 45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
 50 55 60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65 70 75 80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
 85 90 95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
 100 105 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
 115 120 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
 130 135 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
 145 150 155 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
 165 170 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
 180 185 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
 195 200 205

Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
 210 215 220

Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
 225 230 235 240

Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
 245 250 255

Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys

<400> 707																
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ggaacttcta agagcagtgg aatgaaataa tccggtgctg						atg	cag	ggc	aac	tcg	115					
						Met	Gln	Gly	Asn	Ser						
						1				5						
ctt	aat	ctg	gca	gac	aac	agc	gag	aga	aag	aag	ccc	atg	ccg	tca	cca	163
Leu	Asn	Leu	Ala	Asp	Asn	Ser	Glu	Arg	Lys	Lys	Pro	Met	Pro	Ser	Pro	
						10			15					20		
gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca															211	
Gly	Glu	Leu	Leu	Ala	Ala	Arg	Tyr	Gly	Gln	Pro	Ala	Thr	Trp	Thr	Pro	
						25		30					35			
ccg	cag	tgg	aat	gag	acg	ctt	gat	gtc	att	cac	cag	cat	cga	tca	gtt	259
Pro	Gln	Trp	Asn	Glu	Thr	Leu	Asp	Val	Ile	His	Gln	His	Arg	Ser	Val	
						40		45				50				
cgc	agg	tgg	ttg	gat	aaa	ccg	gtt	gat	gat	gac	acc	atc	cgc	acc	att	307
Arg	Arg	Trp	Leu	Asp	Lys	Pro	Val	Asp	Asp	Asp	Thr	Ile	Arg	Thr	Ile	
						55		60			65					
att	tcc	gcc	gca	caa	tcg	gct	gga	acc	tct	tcc	aat	aag	cag	gtc	att	355
Ile	Ser	Ala	Ala	Gln	Ser	Ala	Gly	Thr	Ser	Ser	Asn	Lys	Gln	Val	Ile	
70							75			80					85	
tct	gtc	atc	gtg	gtt	aaa	gat	cct	gag	ctg	agg	aaa	ggc	ctc	gcg	ggg	403
Ser	Val	Ile	Val	Val	Lys	Asp	Pro	Glu	Leu	Arg	Lys	Gly	Leu	Ala	Gly	
						90			95					100		
atc	act	cgc	cag	atg	ttt	ccg	cac	ctt	gag	cag	gtt	ccc	gcg	gtg	ctg	451
Ile	Thr	Arg	Gln	Met	Phe	Pro	His	Leu	Glu	Gln	Val	Pro	Ala	Val	Leu	
						105		110					115			
att	tgg	ttg	att	gat	tat	tcc	cga	atc	agt	gcg	gtg	gca	gcc	aga	gaa	499

Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
 120 125 130
 gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg 547
 Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
 135 140 145
 ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag 595
 Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ile Ala Ala Glu
 150 155 160 165
 tca ctt gga ttg gga acg ctc tat ttg ggt tgc gtg cgc aac gat gcg 643
 Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
 170 175 180
 gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc 691
 Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
 185 190 195
 gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att 739
 Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
 200 205 210
 aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc 787
 Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
 215 220 225
 gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245
 tac tat tct cgc tac ggc cag cac cag ctc tgg tgc aag cag acg gcg 883
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260
 cat agg gcg gcg tgc aaa agc ttt tca aaa acc aac agg cag ttc ctt 931
 His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
 265 270 275
 agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg 977
 Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
 280 285
 attatggacg cct 990

<210> 708

<211> 289

<212> PRT

<213> Corynebacterium glutamicum

<400> 708

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60
 Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80
 Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95
 Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110
 Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125
 Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140
 Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160
 Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175
 Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190
 Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205
 Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220
 Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
 225 230 235 240
 Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
 245 250 255
 Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
 260 265 270
 Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
 275 280 285

Arg

<210> 709
 <211> 922
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(922)
 <223> FRXA02560

<400> 709
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Met Gln Gly Asn Ser	
1 5	
ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca	163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro	
10 15 20	
gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca	211
Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro	
25 30 35	
ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt	259
Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val	
40 45 50	
cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att	307
Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile	
55 60 65	
att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att	355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile	
70 75 80 85	
tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg	403
Ser Val Ile Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly	
90 95 100	
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg	451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu	
105 110 115	
att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa	499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu	
120 125 130	
gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg	547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly	
135 140 145	
ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag	595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu	
150 155 160 165	
tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg	643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala	
170 175 180	
gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc	691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val	
185 190 195	
gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att	739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile	
200 205 210	
aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc	787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr	
215 220 225	

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act 835
 Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
 230 235 240 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg 883
 Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
 250 255 260

cat agg gcg gcg tct aaa cgc tgt tac aag aac caa gaa 922
 His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn Gln Glu
 265 270

<210> 710

<211> 274

<212> PRT

<213> Corynebacterium glutamicum

<400> 710

Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
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Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
 20 25 30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
 35 40 45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
 50 55 60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65 70 75 80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
 85 90 95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
 100 105 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
 115 120 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
 130 135 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
 145 150 155 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
 165 170 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
 180 185 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
 195 200 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
 210 215 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
225 230 235 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
245 250 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Arg Cys Tyr Lys Asn
260 265 270

Gln Glu

<210> 711

<211> 870

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(847)

<223> RXA01311

<400> 711

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tcttcgaatc tgtcccactg cagacaagga actacaagta atg aaa ctt aca ctt 115
Met Lys Leu Thr Leu
1 5

gag atc tgg cgt caa gca ggc cca act gcg gaa ggc aag ttc gaa acc 163
Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu Gly Lys Phe Glu Thr
10 15 20

gtc cag gtt gac gac gcc gtc gcg cag atg tcc atc ctg gag ctg ctt 211
Val Gln Val Asp Ala Val Ala Gln Met Ser Ile Leu Glu Leu Leu
25 30 35

gac cac gta aac aac aag ttc atc gaa gaa ggc aaa gaa cca ttc gcg 259
Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly Lys Glu Pro Phe Ala
40 45 50

ttc gcc tct gac tgc cgc gaa ggc att tgt ggt acc tgt ggt ctc ctc 307
Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly Thr Cys Gly Leu Leu
55 60 65

gtg aac ggt cgc cct cac ggc gcc gac cag aac aag cct gcc tgt gcg 355
Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn Lys Pro Ala Cys Ala
70 75 80 85

cag cgc ctg gtc agc tac aag gaa ggc gac acc ctc aag atc gaa cca 403
Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr Leu Lys Ile Glu Pro
90 95 100

ctg cgt tcc gcc gca tac cca gtg atc aag gac atg gtc gtc gac cgc 451
Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp Met Val Val Asp Arg
105 110 115

tcc gca ctg gac cgt gtc atg gaa cag ggt ggc tac gtg acc atc aac 499
Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly Tyr Val Thr Ile Asn
120 125 130

gca ggt acc gca cct gac gct gat acc ctc cac gtc aac cac gaa acc 547
 Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His Val Asn His Glu Thr
 135 140 145
 gca gaa ctc gca ctt gac cac gca gcc tgc atc ggc tgt ggc gca tgt 595
 Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile Gly Cys Gly Ala Cys
 150 155 160 165
 gtt gct gcc tgc cct aac ggc gca gca cac ctg ttc acc ggc gca aag 643
 Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu Phe Thr Gly Ala Lys
 170 175 180
 ctt gtt cac ctc tcc ctc ctc cca ctg ggt aag gaa gag cgc gga ctg 691
 Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys Glu Glu Arg Gly Leu
 185 190 195
 cgt gca cgt aag atg gtt gat gaa atg gaa acc aac ttc gga cac tgc 739
 Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr Asn Phe Gly His Cys
 200 205 210
 tcc ctc tac ggc gag tgc gca gat gtc tgc ccc gca ggc atc cca ctg 787
 Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro Ala Gly Ile Pro Leu
 215 220 225
 acc gct gtg gca gct gtc acc aag gaa cgt gcg cgt gca gct ttc cga 835
 Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala Arg Ala Ala Phe Arg
 230 235 240 245
 ggc aaa gac gac tagtctttaa tcçaagtaag tac 870
 Gly Lys Asp Asp

<210> 712

<211> 249

<212> PRT

<213> Corynebacterium glutamicum

<400> 712

Met Lys Leu Thr Leu Glu Ile Trp Arg Gln Ala Gly Pro Thr Ala Glu
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 Gly Lys Phe Glu Thr Val Gln Val Asp Asp Ala Val Ala Gln Met Ser
 20 25 30
 Ile Leu Glu Leu Leu Asp His Val Asn Asn Lys Phe Ile Glu Glu Gly
 35 40 45
 Lys Glu Pro Phe Ala Phe Ala Ser Asp Cys Arg Glu Gly Ile Cys Gly
 50 55 60
 Thr Cys Gly Leu Leu Val Asn Gly Arg Pro His Gly Ala Asp Gln Asn
 65 70 75 80
 Lys Pro Ala Cys Ala Gln Arg Leu Val Ser Tyr Lys Glu Gly Asp Thr
 85 90 95
 Leu Lys Ile Glu Pro Leu Arg Ser Ala Ala Tyr Pro Val Ile Lys Asp
 100 105 110

Met Val Val Asp Arg Ser Ala Leu Asp Arg Val Met Glu Gln Gly Gly
 115 120 125

Tyr Val Thr Ile Asn Ala Gly Thr Ala Pro Asp Ala Asp Thr Leu His
 130 135 140

Val Asn His Glu Thr Ala Glu Leu Ala Leu Asp His Ala Ala Cys Ile
 145 150 155 160

Gly Cys Gly Ala Cys Val Ala Ala Cys Pro Asn Gly Ala Ala His Leu
 165 170 175

Phe Thr Gly Ala Lys Leu Val His Leu Ser Leu Leu Pro Leu Gly Lys
 180 185 190

Glu Glu Arg Gly Leu Arg Ala Arg Lys Met Val Asp Glu Met Glu Thr
 195 200 205

Asn Phe Gly His Cys Ser Leu Tyr Gly Glu Cys Ala Asp Val Cys Pro
 210 215 220

Ala Gly Ile Pro Leu Thr Ala Val Ala Ala Val Thr Lys Glu Arg Ala
 225 230 235 240

Arg Ala Ala Phe Arg Gly Lys Asp Asp
 245

<210> 713
 <211> 929
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (1)..(906)
 <223> RXN03014

<400> 713
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 Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt 144
 Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg 192
 Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc 240
 Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg 288
 Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu

85										90					95					
ccg	gac	tcc	tac	ccc	acc	gcg	cca	tcg	ctg	gtc	acc	gcg	gtg	ttc	gca	336				
Pro	Asp	Ser	Tyr	Pro	Thr	Ala	Pro	Ser	Leu	Val	Thr	Ala	Val	Phe	Ala					
100				105				110												
ggt	ctg	ttg	acc	aag	gtg	ggt	gtg	tat	tcc	atc	att	cga	gca	cgc	tcg	384				
Gly	Leu	Leu	Thr	Lys	Val	Gly	Val	Tyr	Ser	Ile	Ile	Arg	Ala	Arg	Ser					
115				120				125												
att	att	ttc	acc	gat	gga	tcc	ctt	gac	acc	atg	ctg	atg	tgg	gtg	gca	432				
Ile	Ile	Phe	Thr	Asp	Gly	Ser	Leu	Asp	Thr	Met	Leu	Met	Trp	Val	Ala					
130				135				140												
ctc	gcc	acc	atg	ctc	att	ggt	att	ttg	ggc	gcg	atg	gcg	caa	aac	gat	480				
Leu	Ala	Thr	Met	Leu	Ile	Gly	Ile	Leu	Gly	Ala	Met	Ala	Gln	Asn	Asp					
145				150				155				160								
atc	aaa	cgt	ttg	ttg	tca	ttt	act	ctg	gtc	agc	cac	atc	ggc	tac	atg	528				
Ile	Lys	Arg	Leu	Leu	Ser	Phe	Thr	Leu	Val	Ser	His	Ile	Gly	Tyr	Met					
165				170				175												
atc	ttc	ggc	gta	gcc	ctt	gga	tct	gca	cag	ggt	ttg	tct	ggt	gcg	atc	576				
Ile	Phe	Gly	Val	Ala	Leu	Gly	Ser	Ala	Gln	Gly	Leu	Ser	Gly	Ala	Ile					
180				185				190												
ttc	tac	gca	atc	cac	cac	att	ctg	gtt	cag	act	tcc	ctg	ttc	ctg	gtg	624				
Phe	Tyr	Ala	Ile	His	His	Ile	Leu	Val	Gln	Thr	Ser	Leu	Phe	Leu	Val					
195				200				205												
gtc	ggt	ctg	gtg	gaa	cgc	caa	gcc	gga	tcc	tcc	tcg	ctg	cga	cgc	ctt	672				
Val	Gly	Leu	Val	Glu	Arg	Gln	Ala	Gly	Ser	Ser	Ser	Leu	Arg	Arg	Leu					
210				215				220												
gga	tcc	ctg	gca	tat	atc	tcc	cca	ctt	ctt	gcg	att	ttg	tac	ttc	atc	720				
Gly	Ser	Leu	Ala	Tyr	Ile	Ser	Pro	Leu	Leu	Ala	Ile	Leu	Tyr	Phe	Ile					
225				230				235				240								
ccc	gcc	atc	aac	ctg	ggt	ggt	atc	cca	ccg	ttc	tcc	ggc	ttc	ctg	ggc	768				
Pro	Ala	Ile	Asn	Leu	Gly	Gly	Ile	Pro	Pro	Phe	Ser	Gly	Phe	Leu	Gly					
245				250				255												
aag	atc	atg	ctc	atc	gaa	gcc	ggc	gcc	cga	aga	tgg	cag	ttg	gct	ggc	816				
Lys	Ile	Met	Leu	Ile	Glu	Ala	Gly	Ala	Arg	Arg	Trp	Gln	Leu	Ala	Gly					
260				265				270												
atg	ggt	cct	tat	cgc	agg	cgc	cgt	tgt	cac	ctc	act	gct	cac	ctt	gta	864				
Met	Gly	Pro	Tyr	Arg	Arg	Arg	Arg	Cys	His	Leu	Thr	Ala	His	Leu	Val					
275				280				285												
cac	cat	ggt	tct	ggt	ctg	gtc	caa	ggc	ctt	ctg	gcg	cga	ccg			906				
His	His	Gly	Ser	Gly	Leu	Val	Gln	Gly	Leu	Leu	Ala	Arg	Pro							
290				295				300												
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<210> 714

<211> 302

<212> PRT

<213> Corynebacterium glutamicum

<400> 714

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Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
 245 250 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Arg Arg Trp Gln Leu Ala Gly
 260 265 270

Met Gly Pro Tyr Arg Arg Arg Arg Cys His Leu Thr Ala His Leu Val
 275 280 285

His His Gly Ser Gly Leu Val Gln Gly Leu Leu Ala Arg Pro
 290 295 300

<210> 715

<211> 1280

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (1)..(1257)

<223> FRXA00910

<400> 715

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1 5 10 15	
ttg ggt gca tcg ccg gca cgt gta cgt tcc ggc gtg ggt tac gtg atg	96
Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met	
20 25 30	
gtg tcc atg gcg tca tcg atg gtg ttc ctg ttt gga ctc gca atg gtt	144
Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val	
35 40 45	
tac gcc tca gtg ggc acg ttg aac atg gct cac gtt ggc cta cgc atg	192
Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met	
50 55 60	
gaa gat gtt ccg tct gga act cgc tcc gcg atc ttc gca gtg ttg ctc	240
Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu	
65 70 75 80	
gtg gca ttc ggt att aaa gct gcc gtg ttc ccc cta gat tcc tgg ctg	288
Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu	
85 90 95	
ccg gac tcc tac ccc acc gcg cca tcg ctg gtc acc gcg gtg ttc gca	336
Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala	
100 105 110	
ggt ctg ttg acc aag gtg ggt gtg tat tcc atc att cga gca cgc tcg	384
Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser	
115 120 125	
att att ttc acc gat gga tcc ctt gac acc atg ctg atg tgg gtg gca	432
Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala	
130 135 140	
ctc gcc acc atg ctc att ggt att ttg ggc gcg atg gcg caa aac gat	480
Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp	
145 150 155 160	
atc aaa cgt ttg ttg tca ttt act ctg gtc agc cac atc ggc tac atg	528
Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met	
165 170 175	
atc ttc ggc gta gcc ctt gga tct gca cag ggt ttg tct ggt gcg atc	576
Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile	
180 185 190	
ttc tac gca atc cac cac att ctg gtt cag act tcc ctg ttc ctg gtg	624
Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val	
195 200 205	

gtc ggt ctg gtg gaa cgc caa gcc gga tcc tcc tcg ctg cga cgc ctt	672
Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu	
210 215 220	
gga tcc ctg gca tat atc tcc cca ctt ctt gcg att ttg tac ttc atc	720
Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile	
225 230 235 240	
ccc gcc atc aac ctg ggt ggt atc cca ccg ttc tcc ggc ttc ctg ggc	768
Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly	
245 250 255	
aag atc atg ctc atc gaa gcc ggc gcc gaa gat ggc agt tgg ctg gca	816
Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala	
260 265 270	
tgg gtc ctt atc gca ggc gcc gtt gtc acc tca ctg ctc acc ttg tac	864
Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr	
275 280 285	
acc atg gtt ctg gtc tgg tcc aag gcc ttc tgg cgc gac cgt aaa gac	912
Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp	
290 295 300	
gcc ccc gat gga gca acc gca ctt gcg cga ccc gca cct ttg gta gat	960
Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp	
305 310 315 320	
gtc caa gac gaa gtc gcc gtt aaa gac cgc aac gat gtc gga cgg atg	1008
Val Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met	
325 330 335	
cct tgg ggc atg gtc ttc tcc act gct ctc ctg gtt tca gca tct ctt	1056
Pro Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu	
340 345 350	
gct gta tcc gtg ctc gca gga cca ctg tca tct att act gga cgc gcc	1104
Ala Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala	
355 360 365	
gcc gaa tcc gca caa gat gtc aac atc tac cgc gcc gca gta ctc ggc	1152
Ala Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly	
370 375 380	
ccc aac tac ctc gac cca tca cgc aca ctc gag atg gag cgt tac gac	1200
Pro Asn Tyr Leu Asp Pro Ser Arg Thr Leu Glu Met Glu Arg Tyr Asp	
385 390 395 400	
gcc aac cgc gat gac atc aac cac cgc gtc gac acc aac gga acg gag	1248
Ala Asn Arg Asp Asp Ile Asn His Arg Val Asp Thr Asn Gly Thr Glu	
405 410 415	
gac caa cca tgatcagtggt attcaaacga cga	1280
Asp Gln Pro	

<210> 716

<211> 419

<212> PRT

<213> Corynebacterium glutamicum

<400> 716

Tyr Val Gly Phe Glu Val Leu Leu Val Ala Ser Tyr Val Leu Leu Thr
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Leu Gly Ala Ser Pro Ala Arg Val Arg Ser Gly Val Gly Tyr Val Met
 20 25 30

Val Ser Met Ala Ser Ser Met Val Phe Leu Phe Gly Leu Ala Met Val
 35 40 45

Tyr Ala Ser Val Gly Thr Leu Asn Met Ala His Val Gly Leu Arg Met
 50 55 60

Glu Asp Val Pro Ser Gly Thr Arg Ser Ala Ile Phe Ala Val Leu Leu
 65 70 75 80

Val Ala Phe Gly Ile Lys Ala Ala Val Phe Pro Leu Asp Ser Trp Leu
 85 90 95

Pro Asp Ser Tyr Pro Thr Ala Pro Ser Leu Val Thr Ala Val Phe Ala
 100 105 110

Gly Leu Leu Thr Lys Val Gly Val Tyr Ser Ile Ile Arg Ala Arg Ser
 115 120 125

Ile Ile Phe Thr Asp Gly Ser Leu Asp Thr Met Leu Met Trp Val Ala
 130 135 140

Leu Ala Thr Met Leu Ile Gly Ile Leu Gly Ala Met Ala Gln Asn Asp
 145 150 155 160

Ile Lys Arg Leu Leu Ser Phe Thr Leu Val Ser His Ile Gly Tyr Met
 165 170 175

Ile Phe Gly Val Ala Leu Gly Ser Ala Gln Gly Leu Ser Gly Ala Ile
 180 185 190

Phe Tyr Ala Ile His His Ile Leu Val Gln Thr Ser Leu Phe Leu Val
 195 200 205

Val Gly Leu Val Glu Arg Gln Ala Gly Ser Ser Ser Leu Arg Arg Leu
 210 215 220

Gly Ser Leu Ala Tyr Ile Ser Pro Leu Leu Ala Ile Leu Tyr Phe Ile
 225 230 235 240

Pro Ala Ile Asn Leu Gly Gly Ile Pro Pro Phe Ser Gly Phe Leu Gly
 245 250 255

Lys Ile Met Leu Ile Glu Ala Gly Ala Glu Asp Gly Ser Trp Leu Ala
 260 265 270

Trp Val Leu Ile Ala Gly Ala Val Val Thr Ser Leu Leu Thr Leu Tyr
 275 280 285

Thr Met Val Leu Val Trp Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp
 290 295 300

Ala Pro Asp Gly Ala Thr Ala Leu Ala Arg Pro Ala Pro Leu Val Asp

<400> 717																
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cacaagcttt	aagatccacg	atcaggagac	tttgacaaat	atg	tca	ggt	aac	cca	115							
				Met	Ser	Val	Asn	Pro								
				1				5								
acc	cgc	ccc	gaa	ggc	ggc	cgt	cac	cac	gtc	gtc	gtc	atc	ggg	tct	ggg	163
Thr	Arg	Pro	Glu	Gly	Gly	Arg	His	His	Val	Val	Val	Ile	Gly	Ser	Gly	
				10					15					20		
ttt	ggg	ggc	ctt	ttt	gct	gcc	aag	aac	ctg	gcc	aag	gca	gac	gtc	gat	211
Phe	Gly	Gly	Leu	Phe	Ala	Ala	Lys	Asn	Leu	Ala	Lys	Ala	Asp	Val	Asp	
			25					30					35			
gtc	act	ctg	att	gac	cgc	acc	aac	cac	cac	ctc	ttc	cag	cca	ctg	ctg	259
Val	Thr	Leu	Ile	Asp	Arg	Thr	Asn	His	His	Leu	Phe	Gln	Pro	Leu	Leu	
		40					45					50				
tac	caa	gtg	gca	acc	ggg	atc	ctc	tcc	tcc	ggg	gaa	atc	gca	cct	tcc	307
Tyr	Gln	Val	Ala	Thr	Gly	Ile	Leu	Ser	Ser	Gly	Glu	Ile	Ala	Pro	Ser	
	55					60					65					
act	cga	cag	atc	ctg	ggc	tcc	cag	gaa	aac	gtc	aac	gtc	atc	aag	ggc	355
Thr	Arg	Gln	Ile	Leu	Gly	Ser	Gln	Glu	Asn	Val	Asn	Val	Ile	Lys	Gly	
70					75				80						85	

gaa gtc acc gac atc aac gtc gag tcc cag act gtg acc gcc tcc ctg	403
Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr Val Thr Ala Ser Leu	
90 95 100	
ggc gag ttc acc cgc gtt ttt gag tac gat tcc ttg gtc gtt ggt gct	451
Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser Leu Val Val Gly Ala	
105 110 115	
ggc gca ggt cag tcc tac ttc ggc aat gat cac ttc gct gag ttc gca	499
Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His Phe Ala Glu Phe Ala	
120 125 130	
cct ggc atg aag tcc atc gac gat gca ctg gag att cgt gca cgc atc	547
Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu Ile Arg Ala Arg Ile	
135 140 145	
atc ggt gct ttc gag cgc gct gag atc tgc gag gat cca gct gag cgc	595
Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu Asp Pro Ala Glu Arg	
150 155 160 165	
gaa cgc ctg ctc acc ttc gtc gtt gtt ggc gct ggc cca acc ggt gtt	643
Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala Gly Pro Thr Gly Val	
170 175 180	
gag ctt gct ggc cag ttg gct gag atg gct cac cgc acc ctt gct ggt	691
Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His Arg Thr Leu Ala Gly	
185 190 195	
gag tac aag aac ttc aac acc aac tcc gca aag atc atc ctg ctt gat	739
Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys Ile Ile Leu Leu Asp	
200 205 210	
ggt gct cca cag gtt ctt cct cca ttc ggt aag cgc cta ggc cgc aac	787
Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys Arg Leu Gly Arg Asn	
215 220 225	
gca cag cgc acc ctg gaa aag atg ggt gtc aac gtt cgc ctg aac gct	835
Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn Val Arg Leu Asn Ala	
230 235 240 245	
atg gtc acc aac gtt gac gct acc tcg gtc acc tac aag acc aag gac	883
Met Val Thr Asn Val Asp Ala Thr Ser Val Thr Tyr Lys Thr Lys Asp	
250 255 260	
ggc gaa gag cac acc atc gaa tct ttc tgc aag att tgg tcc gct ggt	931
Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys Ile Trp Ser Ala Gly	
265 270 275	
gtt gcg gca tcc cca ctg ggc aag ctc gtc gca gag cag acc ggt gtt	979
Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala Glu Gln Thr Gly Val	
280 285 290	
gag acc gac cgc gca ggc cgc gtc atg gtt aac gat gac ctg tct gtt	1027
Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn Asp Asp Leu Ser Val	
295 300 305	
ggc gat cag aag aac gtc ttc gtt	1051
Gly Asp Gln Lys Asn Val Phe Val	
310 315	

<210> 718

<211> 317

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 718

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Met Ser Val Asn Pro Thr Arg Pro Glu Gly Gly Arg His His Val Val
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Val Ile Gly Ser Gly Phe Gly Gly Leu Phe Ala Ala Lys Asn Leu Ala
      20           25           30

Lys Ala Asp Val Asp Val Thr Leu Ile Asp Arg Thr Asn His His Leu
      35           40           45

Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu Ser Ser Gly
      50           55           60

Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln Glu Asn Val
      65           70           75           80

Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu Ser Gln Thr
      85           90           95

Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu Tyr Asp Ser
      100          105          110

Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly Asn Asp His
      115          120          125

Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp Ala Leu Glu
      130          135          140

Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu Ile Cys Glu
      145          150          155          160

Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val Val Gly Ala
      165          170          175

Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu Met Ala His
      180          185          190

Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn Ser Ala Lys
      195          200          205

Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro Phe Gly Lys
      210          215          220

Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met Gly Val Asn
      225          230          235          240

Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr Ser Val Thr
      245          250          255

Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser Phe Cys Lys
      260          265          270

Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys Leu Val Ala
      275          280          285

Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val Met Val Asn

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Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
305              310              315

<210> 719
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(816)
<223> FRXA01895

<400> 719
cac cac ctc ttc cag cca ctg ctg tac caa gtg gca acc ggt atc ctc 48
His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
1              5              10              15

tcc tcc ggt gaa atc gca cct tcc act cga cag atc ctg ggc tcc cag 96
Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
20              25              30

gaa aac gtc aac gtc atc aag ggc gaa gtc acc gac atc aac gtc gag 144
Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
35              40              45

tcc cag act gtg acc gcc tcc ctg ggc gag ttc acc cgc gtt ttt gag 192
Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
50              55              60

tac gat tcc ttg gtc gtt ggt gct ggc gca ggt cag tcc tac ttc ggc 240
Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
65              70              75              80

aat gat cac ttc gct gag ttc gca cct ggc atg aag tcc atc gac gat 288
Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
85              90              95

gca ctg gag att cgt gca cgc atc atc ggt gct ttc gag cgc gct gag 336
Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
100              105              110

atc tgc gag gat cca gct gag cgc gaa cgc ctg ctc acc ttc gtc gtt 384
Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
115              120              125

gtt ggc gct ggc cca acc ggt gtt gag ctt gct ggc cag ttg gct gag 432
Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
130              135              140

atg gct cac cgc acc ctt gct ggt gag tac aag aac ttc aac acc aac 480
Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
145              150              155              160

tcc gca aag atc atc ctg ctt gat ggt gct cca cag gtt ctt cct cca 528
Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
165              170              175

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ttc ggt aag cgc cta ggc cgc aac gca cag cgc acc ctg gaa aag atg 576
 Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
 180 185 190

ggt gtc aac gtt cgc ctg aac gct atg gtc acc aac gtt gac gct acc 624
 Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
 195 200 205

tcg gtc acc tac aag acc aag gac ggc gaa gag cac acc atc gaa tct 672
 Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
 210 215 220

ttc tgc aag att tgg tcc gct ggt gtt gcg gca tcc cca ctg ggc aag 720
 Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
 225 230 235 240

ctc gtc gca gag cag acc ggt gtt gag acc gac cgc gca ggc cgc gtc 768
 Leu Val Ala Glu Gln Thr Gly Val Glu Thr Asp Arg Ala Gly Arg Val
 245 250 255

atg gtt aac gat gac ctg tct gtt ggc gat cag aag aac gtc ttc gtt 816
 Met Val Asn Asp Asp Leu Ser Val Gly Asp Gln Lys Asn Val Phe Val
 260 265 270

<210> 720

<211> 272

<212> PRT

<213> Corynebacterium glutamicum

<400> 720

His His Leu Phe Gln Pro Leu Leu Tyr Gln Val Ala Thr Gly Ile Leu
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Ser Ser Gly Glu Ile Ala Pro Ser Thr Arg Gln Ile Leu Gly Ser Gln
 20 25 30

Glu Asn Val Asn Val Ile Lys Gly Glu Val Thr Asp Ile Asn Val Glu
 35 40 45

Ser Gln Thr Val Thr Ala Ser Leu Gly Glu Phe Thr Arg Val Phe Glu
 50 55 60

Tyr Asp Ser Leu Val Val Gly Ala Gly Ala Gly Gln Ser Tyr Phe Gly
 65 70 75 80

Asn Asp His Phe Ala Glu Phe Ala Pro Gly Met Lys Ser Ile Asp Asp
 85 90 95

Ala Leu Glu Ile Arg Ala Arg Ile Ile Gly Ala Phe Glu Arg Ala Glu
 100 105 110

Ile Cys Glu Asp Pro Ala Glu Arg Glu Arg Leu Leu Thr Phe Val Val
 115 120 125

Val Gly Ala Gly Pro Thr Gly Val Glu Leu Ala Gly Gln Leu Ala Glu
 130 135 140

Met Ala His Arg Thr Leu Ala Gly Glu Tyr Lys Asn Phe Asn Thr Asn
 145 150 155 160

Ser Ala Lys Ile Ile Leu Leu Asp Gly Ala Pro Gln Val Leu Pro Pro
 165 170 175

Phe Gly Lys Arg Leu Gly Arg Asn Ala Gln Arg Thr Leu Glu Lys Met
 180 185 190

Gly Val Asn Val Arg Leu Asn Ala Met Val Thr Asn Val Asp Ala Thr
 195 200 205

Ser Val Thr Tyr Lys Thr Lys Asp Gly Glu Glu His Thr Ile Glu Ser
 210 215 220

Phe Cys Lys Ile Trp Ser Ala Gly Val Ala Ala Ser Pro Leu Gly Lys
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 Asp Val Gly Arg Arg Ile Thr Ser Ala Ala Gly Val Pro Gly Val Leu
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 His Ala Leu Gln His Ala Val Pro Asn Arg Ala Leu Leu Pro Leu Leu
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 Thr Met Asn Lys Pro Gly Gly Ile Asp Cys Pro Gly Cys Ala Trp Pro
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Trp Leu Gly Lys Arg Gly Arg Ile Thr Glu Pro Met Phe Tyr Asp Arg	
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Ser Ser Gly Asp Asp His Tyr Arg Pro Ile Ser Trp Asp Arg Ala Phe	
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Ala Ile Ile Ala Ser Lys Leu Arg Glu Ile Glu Pro Asp Glu Ala Val	
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Ala Pro Leu Arg Gly His Ser Asn Val Gln Gly Asp Arg Thr Met Gly	
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Ile Trp Glu Lys Met Pro Glu Ala Phe Leu Ala Ala Leu Glu Asn Glu	
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 Pro Asp Glu Ala Val Phe Tyr Thr Ser Gly Arg Ala Pro Asn Glu Pro
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 Ala Tyr Met Leu Gln Leu Leu Ala Arg Arg Leu Gly Thr Asn Asn Leu
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 Pro Asp Cys Gly Asn Met Cys His Glu Ser Thr Gly Thr Ala Leu Gly
 195 200 205
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Ser	Thr	Ile	Tyr	Gly	Leu	Asp	Asp	Arg	Tyr	Arg	Gly	Val	Arg	Asn	Gly				
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Lys Asp Gly Asp Ile Val Asp Ile Val Ser Val Phe Asp Asp Gly Glu
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Cys Val Thr Thr Tyr Phe Pro Glu Ala Asn Val Leu Val Pro Leu Asp
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gat att gag ttg gtg cat ggc ctc ctc ttg tca gaa ggt ctg atc acg 307
 Asp Ile Glu Leu Val His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr
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 Asp Ala Ser Glu Val Phe Thr Ala Arg Tyr Cys Ala Gly Ala Val Gly
 70 75 80 85

cca gat aat caa aat acg tac aac gtc tta gaa ctt gat gtc atc ccc 403
 Pro Asp Asn Gln Asn Thr Tyr Asn Val Leu Glu Leu Asp Val Ile Pro
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gaa ggc agc caa cac gaa gca ctc cac atc cca act ttc caa ccg gta 499
Glu Gly Ser Gln His Glu Ala Leu His Ile Pro Thr Phe Gln Pro Val
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cgc gaa cta aac ctc gtg gca gcc caa cgc aat gtg ctg act acg tct 547
Arg Glu Leu Asn Leu Val Ala Ala Gln Arg Asn Val Leu Thr Thr Ser
135 140 145

gct tgt ggt gtt tgt ggc acg acg tct att gag cag ttg atg aac aag 595
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aag ggc tgg ccc att acg ccg att aca ccg gat cct cgg atg att gtg 643
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170 175 180

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Ile Ile Arg Glu Asp Val Gly Arg His Asn Ala Ala Asp Lys Val Ile
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gga aac atg ctg atg gcg gga aag ctc ccc ttg gaa aac act att ttg 835
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 Asp Thr Val Ala Val Glu Glu Pro Leu Glu Ile Arg Val Asn Gly Thr
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 Ala Leu Thr Thr Thr Met Arg Thr Pro Gly His Asp Ile Glu Leu Val
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 His Gly Leu Leu Leu Ser Glu Gly Leu Ile Thr Asp Ala Ser Glu Val
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 145 150 155 160
 acg ccg att aca ccg gat cct cgg atg att gtg tcg ttg cca gat aag 528
 Thr Pro Ile Thr Pro Asp Pro Arg Met Ile Val Ser Leu Pro Asp Lys
 165 170 175
 ttg aag tcg aag cag aag att ttc gac aaa act ggt ggg gtt cat gct 576
 Leu Lys Ser Lys Gln Lys Ile Phe Asp Lys Thr Gly Gly Val His Ala
 180 185 190
 gct ggt ttg gcc acg ctt gat ggt gag atg ttg att att cga gag gat 624
 Ala Gly Leu Ala Thr Leu Asp Gly Glu Met Leu Ile Ile Arg Glu Asp

195	200	205	
gtc ggt cgg cat aac gca gct gac aaa gtt ata gga aac atg ctg atg			672
Val Gly Arg His Asn Ala Ala Asp Lys Val Ile Gly Asn Met Leu Met			
210	215	220	
gcg gga aag ctc ccc ttg gaa aac act att ttg gtg atg agt tct agg			720
Ala Gly Lys Leu Pro Leu Glu Asn Thr Ile Leu Val Met Ser Ser Arg			
225	230	235	240
gcg tct ttt gag ctt gtc caa aag gct gcc atg gct gga att tcg ggt			768
Ala Ser Phe Glu Leu Val Gln Lys Ala Ala Met Ala Gly Ile Ser Gly			
245	250	255	
gta atc gct gtt ggt gct gca aca tcg ctg gca atc gag gcg gcg cag			816
Val Ile Ala Val Gly Ala Ala Thr Ser Leu Ala Ile Glu Ala Ala Gln			
260	265	270	
gat tca ggt att ttc ctt gct ggt ttt gtt cgg ggc aac aag ttt aac			864
Asp Ser Gly Ile Phe Leu Ala Gly Phe Val Arg Gly Asn Lys Phe Asn			
275	280	285	
cac tat gcg ggc gag ctc gga taatgccaga acaggtagaa cag			~ 908
His Tyr Ala Gly Glu Leu Gly			
290	295		

<210> 726

<211> 295

<212> PRT

<213> Corynebacterium glutamicum

<400> 726

Pro	Arg	Val	Val	Ser	Thr	Asp	Glu	Gln	Val	Phe	Val	Asn	Thr	Arg	Pro
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Asp	Thr	Val	Ala	Val	Glu	Glu	Pro	Leu	Glu	Ile	Arg	Val	Asn	Gly	Thr
		20						25					30		

Ala	Leu	Thr	Thr	Thr	Met	Arg	Thr	Pro	Gly	His	Asp	Ile	Glu	Leu	Val
		35					40					45			

His	Gly	Leu	Leu	Leu	Ser	Glu	Gly	Leu	Ile	Thr	Asp	Ala	Ser	Glu	Val
	50					55					60				

Phe	Thr	Ala	Arg	Tyr	Cys	Ala	Gly	Ala	Val	Gly	Pro	Asp	Asn	Gln	Asn
65					70					75				80	

Thr	Tyr	Asn	Val	Leu	Glu	Leu	Asp	Val	Ile	Pro	Lys	Asp	Asn	Pro	Ala
		85						90						95	

Arg	Asp	Pro	Val	Gln	Asn	Pro	Ser	His	Asn	Pro	Glu	Gly	Ser	Gln	His
		100						105					110		

Glu	Ala	Leu	His	Ile	Pro	Thr	Phe	Gln	Pro	Val	Arg	Glu	Leu	Asn	Leu
	115						120					125			

Val	Ala	Ala	Gln	Arg	Asn	Val	Leu	Thr	Thr	Ser	Ala	Cys	Gly	Val	Cys
	130					135					140				

Gly	Thr	Thr	Ser	Ile	Glu	Gln	Leu	Met	Asn	Lys	Lys	Gly	Trp	Pro	Ile
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

<400> 727																
gaagagtact tgcaccacga cgactaacac cgcaatttaa aggccttttca agcctgcccc																60
acatcgaagc agttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac																115
Met Leu Pro Val Asn																
1 5																
caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc																163
Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile																
10 15 20																
atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa																211
Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln																
25 30 35																
caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc																259
Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu																
40 45 50																
gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac																307
Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp																

55	60	65	
atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu 70 75 80 85			355
acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly 90 95 100			403
gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser 105 110 115			451
cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu 120 125 130			499
ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg 135 140 145			547
gtg gta tgg cca tgg atc ctc acc cca atg ctg gca ctg ctc ttc tac Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu Ala Leu Leu Phe Tyr 150 155 160 165			595
ggt ggc acc cag ctg tac tcc gac gca gca cca gtc gtt cca gca ctg Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro Val Val Pro Ala Leu 170 175 180			643
cag tcc ttc tgg ttc ccg atc cac gtt tcc tcc gtc tcc atc ggc gca Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser Val Ser Ile Gly Ala 185 190 195			691
tcc atc ggt atc gtc tcc ggt att gca tcc ctg ctg tac ata ctg cgc Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu Leu Tyr Ile Leu Arg 200 205 210			739
atg tgg caa cca aag ggt aaa gaa aag ggc ttc ttc ggc gca gta gca Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe Phe Gly Ala Val Ala 215 220 225			787
aaa cca ctc cca tcc gga aaa acc ctg gat aac ctg gca tac aag acc Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn Leu Ala Tyr Lys Thr 230 235 240 245			835
gcg atc tgg act gtc cca atc ttc ggc ctg ggc atc atc ttg ggt gcc Ala Ile Trp Thr Val Pro Ile Phe Gly Leu Gly Ile Ile Leu Gly Ala 250 255 260			883
atc tgg gca gaa gca gcc tgg ggt cgt ttc tgg gga tgg gat cct aag Ile Trp Ala Glu Ala Ala Trp Gly Arg Phe Trp Gly Trp Asp Pro Lys 265 270 275			931
gaa aca gtc tcc ttc atc acc tgg gtt ctc tac gct ggt tac ctc cac Glu Thr Val Ser Phe Ile Thr Trp Val Leu Tyr Ala Gly Tyr Leu His 280 285 290			979
gca cgt gca act gct ggt tgg cgc aac acc aac gct gca tgg atc aac Ala Arg Ala Thr Ala Gly Trp Arg Asn Thr Asn Ala Ala Trp Ile Asn 295 300 305			1027

atc ctg gcg ctg gtc acg atg att ttt aat ctg ttc ttc atc aac atg 1075
 Ile. Leu Ala Leu Val Thr Met Ile Phe Asn Leu Phe Phe Ile Asn Met
 310 315 320 325

gtc gta tct ggt ctg cac tct tac gcc gga ctg aac taagcacttt 1121
 Val Val Ser Gly Leu His Ser Tyr Ala Gly Leu Asn
 330 335

tggttggcgg ggt 1134

<210> 728

<211> 337

<212> PRT

<213> Corynebacterium glutamicum

<400> 728

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Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
 35 40 45

Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr
 50 55 60

Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu
 65 70 75 80

Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser
 85 90 95

Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg
 100 105 110

Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile
 115 120 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln
 130 135 140

Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Leu
 145 150 155 160

Ala Leu Leu Phe Tyr Gly Gly Thr Gln Leu Tyr Ser Asp Ala Ala Pro
 165 170 175

Val Val Pro Ala Leu Gln Ser Phe Trp Phe Pro Ile His Val Ser Ser
 180 185 190

Val Ser Ile Gly Ala Ser Ile Gly Ile Val Ser Gly Ile Ala Ser Leu
 195 200 205

Leu Tyr Ile Leu Arg Met Trp Gln Pro Lys Gly Lys Glu Lys Gly Phe
 210 215 220

Phe Gly Ala Val Ala Lys Pro Leu Pro Ser Gly Lys Thr Leu Asp Asn

<400> 729																
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Thr	Leu	Asp	Asn	Leu	Ala	Tyr	Lys	Thr	Ala	Ile	Trp	Thr	Val	Pro	Ile	
1				5					10					15		
ttc	ggc	ctg	ggc	atc	atc	ttg	ggt	gcc	atc	tgg	gca	gaa	gca	gcc	tgg	96
Phe	Gly	Leu	Gly	Ile	Ile	Leu	Gly	Ala	Ile	Trp	Ala	Glu	Ala	Ala	Trp	
			20					25					30			
ggt	cgt	ttc	tgg	gga	tgg	gat	cct	aag	gaa	aca	gtc	tcc	ttc	atc	acc	144
Gly	Arg	Phe	Trp	Gly	Trp	Asp	Pro	Lys	Glu	Thr	Val	Ser	Phe	Ile	Thr	
		35					40					45				
tgg	gtt	ctc	tac	gct	ggt	tac	ctc	cac	gca	cgt	gca	act	gct	ggt	tgg	192
Trp	Val	Leu	Tyr	Ala	Gly	Tyr	Leu	His	Ala	Arg	Ala	Thr	Ala	Gly	Trp	
	50					55					60					
cgc	aac	acc	aac	gct	gca	tgg	atc	aac	atc	ctg	gcg	ctg	gtc	acg	atg	240
Arg	Asn	Thr	Asn	Ala	Ala	Trp	Ile	Asn	Ile	Leu	Ala	Leu	Val	Thr	Met	
65					70					75					80	
att	ttt	aat	ctg	ttc	ttc	atc	aac	atg	gtc	gta	tct	ggt	ctg	cac	tct	288
Ile	Phe	Asn	Leu	Phe	Phe	Ile	Asn	Met	Val	Val	Ser	Gly	Leu	His	Ser	
				85					90					95		
tac	gcc	gga	ctg	aac	taagcacttt tggttggcgg ggt										326	
Tyr	Ala	Gly	Leu	Asn												

100

<210> 730
 <211> 101
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 730
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 Phe Gly Leu Gly Ile Ile Leu Gly Ala Ile Trp Ala Glu Ala Ala Trp
 20 25 30
 Gly Arg Phe Trp Gly Trp Asp Pro Lys Glu Thr Val Ser Phe Ile Thr
 35 40 45
 Trp Val Leu Tyr Ala Gly Tyr Leu His Ala Arg Ala Thr Ala Gly Trp
 50 55 60
 Arg Asn Thr Asn Ala Ala Trp Ile Asn Ile Leu Ala Leu Val Thr Met
 65 70 75 80
 Ile Phe Asn Leu Phe Phe Ile Asn Met Val Val Ser Gly Leu His Ser
 85 90 95
 Tyr Ala Gly Leu Asn
 100

<210> 731
 <211> 610
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(610)
 <223> FRXA00386

<400> 731
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 acatcgaagc agtttttcaca aagaataagg ttggaaaatt atg ttg ccc gtc aac 115
 Met Leu Pro Val Asn
 1 5
 caa acg tat gcg cag ttc tca gac act gcc ttc gta tcg gca tac atc 163
 Gln Thr Tyr Ala Gln Phe Ser Asp Thr Ala Phe Val Ser Ala Tyr Ile
 10 15 20
 atc tac gtt ctg gca ctc atc ctc tcc ctc gtc tac tac gta aaa caa 211
 Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val Tyr Tyr Val Lys Gln
 25 30 35
 caa ggc att atc gac gcc cgc cgc gag caa acc cgc gtc agc gaa ctc 259
 Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr Arg Val Ser Glu Leu
 40 45 50
 gtt ggt gca ggc ggc agc gct gat gtt gat act gac ctg cct gat gac 307

Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr Asp Leu Pro Asp Asp
 55 60 65
 atc gcc gac ggt gtc ctc gcc gac gaa gac ctt gca aaa cgc gaa gaa 355
 Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu Ala Lys Arg Glu Glu
 70 75 80 85
 acc gca cgc aaa cta gcc aac atg acc caa tct ctc atg tgg ctc ggc 403
 Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser Leu Met Trp Leu Gly
 90 95 100
 gtc atg gtg cac ctc gta tcc gtc gtg atg cgc gcg ctg tct gcc agc 451
 Val Met Val His Leu Val Ser Val Val Met Arg Ala Leu Ser Ala Ser
 105 110 115
 cga ttc ccc ttc ggc aac ctg tat gaa tac atc ctc atg gtc acc ctc 499
 Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile Leu Met Val Thr Leu
 120 125 130
 ttc gcc atg atc gga gcc gta ctc atc ctg cag cgc cca caa ttc cgc 547
 Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln Arg Pro Gln Phe Arg
 135 140 145
 gtg gta tgg cca tgg atc ctc acc cca atg gct ggc act tgg ttt tct 595
 Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala Gly Thr Trp Phe Ser
 150 155 160 165
 acg gtg gca ccc agc 610
 Thr Val Ala Pro Ser
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<210> 732
 <211> 170
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 732
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 Val Ser Ala Tyr Ile Ile Tyr Val Leu Ala Leu Ile Leu Ser Leu Val
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 Tyr Tyr Val Lys Gln Gln Gly Ile Ile Asp Ala Arg Arg Glu Gln Thr
 35 40 45
 Arg Val Ser Glu Leu Val Gly Ala Gly Gly Ser Ala Asp Val Asp Thr
 50 55 60
 Asp Leu Pro Asp Asp Ile Ala Asp Gly Val Leu Ala Asp Glu Asp Leu
 65 70 75 80
 Ala Lys Arg Glu Glu Thr Ala Arg Lys Leu Ala Asn Met Thr Gln Ser
 85 90 95
 Leu Met Trp Leu Gly Val Met Val His Leu Val Ser Val Val Met Arg
 100 105 110
 Ala Leu Ser Ala Ser Arg Phe Pro Phe Gly Asn Leu Tyr Glu Tyr Ile
 115 120 125

Leu Met Val Thr Leu Phe Ala Met Ile Gly Ala Val Leu Ile Leu Gln
 130 135 140

Arg Pro Gln Phe Arg Val Val Trp Pro Trp Ile Leu Thr Pro Met Ala
 145 150 155 160

Gly Thr Trp Phe Ser Thr Val Ala Pro Ser
 165 170

<210> 733

<211> 1095

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1072)

<223> RXA00945

<400> 733

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ttcccggtgt ttgaggcgat tgcaccgtac actaatgtgc atg ctt gaa cgc ctc 115
 Met Leu Glu Arg Leu
 1 5

aaa cgc cta gat ccg ctc att gtc ctc att gtg ctg gct gtc att gtg 163
 Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val Leu Ala Val Ile Val
 10 15 20

gcg atc atc att cca gtt cgc ggg gtt gct gcg gat tgg ttt gat gtc 211
 Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala Asp Trp Phe Asp Val
 25 30 35

gcc gtc aag att gcc att gcg ctg ctg ttt ttt ctt tat ggt gcc cgc 259
 Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe Leu Tyr Gly Ala Arg
 40 45 50

cta tcc acc caa gag gcg ctg aat ggt ctg aag cac tgg agg ctt cac 307
 Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys His Trp Arg Leu His
 55 60 65

ctg act att ttg gcg atc act ttc gga ata ttc cca ctt atc ggc att 355
 Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe Pro Leu Ile Gly Ile
 70 75 80 85

ggg ctc gag ccg atg act gca ttt gtg tcg gaa gat att tat cgg gga 403
 Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu Asp Ile Tyr Arg Gly
 90 95 100

att ttg ttc ctc acg ctc gtt ccg tcc acc gtg cag tca tcg gtg gcg 451
 Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val Gln Ser Ser Val Ala
 105 110 115

ttt acc tcg atc gct aaa ggc aac gta gct ggt gcg att gtg tcg gca 499
 Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly Ala Ile Val Ser Ala
 120 125 130

tcg ctc tcc aac ctt gcg ggt gtt ttc ctc act ccg ctg ctg gtc atg 547

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Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr Pro Leu Leu Val Met
 135                               140               145

ctc atc atg tct gcg ggc ggg gga gtt cac gtg gat tcc cag gtc ttc   595
Leu Ile Met Ser Ala Gly Gly Gly Val His Val Asp Ser Gln Val Phe
150                               155               160               165

ctc gac att gcg att cag ctt ctg ctg ccg ttc atc ctc ggc cag gta   643
Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe Ile Leu Gly Gln Val
                               170               175               180

tgt agg cgt tgg gtg aag aat ttt gcg gcc aac aaa gca aca aaa atc   691
Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn Lys Ala Thr Lys Ile
                               185               190               195

gtg gac cgc ggc tcg atc gcg atg gtc gtg tac tcc gcg ttt tct gcc   739
Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr Ser Ala Phe Ser Ala
                               200               205               210

ggc atg gtg gct ggc att tgg tcc act gtg agc gtt cta gag att atc   787
Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser Val Leu Glu Ile Ile
                               215               220               225

tac ctc att gtt ttc gct att ctg ctg gtg atg gcc atg ctg tgg ttc   835
Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met Ala Met Leu Trp Phe
230                               235               240               245

acg ctg ttc atg gct aca cgc ctt gga ttt aac cgg gca gat tcc atc   883
Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn Arg Ala Asp Ser Ile
                               250               255               260

gct att cag ttc tgc gga acc aag aaa tcc ctg gcc aca ggc ctc cca   931
Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu Ala Thr Gly Leu Pro
                               265               270               275

atg gcg gca gtc atc ttc ggt ggc gcc aat atc ggc ctg ctc atc ttg   979
Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile Gly Leu Leu Ile Leu
                               280               285               290

ccg ttg atg atc ttc cac caa gtc cag ctg atg att tgt gca tgg ctt   1027
Pro Leu Met Ile Phe His Gln Val Gln Leu Met Ile Cys Ala Trp Leu
                               295               300               305

gca gct cgt tat ggt cgt gat gcg cag gaa cag aaa gcc aac gcc   1072
Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln Lys Ala Asn Ala
310                               315               320

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<210> 734

<211> 324

<212> PRT

<213> Corynebacterium glutamicum

<400> 734

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Met Leu Glu Arg Leu Lys Arg Leu Asp Pro Leu Ile Val Leu Ile Val
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Leu Ala Val Ile Val Ala Ile Ile Ile Pro Val Arg Gly Val Ala Ala
 20                               25               30

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Asp Trp Phe Asp Val Ala Val Lys Ile Ala Ile Ala Leu Leu Phe Phe
 35 40 45
 Leu Tyr Gly Ala Arg Leu Ser Thr Gln Glu Ala Leu Asn Gly Leu Lys
 50 55 60
 His Trp Arg Leu His Leu Thr Ile Leu Ala Ile Thr Phe Gly Ile Phe
 65 70 75 80
 Pro Leu Ile Gly Ile Gly Leu Glu Pro Met Thr Ala Phe Val Ser Glu
 85 90 95
 Asp Ile Tyr Arg Gly Ile Leu Phe Leu Thr Leu Val Pro Ser Thr Val
 100 105 110
 Gln Ser Ser Val Ala Phe Thr Ser Ile Ala Lys Gly Asn Val Ala Gly
 115 120 125
 Ala Ile Val Ser Ala Ser Leu Ser Asn Leu Ala Gly Val Phe Leu Thr
 130 135 140
 Pro Leu Leu Val Met Leu Ile Met Ser Ala Gly Gly Gly Val His Val
 145 150 155 160
 Asp Ser Gln Val Phe Leu Asp Ile Ala Ile Gln Leu Leu Leu Pro Phe
 165 170 175
 Ile Leu Gly Gln Val Cys Arg Arg Trp Val Lys Asn Phe Ala Ala Asn
 180 185 190
 Lys Ala Thr Lys Ile Val Asp Arg Gly Ser Ile Ala Met Val Val Tyr
 195 200 205
 Ser Ala Phe Ser Ala Gly Met Val Ala Gly Ile Trp Ser Thr Val Ser
 210 215 220
 Val Leu Glu Ile Ile Tyr Leu Ile Val Phe Ala Ile Leu Leu Val Met
 225 230 235 240
 Ala Met Leu Trp Phe Thr Leu Phe Met Ala Thr Arg Leu Gly Phe Asn
 245 250 255
 Arg Ala Asp Ser Ile Ala Ile Gln Phe Cys Gly Thr Lys Lys Ser Leu
 260 265 270
 Ala Thr Gly Leu Pro Met Ala Ala Val Ile Phe Gly Gly Ala Asn Ile
 275 280 285
 Gly Leu Leu Ile Leu Pro Leu Met Ile Phe His Gln Val Gln Leu Met
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 Ile Cys Ala Trp Leu Ala Ala Arg Tyr Gly Arg Asp Ala Gln Glu Gln
 305 310 315 320
 Lys Ala Asn Ala

<210> 735

<211> 1281

<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(1258)

<223> RXN02556

<400> 735

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                                   Leu Ile Val Ser Thr
                                   1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
                                   10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
                                   25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
                                   40 45 50

aac acc ttc aac cgt ggc aat cag aag caa ggc gat cag cag aag gcg 307
Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
                                   55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
                                   70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
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tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
                                   105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
                                   120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg 547
Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu
                                   135 140 145

atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc 595
Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly
                                   150 155 160 165

gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca 643
Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala
                                   170 175 180

acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca 691
Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro

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	185	190	195	
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag				739
Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln				
200 . 205 210				
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att				787
Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile				
215 220 225				
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta				835
Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val				
230 235 240 245				
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt				883
Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val				
250 255 260				
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc				931
Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly				
265 270 275				
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac				979
Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp				
280 285 290				
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg				1027
Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val				
295 300 305				
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa				1075
Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu				
310 315 320 325				
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att				1123
Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile				
330 335 340				
cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag				1171
Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys				
345 350 355				
aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta				1219
Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val				
360 365 370				
aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca				1268
Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser				
375 380 385				
ccccagaact tcc				1281

<210> 736

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 736

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 20 25 30
 Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45
 Pro Glu Leu Ile Ala Asn Thr Phe Asn Arg Gly Asn Gln Lys Gln Gly
 50 55 60
 Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80
 Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95
 Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110
 Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125
 Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140
 Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160
 Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175
 Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190
 Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205
 Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220
 Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240
 Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255
 Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270
 Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285
 Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300
 Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320
 Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
370 375 380

Ile Ser
385

<210> 737

<211> 1281

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1258)

<223> FRXA02556

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gtagaaatta gcccatgaag catggaaagg cgaaaacccc ttg atc gtt tcc acc 115
Leu Ile Val Ser Thr
1 5

cag ccc att act gat cgc agc gca ctc tcg gca gaa cac gca gag gtg 163
Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala Glu His Ala Glu Val
10 15 20

atc aaa gca acg ctt cct ctc gtg ggc ggc aag att aat gag atc acg 211
Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys Ile Asn Glu Ile Thr
25 30 35

ccg gtt ttc tac aac aag atg ttt gcg gct cac cca gaa ttg atc gct 259
Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His Pro Glu Leu Ile Ala
40 45 50

aac acc ttc aac ggt ggc aat cag aag caa ggc gat cag cag aag gcg 307
Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly Asp Gln Gln Lys Ala
55 60 65

ctg gcg gct tcg att gca acg ttt gcc acc atg ctc gtt act cct gat 355
Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met Leu Val Thr Pro Asp
70 75 80 85

gct cct gac cca gtt cag ctg ctg tcc cgc att ggc cac aag cac gtg 403
Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile Gly His Lys His Val
90 95 100

tcc ctc ggc att act gct gat cag tac gac att gtt cac gag cac ctg 451
Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile Val His Glu His Leu
105 110 115

ttc gcc gca atc gtt gag gtt ttg gga gcg gaa act gtc acc gca cct 499
Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu Thr Val Thr Ala Pro
120 125 130

gtc gct gaa gcc tgg gat gct gtc tac tgg atc atg gca aat gtg ctg Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile Met Ala Asn Val Leu 135 140 145	547
atc ggt ttt gag aac aac ctt tat gct tcc aac gat ctg gag cct ggc Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn Asp Leu Glu Pro Gly 150 155 160 165	595
gac gtc ttc cgc gaa gtc acc gtg acc gcg aag aag cag ctc agc gca Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys Lys Gln Leu Ser Ala 170 175 180	643
acc gtc tgg gaa tac acc ctg gca ggt gag ctg gtt gcc cca gag cca Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu Val Ala Pro Glu Pro 185 190 195	691
ggt cag tac acc tcc atc gga gta gtg ctt gac gac ggc gcc cgc cag Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp Asp Gly Ala Arg Gln 200 205 210	739
ctg cgc cag tac agc ttg ctc ggc ggc tcc gac acc gag tac cgc att Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp Thr Glu Tyr Arg Ile 215 220 225	787
gcg gtt gag gat aac ggc gag gtt tct gga ttc ctg cgt gat cgc gta Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe Leu Arg Asp Arg Val 230 235 240 245	835
tcc gtt ggt gac aag att gaa gcc acc atc gcg gcc ggc gac ctg gtt Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala Ala Gly Asp Leu Val 250 255 260	883
ctt aac aag gac acc aat cca gtt gtg ctg att tcc cag ggc atc ggc Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile Ser Gln Gly Ile Gly 265 270 275	931
tcc acc cca atg gtg ggc atg ctc gca ggt atg aac cct gaa cgt gac Ser Thr Pro Met Val Gly Met Leu Ala Gly Met Asn Pro Glu Arg Asp 280 285 290	979
gtt gtg gtt ttg cat gct gac cag gcc gag tcc acc tac gcg cag gtg Val Val Val Leu His Ala Asp Gln Ala Glu Ser Thr Tyr Ala Gln Val 295 300 305	1027
gag gaa gtg cag ggg ctc gtc gaa aag ctc cct aag gct gcg ttt gaa Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro Lys Ala Ala Phe Glu 310 315 320 325	1075
atc ttc tac cgc gac aac gac cag tgg ctc gag gtc gct ggc cgc att Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu Val Ala Gly Arg Ile 330 335 340	1123
cca tca ggt gcg tcc gtg tac ctg tgc ggt ggc gtg gaa ttc ttg aag Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly Val Glu Phe Leu Lys 345 350 355	1171
aac gtg cgt gag cag atc gag gcg ctc gat gag cag cct cgc gac gta Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu Gln Pro Arg Asp Val 360 365 370	1219

aac ttc gag ctc ttc gca cca aac gac tgg ctg att tcc taagcccaca 1268
 Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu Ile Ser
 375 380 385

ccccagaact tcc 1281

<210> 738

<211> 386

<212> PRT

<213> Corynebacterium glutamicum

<400> 738

Leu Ile Val Ser Thr Gln Pro Ile Thr Asp Arg Ser Ala Leu Ser Ala
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Glu His Ala Glu Val Ile Lys Ala Thr Leu Pro Leu Val Gly Gly Lys
 20 25 30

Ile Asn Glu Ile Thr Pro Val Phe Tyr Asn Lys Met Phe Ala Ala His
 35 40 45

Pro Glu Leu Ile Ala Asn Thr Phe Asn Gly Gly Asn Gln Lys Gln Gly
 50 55 60

Asp Gln Gln Lys Ala Leu Ala Ala Ser Ile Ala Thr Phe Ala Thr Met
 65 70 75 80

Leu Val Thr Pro Asp Ala Pro Asp Pro Val Gln Leu Leu Ser Arg Ile
 85 90 95

Gly His Lys His Val Ser Leu Gly Ile Thr Ala Asp Gln Tyr Asp Ile
 100 105 110

Val His Glu His Leu Phe Ala Ala Ile Val Glu Val Leu Gly Ala Glu
 115 120 125

Thr Val Thr Ala Pro Val Ala Glu Ala Trp Asp Ala Val Tyr Trp Ile
 130 135 140

Met Ala Asn Val Leu Ile Gly Phe Glu Asn Asn Leu Tyr Ala Ser Asn
 145 150 155 160

Asp Leu Glu Pro Gly Asp Val Phe Arg Glu Val Thr Val Thr Ala Lys
 165 170 175

Lys Gln Leu Ser Ala Thr Val Trp Glu Tyr Thr Leu Ala Gly Glu Leu
 180 185 190

Val Ala Pro Glu Pro Gly Gln Tyr Thr Ser Ile Gly Val Val Leu Asp
 195 200 205

Asp Gly Ala Arg Gln Leu Arg Gln Tyr Ser Leu Leu Gly Gly Ser Asp
 210 215 220

Thr Glu Tyr Arg Ile Ala Val Glu Asp Asn Gly Glu Val Ser Gly Phe
 225 230 235 240

Leu Arg Asp Arg Val Ser Val Gly Asp Lys Ile Glu Ala Thr Ile Ala
 245 250 255

Ala Gly Asp Leu Val Leu Asn Lys Asp Thr Asn Pro Val Val Leu Ile
 260 265 270

Ser Gln Gly Ile Gly Ser Thr Pro Met Val Gly Met Leu Ala Gly Met
 275 280 285

Asn Pro Glu Arg Asp Val Val Val Leu His Ala Asp Gln Ala Glu Ser
 290 295 300

Thr Tyr Ala Gln Val Glu Glu Val Gln Gly Leu Val Glu Lys Leu Pro
 305 310 315 320

Lys Ala Ala Phe Glu Ile Phe Tyr Arg Asp Asn Asp Gln Trp Leu Glu
 325 330 335

Val Ala Gly Arg Ile Pro Ser Gly Ala Ser Val Tyr Leu Cys Gly Gly
 340 345 350

Val Glu Phe Leu Lys Asn Val Arg Glu Gln Ile Glu Ala Leu Asp Glu
 355 360 365

Gln Pro Arg Asp Val Asn Phe Glu Leu Phe Ala Pro Asn Asp Trp Leu
 370 375 380

Ile Ser
 385

<210> 739
 <211> 1200
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1177)
 <223> RXA01392

<400> 739
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ttgacatatc atctaaatctt ccaagagagg acaccacaca gtg gct aac acg tca 115
 Val Ala Asn Thr Ser
 1 5

tcc gat tgg gca ggc gcc cca caa aat gca tca gca gac ggc gag ttc 163
 Ser Asp Trp Ala Gly Ala Pro Gln Asn Ala Ser Ala Asp Gly Glu Phe
 10 15 20

gtt cgc gat acc aac tac atc gat gac cgc atc gtc gca gac gtt cca 211
 Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile Val Ala Asp Val Pro
 25 30 35

gcg gga tcc gaa cca att gct cag gaa gat ggc act ttc cat tgg cct 259
 Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly Thr Phe His Trp Pro
 40 45 50

gtc gag gct ggt cgc tac cgt tta gtc gct gcc cgc gca tgt cca tgg 307
 Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala Arg Ala Cys Pro Trp
 55 60 65

gca cac cgc act gtt atc acc cgt cgt ctt ctc ggc ctg gag aac gtg	355
Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu Gly Leu Glu Asn Val	
70 75 80 85	
atc tcg ctt ggt ctg acc ggc ccg act cac gac gtt cgt tcc tgg act	403
Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp Val Arg Ser Trp Thr	
90 95 100	
ttc gat tta gat cca aac cat ctt gat ccc gtg ctg cag att cct cgt	451
Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val Leu Gln Ile Pro Arg	
105 110 115	
cta cag gac gcg tat ttc aac cgc ttc ccc gat tac ccg cgc ggc att	499
Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp Tyr Pro Arg Gly Ile	
120 125 130	
act gtc cca gcg ctc gtg gag gaa tcg tct aag aag gtc gtc acc aac	547
Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys Lys Val Val Thr Asn	
135 140 145	
gat tac cct tcc atc acc atc gat ttc aat ctt gag tgg aag cag ttc	595
Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu Glu Trp Lys Gln Phe	
150 155 160 165	
cac cgt gag ggt gcg cct aac ctc tac ccc gcg gag ctg cgc gag gag	643
His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala Glu Leu Arg Glu Glu	
170 175 180	
atg gcg ccg gtg atg aag cgc atc ttc act gag gtc aac aac ggc gta	691
Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu Val Asn Asn Gly Val	
185 190 195	
tac agg acc ggc ttt gcc ggt agc cag gaa gcg cac aac gag gcg tac	739
Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala His Asn Glu Ala Tyr	
200 205 210	
aag cgg ctt tgg gtt gcg ttg gac tgg cta gaa gat cgc tta tcg acg	787
Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu Asp Arg Leu Ser Thr	
215 220 225	
cga cgt tac ctc atg ggg gat cac atc acc gag gcg gat atc cgc ctc	835
Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu Ala Asp Ile Arg Leu	
230 235 240 245	
tac cca acc ctc gtg cgt ttc gat gcc gtc tac cac gga cac ttc aag	883
Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr His Gly His Phe Lys	
250 255 260	
tgt ggc cgc aac aag atc acc gaa atg ccg aat cta tgg ggc tac ctg	931
Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn Leu Trp Gly Tyr Leu	
265 270 275	
cgg gat ctt ttc cag acc cca ggc ttt ggc gac acc acc gat ttc acc	979
Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp Thr Thr Asp Phe Thr	
280 285 290	
gaa atc aag cag cac tac tac atc acc cac gcg gag att aac ccc acc	1027
Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala Glu Ile Asn Pro Thr	
295 300 305	
cgg atc gtt cca gtc gga cca gat ctg tct ggt ttc gcg aca cca cac	1075

Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly Phe Ala Thr Pro His
 310 315 320 325

ggc cgt gaa aag ctc ggc gga tcc cca ttt gct gaa ggt gtt act ctg 1123
 Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala Glu Gly Val Thr Leu
 330 335 340

cct ggc cca att cct gcg ggc gaa gaa gtg aaa aac cct gaa cct ttt 1171
 Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys Asn Pro Glu Pro Phe
 345 350 355

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 Gln Lys

<210> 740
 <211> 359
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 740
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Ala Asp Gly Glu Phe Val Arg Asp Thr Asn Tyr Ile Asp Asp Arg Ile
 20 25 30

Val Ala Asp Val Pro Ala Gly Ser Glu Pro Ile Ala Gln Glu Asp Gly
 35 40 45

Thr Phe His Trp Pro Val Glu Ala Gly Arg Tyr Arg Leu Val Ala Ala
 50 55 60

Arg Ala Cys Pro Trp Ala His Arg Thr Val Ile Thr Arg Arg Leu Leu
 65 70 75 80

Gly Leu Glu Asn Val Ile Ser Leu Gly Leu Thr Gly Pro Thr His Asp
 85 90 95

Val Arg Ser Trp Thr Phe Asp Leu Asp Pro Asn His Leu Asp Pro Val
 100 105 110

Leu Gln Ile Pro Arg Leu Gln Asp Ala Tyr Phe Asn Arg Phe Pro Asp
 115 120 125

Tyr Pro Arg Gly Ile Thr Val Pro Ala Leu Val Glu Glu Ser Ser Lys
 130 135 140

Lys Val Val Thr Asn Asp Tyr Pro Ser Ile Thr Ile Asp Phe Asn Leu
 145 150 155 160

Glu Trp Lys Gln Phe His Arg Glu Gly Ala Pro Asn Leu Tyr Pro Ala
 165 170 175

Glu Leu Arg Glu Glu Met Ala Pro Val Met Lys Arg Ile Phe Thr Glu
 180 185 190

Val Asn Asn Gly Val Tyr Arg Thr Gly Phe Ala Gly Ser Gln Glu Ala
 195 200 205

His Asn Glu Ala Tyr Lys Arg Leu Trp Val Ala Leu Asp Trp Leu Glu
 210 215 220
 Asp Arg Leu Ser Thr Arg Arg Tyr Leu Met Gly Asp His Ile Thr Glu
 225 230 235 240
 Ala Asp Ile Arg Leu Tyr Pro Thr Leu Val Arg Phe Asp Ala Val Tyr
 245 250 255
 His Gly His Phe Lys Cys Gly Arg Asn Lys Ile Thr Glu Met Pro Asn
 260 265 270
 Leu Trp Gly Tyr Leu Arg Asp Leu Phe Gln Thr Pro Gly Phe Gly Asp
 275 280 285
 Thr Thr Asp Phe Thr Glu Ile Lys Gln His Tyr Tyr Ile Thr His Ala
 290 295 300
 Glu Ile Asn Pro Thr Arg Ile Val Pro Val Gly Pro Asp Leu Ser Gly
 305 310 315 320
 Phe Ala Thr Pro His Gly Arg Glu Lys Leu Gly Gly Ser Pro Phe Ala
 325 330 335
 Glu Gly Val Thr Leu Pro Gly Pro Ile Pro Ala Gly Glu Glu Val Lys
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 Asn Pro Glu Pro Phe Gln Lys
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 <212> DNA
 <213> Corynebacterium glutamicum

<220>
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 <222> (101)..(1204)
 <223> RXA00800

<400> 741
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 Met Ser Thr Val Val
 1 5
 cct gga att gtc gca ctg tcc aag ggt gca ccg gta gaa aaa gta aac 163
 Pro Gly Ile Val Ala Leu Ser Lys Gly Ala Pro Val Glu Lys Val Asn
 10 15 20
 gtt gtt gtc cct gat cca ggt gct aac gat gtc atc gtc aag att cag 211
 Val Val Val Pro Asp Pro Gly Ala Asn Asp Val Ile Val Lys Ile Gln
 25 30 35
 gcc tgc ggt gtg tgc cac acc gac ttg gcc tac cgc gat ggc gat att 259
 Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr Arg Asp Gly Asp Ile
 40 45 50
 tca gat gag ttc cct tac ctc ctc ggc cac gag gca gca ggc att gtt 307

Ser	Asp	Glu	Phe	Pro	Tyr	Leu	Leu	Gly	His	Glu	Ala	Ala	Gly	Ile	Val		
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gag	gag	gta	ggc	gag	tcc	gtc	acc	cac	ggt	gag	gtc	ggc	gat	ttc	gtc	355	
Glu	Glu	Val	Gly	Glu	Ser	Val	Thr	His	Val	Glu	Val	Gly	Asp	Phe	Val	85	
70					75					80							
atc	ttg	aac	tgg	cgt	gca	gtg	tgc	ggc	gag	tgc	cgt	gca	tgt	aag	aag	403	
Ile	Leu	Asn	Trp	Arg	Ala	Val	Cys	Gly	Glu	Cys	Arg	Ala	Cys	Lys	Lys	100	
				90					95								
ggc	gag	cca	aag	tac	tgc	ttt	aac	acc	cac	aac	gcc	tct	aag	aag	atg	451	
Gly	Glu	Pro	Lys	Tyr	Cys	Phe	Asn	Thr	His	Asn	Ala	Ser	Lys	Lys	Met	115	
			105					110									
acc	ctg	gaa	gac	ggc	acc	gag	ctg	tcc	cca	gca	ctg	ggt	att	ggc	gcg	499	
Thr	Leu	Glu	Asp	Gly	Thr	Glu	Leu	Ser	Pro	Ala	Leu	Gly	Ile	Gly	Ala	130	
		120					125										
ttc	ttg	gaa	aag	acc	ctg	gtc	cac	gaa	ggc	cag	tgc	acc	aag	gtt	aac	547	
Phe	Leu	Glu	Lys	Thr	Leu	Val	His	Glu	Gly	Gln	Cys	Thr	Lys	Val	Asn	145	
	135					140											
cct	gag	gaa	gat	cca	gca	gca	gct	ggc	ctt	ctg	ggt	tgt	ggc	atc	atg	595	
Pro	Glu	Glu	Asp	Pro	Ala	Ala	Ala	Gly	Leu	Leu	Gly	Cys	Gly	Ile	Met	165	
150					155					160							
gca	ggc	ctt	ggc	gct	gcg	gtg	aac	acc	ggt	gat	att	aag	cgt	ggc	gag	643	
Ala	Gly	Leu	Gly	Ala	Ala	Val	Asn	Thr	Gly	Asp	Ile	Lys	Arg	Gly	Glu	180	
				170					175								
tcc	gta	gca	gtc	ttc	ggc	ctt	ggt	ggc	gtg	ggc	atg	gca	gct	att	gct	691	
Ser	Val	Ala	Val	Phe	Gly	Leu	Gly	Gly	Val	Gly	Met	Ala	Ala	Ile	Ala	195	
			185					190									
ggc	gcc	aag	att	gct	ggc	gct	tcc	aag	atc	att	gct	gtt	gat	atc	gat	739	
Gly	Ala	Lys	Ile	Ala	Gly	Ala	Ser	Lys	Ile	Ile	Ala	Val	Asp	Ile	Asp	210	
		200					205										
gag	aag	aag	ctg	gag	tgg	gcg	aag	gaa	ttc	ggc	gca	acc	cac	acc	att	787	
Glu	Lys	Lys	Leu	Glu	Trp	Ala	Lys	Glu	Phe	Gly	Ala	Thr	His	Thr	Ile	225	
	215					220											
aat	tcc	tct	ggt	ctt	ggt	ggc	gaa	ggt	gat	gcc	tct	gag	gtc	gtg	gca	835	
Asn	Ser	Ser	Gly	Leu	Gly	Gly	Glu	Gly	Asp	Ala	Ser	Glu	Val	Val	Ala	245	
230					235					240							
aag	gtt	cgt	gag	ctc	acc	gat	ggt	ttc	ggc	acc	gat	gtc	tcc	atc	gat	883	
Lys	Val	Arg	Glu	Leu	Thr	Asp	Gly	Phe	Gly	Thr	Asp	Val	Ser	Ile	Asp	260	
				250					255								
gcg	gta	ggc	atc	atg	ccg	acc	tgg	cag	cag	gcg	ttt	tac	tcc	cgt	gac	931	
Ala	Val	Gly	Ile	Met	Pro	Thr	Trp	Gln	Gln	Ala	Phe	Tyr	Ser	Arg	Asp	275	
			265					270									
cat	gca	ggc	cgc	atg	gtg	atg	gtg	ggc	gtt	cca	aac	ctg	acg	tct	cgc	979	
His	Ala	Gly	Arg	Met	Val	Met	Val	Gly	Val	Pro	Asn	Leu	Thr	Ser	Arg	290	
		280					285										
gta	gat	gtt	cct	gcg	att	gat	ttt	tac	ggt	cgc	ggt	gga	tcc	gtg	cgc	1027	
Val	Asp	Val	Pro	Ala	Ile	Asp	Phe	Tyr	Gly	Arg	Gly	Gly	Ser	Val	Arg		

295 300 305
 cct gca tgg tac ggc gac tgc ctg cct gag cgt gat ttc cca act tat 1075
 Pro Ala Trp Tyr Gly Asp Cys Leu Pro Glu Arg Asp Phe Pro Thr Tyr
 310 315 320 325
 gtg gat ctg cac ctg cag ggt cgt ttc cca ctg gat aag ttt gtt tct 1123
 Val Asp Leu His Leu Gln Gly Arg Phe Pro Leu Asp Lys Phe Val Ser
 330 335 340
 gag cgt att ggt ctt gat gat gtt gaa gag gct ttc aac acc atg aag 1171
 Glu Arg Ile Gly Leu Asp Asp Val Glu Glu Ala Phe Asn Thr Met Lys
 345 350 355
 gct ggc gac gtg ctg cgt tct gtg gtg gag atc taaatggctc acgacggatt 1224
 Ala Gly Asp Val Leu Arg Ser Val Val Glu Ile
 360 365
 gcg 1227

<210> 742
 <211> 368
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 742
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 Val Glu Lys Val Asn Val Val Val Pro Asp Pro Gly Ala Asn Asp Val
 20 25 30
 Ile Val Lys Ile Gln Ala Cys Gly Val Cys His Thr Asp Leu Ala Tyr
 35 40 45
 Arg Asp Gly Asp Ile Ser Asp Glu Phe Pro Tyr Leu Leu Gly His Glu
 50 55 60
 Ala Ala Gly Ile Val Glu Glu Val Gly Glu Ser Val Thr His Val Glu
 65 70 75 80
 Val Gly Asp Phe Val Ile Leu Asn Trp Arg Ala Val Cys Gly Glu Cys
 85 90 95
 Arg Ala Cys Lys Lys Gly Glu Pro Lys Tyr Cys Phe Asn Thr His Asn
 100 105 110
 Ala Ser Lys Lys Met Thr Leu Glu Asp Gly Thr Glu Leu Ser Pro Ala
 115 120 125
 Leu Gly Ile Gly Ala Phe Leu Glu Lys Thr Leu Val His Glu Gly Gln
 130 135 140
 Cys Thr Lys Val Asn Pro Glu Glu Asp Pro Ala Ala Ala Gly Leu Leu
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 Gly Cys Gly Ile Met Ala Gly Leu Gly Ala Ala Val Asn Thr Gly Asp
 165 170 175
 Ile Lys Arg Gly Glu Ser Val Ala Val Phe Gly Leu Gly Gly Val Gly

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<223> RXA02143
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                                         Met Met Glu Thr Asn
                                         1                               5

ccg cag acc cca gag gga aat agc atg gct aaa ccc tct gct aag aag 163
Pro Gln Thr Pro Glu Gly Asn Ser Met Ala Lys Pro Ser Ala Lys Lys
                        10                                15                                20

gtc aaq aat cgc cgc aag gtc cgg cgc acc gtc gca ggt gca ttg gct 211

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Val	Lys	Asn	Arg	Arg	Lys	Val	Arg	Arg	Thr	Val	Ala	Gly	Ala	Leu	Ala	
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ctg	acc	att	gga	ctg	agc	gga	gca	gga	atc	ctc	gca	acc	gcg	atc	act	259
Leu	Thr	Ile	Gly	Leu	Ser	Gly	Ala	Gly	Ile	Leu	Ala	Thr	Ala	Ile	Thr	
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cca	gat	gct	caa	gtt	gct	acc	gct	cag	cgt	gac	gat	cag	gca	ctt	atc	307
Pro	Asp	Ala	Gln	Val	Ala	Thr	Ala	Gln	Arg	Asp	Asp	Gln	Ala	Leu	Ile	
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Ser	Glu	Gly	Lys	Asp	Leu	Tyr	Asp	Val	Ala	Cys	Ile	Thr	Cys	His	Gly	
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Val	Asn	Leu	Gln	Gly	Val	Glu	Asp	Arg	Gly	Pro	Ser	Leu	Val	Gly	Val	
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Gly	Glu	Gly	Ala	Val	Tyr	Phe	Gln	Val	His	Ser	Gly	Arg	Met	Pro	Ile	
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Leu	Arg	Asn	Glu	Ala	Gln	Ala	Glu	Arg	Lys	Ala	Pro	Arg	Tyr	Thr	Glu	
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gca	cag	acc	ctt	gcg	atc	gct	gca	tat	gtt	gca	gct	aat	ggc	ggg	ggc	547
Ala	Gln	Thr	Leu	Ala	Ile	Ala	Ala	Tyr	Val	Ala	Ala	Asn	Gly	Gly	Gly	
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cca	gga	ctc	gtt	tac	aac	gag	gac	ggc	acc	ctc	gcc	atg	gag	gag	ctc	595
Pro	Gly	Leu	Val	Tyr	Asn	Glu	Asp	Gly	Thr	Leu	Ala	Met	Glu	Glu	Leu	
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Arg	Gly	Glu	Asn	Tyr	Asp	Gly	Gln	Ile	Thr	Ser	Ala	Asp	Val	Ala	Arg	
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ggc	gga	gat	ctg	ttc	cgc	ctg	aac	tgt	gca	tcc	tgc	cac	aac	ttc	act	691
Gly	Gly	Asp	Leu	Phe	Arg	Leu	Asn	Cys	Ala	Ser	Cys	His	Asn	Phe	Thr	
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Gly	Arg	Gly	Gly	Ala	Leu	Ser	Ser	Gly	Lys	Tyr	Ala	Pro	Asn	Leu	Asp	
	200					205						210				
gct	gca	aac	gag	cag	gaa	atc	tac	cag	gct	atg	ctt	acc	ggg	cct	cag	787
Ala	Ala	Asn	Glu	Gln	Glu	Ile	Tyr	Gln	Ala	Met	Leu	Thr	Gly	Pro	Gln	
	215					220					225					
aac	atg	cct	aag	ttc	tcc	gat	cgt	cag	ctc	tcc	gca	gat	gag	aag	aag	835
Asn	Met	Pro	Lys	Phe	Ser	Asp	Arg	Gln	Leu	Ser	Ala	Asp	Glu	Lys	Lys	
	230				235					240					245	
gac	atc	atc	gcc	ttc	atc	aag	tcc	acc	aag	gag	act	cca	tca	cct	ggg	883
Asp	Ile	Ile	Ala	Phe	Ile	Lys	Ser	Thr	Lys	Glu	Thr	Pro	Ser	Pro	Gly	
			250						255					260		
ggg	tac	tca	ctc	ggg	agc	ttg	ggc	cca	gtg	gct	gag	ggg	ctg	ttc	atg	931
Gly	Tyr	Ser	Leu	Gly	Ser	Leu	Gly	Pro	Val	Ala	Glu	Gly	Leu	Phe	Met	

265 270 275
 tgg gta ttc ggc atc ttg gtc ctc gtg gcc gcc gct atg tgg att gga 979
 Trp Val Phe Gly Ile Leu Val Leu Val Ala Ala Ala Met Trp Ile Gly
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 Ser Arg Ser
 295
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 Ala Gly Ala Leu Ala Leu Thr Ile Gly Leu Ser Gly Ala Gly Ile Leu
 35 40 45
 Ala Thr Ala Ile Thr Pro Asp Ala Gln Val Ala Thr Ala Gln Arg Asp
 50 55 60
 Asp Gln Ala Leu Ile Ser Glu Gly Lys Asp Leu Tyr Asp Val Ala Cys
 65 70 75 80
 Ile Thr Cys His Gly Val Asn Leu Gln Gly Val Glu Asp Arg Gly Pro
 85 90 95
 Ser Leu Val Gly Val Gly Glu Gly Ala Val Tyr Phe Gln Val His Ser
 100 105 110
 Gly Arg Met Pro Ile Leu Arg Asn Glu Ala Gln Ala Glu Arg Lys Ala
 115 120 125
 Pro Arg Tyr Thr Glu Ala Gln Thr Leu Ala Ile Ala Ala Tyr Val Ala
 130 135 140
 Ala Asn Gly Gly Gly Pro Gly Leu Val Tyr Asn Glu Asp Gly Thr Leu
 145 150 155 160
 Ala Met Glu Glu Leu Arg Gly Glu Asn Tyr Asp Gly Gln Ile Thr Ser
 165 170 175
 Ala Asp Val Ala Arg Gly Gly Asp Leu Phe Arg Leu Asn Cys Ala Ser
 180 185 190
 Cys His Asn Phe Thr Gly Arg Gly Gly Ala Leu Ser Ser Gly Lys Tyr
 195 200 205
 Ala Pro Asn Leu Asp Ala Ala Asn Glu Gln Glu Ile Tyr Gln Ala Met
 210 215 220
 Leu Thr Gly Pro Gln Asn Met Pro Lys Phe Ser Asp Arg Gln Leu Ser
 225 230 235 240

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Met Val Leu Val Trp																1 5
tcc aag gcc ttc tgg cgc gac cgt aaa gac gcc ccc gat gga gca acc																163
Ser Lys Ala Phe Trp Arg Asp Arg Lys Asp Ala Pro Asp Gly Ala Thr																10 15 20
gca cta gca aga ccc gca cct ttg gta gat atc caa gac gaa gtc gcc																211
Ala Leu Ala Arg Pro Ala Pro Leu Val Asp Ile Gln Asp Glu Val Ala																25 30 35
gtt aaa gac cgc aac gat gtc gga cgg atg cct tgg ggc atg gtc ttc																259
Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro Trp Gly Met Val Phe																40 45 50
tcc act gcc ctg ttg gtt tcc gca tcc ctt gct gta tcc gtg ctc gca																307
Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala Val Ser Val Leu Ala																55 60 65
gga cca ctg tca tct att act gga cgc gcc gcc gaa tcc gca caa gat																355
Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala Glu Ser Ala Gln Asp																70 75 80 85
gtc aac atc tac cgc gcc gca gta ctc ggc cca act acc tcg acc cat																403
Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro Thr Thr Ser Thr His																90 95 100
cac gca cac tcg aga tgg agc gtt acg acg cca acc gcg atg aca tca																451
His Ala His Ser Arg Trp Ser Val Thr Thr Pro Thr Ala Met Thr Ser																105 110 115
acc acc gcg tcg aca cca atg gaa cgg agg acc aac cat gat cag tgg																499
Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr Asn His Asp Gln Trp																

120 125 130 502

att
Ile

<210> 746
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<212> PRT
<213> Corynebacterium glutamicum

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Gln Asp Glu Val Ala Val Lys Asp Arg Asn Asp Val Gly Arg Met Pro
35 40 45
Trp Gly Met Val Phe Ser Thr Ala Leu Leu Val Ser Ala Ser Leu Ala
50 55 60
Val Ser Val Leu Ala Gly Pro Leu Ser Ser Ile Thr Gly Arg Ala Ala
65 70 75 80
Glu Ser Ala Gln Asp Val Asn Ile Tyr Arg Ala Ala Val Leu Gly Pro
85 90 95
Thr Thr Ser Thr His His Ala His Ser Arg Trp Ser Val Thr Thr Pro
100 105 110
Thr Ala Met Thr Ser Thr Thr Ala Ser Thr Pro Met Glu Arg Arg Thr
115 120 125
Asn His Asp Gln Trp Ile
130

<210> 747
<211> 504
<212> DNA
<213> Corynebacterium glutamicum

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<222> (101)..(481)
<223> RXN02036

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Val His Ile Pro Phe
1 5
ggg cac ctc gcc gac acc gtc tcc tgg gac tgc ggg gga ggc agc tgc 163
Gly His Leu Ala Asp Thr Val Ser Trp Asp Cys Gly Gly Gly Ser Cys
10 15 20

gcc acc aac gat ttg gta tcc ctg ttc atg ccg gcc gcc ttc atg agt 211
 Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro Ala Ala Phe Met Ser
 25 30 35

acc ctc gcc gcc tgc gta ttt ggc gcg tgg gcc ata ggt ttg atc gct 259
 Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala Ile Gly Leu Ile Ala
 40 45 50

ccc gca cta ttc atc gcg gtg act gcc tgg gca ttt cgc tcc ggc gtg 307
 Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala Phe Arg Ser Gly Val
 55 60 65

cag gct gcg att gcc gac ggc tac acg tcc gcg act tcc gtc ggc ttc 355
 Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala Thr Ser Val Gly Phe
 70 75 80 85

gaa atg act gtc tcg ctc att ctt ttc atc atc gca ggt ctg tgc ttt 403
 Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile Ala Gly Leu Cys Phe
 90 95 100

ctg ggc tgg atc ccc atg ttc atc aac aac cgc caa gtc gcg cgc aag 451
 Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg Gln Val Ala Arg Lys
 105 110 115

gtc cgc gag agg gct gcg ggc ttg agc aat taggctctcg cttttcgacg 501
 Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
 120 125

ttt 504

<210> 748

<211> 127

<212> PRT

<213> Corynebacterium glutamicum

<400> 748

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Gly Gly Gly Ser Cys Ala Thr Asn Asp Leu Val Ser Leu Phe Met Pro
 20 25 30

Ala Ala Phe Met Ser Thr Leu Ala Ala Cys Val Phe Gly Ala Trp Ala
 35 40 45

Ile Gly Leu Ile Ala Pro Ala Leu Phe Ile Ala Val Thr Ala Trp Ala
 50 55 60

Phe Arg Ser Gly Val Gln Ala Ala Ile Ala Asp Gly Tyr Thr Ser Ala
 65 70 75 80

Thr Ser Val Gly Phe Glu Met Thr Val Ser Leu Ile Leu Phe Ile Ile
 85 90 95

Ala Gly Leu Cys Phe Leu Gly Trp Ile Pro Met Phe Ile Asn Asn Arg
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Gln Val Ala Arg Lys Val Arg Glu Arg Ala Ala Gly Leu Ser Asn
 115 120 125

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				Met	Ser	Asn	Gln	Leu								
				1				5								
ccc	gat	cac	gtc	cgc	gac	gcc	ttc	caa	gta	ggg	gcg	gga	cct	gcc	gaa	163
Pro	Asp	His	Val	Arg	Asp	Ala	Phe	Gln	Val	Gly	Ala	Gly	Pro	Ala	Glu	
				10					15					20		
caa	ctc	ggg	caa	gct	tgg	gac	ttc	gga	ttc	cgc	gtc	ggc	aac	act	gtg	211
Gln	Leu	Gly	Gln	Ala	Trp	Asp	Phe	Gly	Phe	Arg	Val	Gly	Asn	Thr	Val	
			25					30					35			
ttc	gcc	aaa	gtg	acg	gcg	ccg	gaa	gtg	tcg	ggc	tgg	tcg	tcg	aaa	acc	259
Phe	Ala	Lys	Val	Thr	Ala	Pro	Glu	Val	Ser	Gly	Trp	Ser	Ser	Lys	Thr	
		40					45					50				
cgc	gaa	acc	ctg	aaa	cca	gaa	ggc	gtg	cgc	gtc	gta	cga	ccg	atc	cgc	307
Arg	Glu	Thr	Leu	Lys	Pro	Glu	Gly	Val	Arg	Val	Val	Arg	Pro	Ile	Arg	
	55					60					65					
tcc	acc	gac	ggc	cga	ttt	gtg	gtt	gcg	ggg	tgg	cgc	gca	tcg	gtg	ttc	355
Ser	Thr	Asp	Gly	Arg	Phe	Val	Val	Ala	Gly	Trp	Arg	Ala	Ser	Val	Phe	
70					75					80					85	
tct	acg	gga	acg	atc	agc	aag	cga	gtc	gat	gag	acg	gtc	gtt	gcg	ggg	403
Ser	Thr	Gly	Thr	Ile	Ser	Lys	Arg	Val	Asp	Glu	Thr	Val	Val	Ala	Gly	
				90					95					100		
ctt	cgt	ttg	gca	gat	gca	tta	gtg	gat	acg	cat	gca	ccg	gaa	cct	gtg	451
Leu	Arg	Leu	Ala	Asp	Ala	Leu	Val	Asp	Thr	His	Ala	Pro	Glu	Pro	Val	
			105					110					115			
gac	aat	gtg	ttt	aac	cgt	gct	gat	gtg	cag	gcc	tgg	gaa	gag	cag	ccc	499
Asp	Asn	Val	Phe	Asn	Arg	Ala	Asp	Val	Gln	Ala	Trp	Glu	Glu	Gln	Pro	
		120					125					130				
ggg	cga	atc	ggg	gaa	ttg	ttg	gag	ccg	att	aat	cgc	gtg	aac	cag	gtt	547
Gly	Arg	Ile	Gly	Glu	Leu	Leu	Glu	Pro	Ile	Asn	Arg	Val	Asn	Gln	Val	
	135					140					145					
ggg	cat	gcg	gat	atg	ttg	gcg	aca	acg	ctg	tat	gcg	gga	act	cag	cca	595
Gly	His	Ala	Asp	Met	Leu	Ala	Thr	Thr	Leu	Tyr	Ala	Gly	Thr	Gln	Pro	
150					155					160					165	
cct	gca	gtg	acg	gat	ttg	gtg	cca	gtg	ctg	cgt	ccg	cat	ggg	ttc	act	643
Pro	Ala	Val	Thr	Asp	Leu	Val	Pro	Val	Leu	Arg	Pro	His	Gly	Phe	Thr	

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gcg gca ttg gtg atc gtt gat ggg ttg ctg ctg ggt gcg gtt gat gag			691
Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu Gly Ala Val Asp Glu			
185	190	195	
gga att ctg cgg agg ttt tcg cat ttg ccg gaa att gag cag ctg gtt			739
Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu Ile Glu Gln Leu Val			
200	205	210	
ttg agg gca ttt ttg ttc cgt cga aac ttg cag gag ttc tct gag aac			787
Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln Glu Phe Ser Glu Asn			
215	220	225	
aac gat ccg aat gtt att tcg aac cta aac agg gtg gaa tcg aca ctc			835
Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg Val Glu Ser Thr Leu			
230	235	240	245
gtg tcg tat gtt tct gac aag att tgaggtatgt cggaatacaa acc			882
Val Ser Tyr Val Ser Asp Lys Ile			
250			

<210> 750

<211> 253

<212> PRT

<213> Corynebacterium glutamicum

<400> 750

Met Ser Asn Gln Leu Pro Asp His Val Arg Asp Ala Phe Gln Val Gly	
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20	25
Val Gly Asn Thr Val Phe Ala Lys Val Thr Ala Pro Glu Val Ser Gly	
35	40
Trp Ser Ser Lys Thr Arg Glu Thr Leu Lys Pro Glu Gly Val Arg Val	
50	55
Val Arg Pro Ile Arg Ser Thr Asp Gly Arg Phe Val Val Ala Gly Trp	
65	70
Arg Ala Ser Val Phe Ser Thr Gly Thr Ile Ser Lys Arg Val Asp Glu	
85	90
Thr Val Val Ala Gly Leu Arg Leu Ala Asp Ala Leu Val Asp Thr His	
100	105
Ala Pro Glu Pro Val Asp Asn Val Phe Asn Arg Ala Asp Val Gln Ala	
115	120
Trp Glu Glu Gln Pro Gly Arg Ile Gly Glu Leu Leu Glu Pro Ile Asn	
130	135
Arg Val Asn Gln Val Gly His Ala Asp Met Leu Ala Thr Thr Leu Tyr	
145	150
Ala Gly Thr Gln Pro Pro Ala Val Thr Asp Leu Val Pro Val Leu Arg	
165	170
	175

Pro His Gly Phe Thr Ala Ala Leu Val Ile Val Asp Gly Leu Leu Leu
 180 185 190

Gly Ala Val Asp Glu Gly Ile Leu Arg Arg Phe Ser His Leu Pro Glu
 195 200 205

Ile Glu Gln Leu Val Leu Arg Ala Phe Leu Phe Arg Arg Asn Leu Gln
 210 215 220

Glu Phe Ser Glu Asn Asn Asp Pro Asn Val Ile Ser Asn Leu Asn Arg
 225 230 235 240

Val Glu Ser Thr Leu Val Ser Tyr Val Ser Asp Lys Ile
 245 250

<210> 751
 <211> 1059
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(1036)
 <223> RXN02206

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 Met Val Gly Ser Ser
 1 5

ggt ttg cgg gta tcc agg ctc ggt ttg ggc acc tca aca tgg ggc tcg 163
 Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr Ser Thr Trp Gly Ser
 10 15 20

ggc acc gag ctg gct gag gca ggc gat atc ttt aag gcg ttc atc aat 211
 Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe Lys Ala Phe Ile Asn
 25 30 35

tct ggt ggc acg ctt atc gac gtc tcc ccc aac tac acc acc ggc gtc 259
 Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn Tyr Thr Thr Gly Val
 40 45 50

gcg gaa gaa atg ctc ggc acg atg ttg gat gcg gaa gtc tct cgt tcg 307
 Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala Glu Val Ser Arg Ser
 55 60 65

gct gtc gtc att tcc tcc agc gca ggt gtc aac ccc gct ctg ccg ctc 355
 Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn Pro Ala Leu Pro Leu
 70 75 80 85

ggc cga cgt gtg gat tgc tcc cgc cgc aat ttg att gcc caa tta gat 403
 Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu Ile Ala Gln Leu Asp
 90 95 100

gtc acc ctg cgg gca tta aac act gac tat ttg gat ttg tgg tct gtg 451
 Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu Asp Leu Trp Ser Val
 105 110 115

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ggc tat tgg gat gag ggc acc cca ccg cat gag gtg gcc gat act ttg 499
Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu Val Ala Asp Thr Leu
120 125 130

gat tac gcc gtg cgc acc ggc cga gtc cga tat gcc ggt gtc cga gga 547
Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr Ala Gly Val Arg Gly
135 140 145

tat tcc ggt tgg cag tta gcg gtc acc cac gct gca tcc aat cat gca 595
Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala Ala Ser Asn His Ala
150 155 160

gcg gcc tcc gcc cgc ccc gtg gtc gtt gca caa aat gaa tac agc ctg 643
Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln Asn Glu Tyr Ser Leu
170 175 180

ctg gaa cgc cgc gca gaa caa gaa ctc ctc cct gcc acc caa cac cta 691
Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro Ala Thr Gln His Leu
185 190 195

ggt gtc gga ttc ttt gct ggc gct ccg ctg ggg caa ggc gtg ctg act 739
Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly Gln Gly Val Leu Thr
200 205 210

gct aaa tac cgc tcc gaa att ccc cat gat tcc aga gct gca tcc aca 787
Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser Arg Ala Ala Ser Thr
215 220 225

gga cgc gac gca gaa gtc caa agc tac cta gat aat cga ggc cgc atc 835
Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp Asn Arg Gly Arg Ile
230 235 240 245

att gtc gat gct ctt gat act gca gcc aaa gga tta ggc att agc ccc 883
Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly Leu Gly Ile Ser Pro
250 255 260

gct gtc aca gcc acc acc tgg gtg cgt gat cgt ccc gga gtg aca gct 931
Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg Pro Gly Val Thr Ala
265 270 275

gtc atc gtg ggc gct cgc aca cat gaa cag ctg tca cat ctt ctc aag 979
Val Ile Val Gly Ala Arg Thr His Glu Gln Leu Ser His Leu Leu Lys
280 285 290

gcg gaa tcg gtg act ttg cca aca cca atc aca caa gcc ctt gat gat 1027
Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr Gln Ala Leu Asp Asp
295 300 305

gtc tcc ctg tgacttggtc caattacatt cac 1059
Val Ser Leu
310

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<210> 752

<211> 312

<212> PRT

<213> Corynebacterium glutamicum

<400> 752

Met Val Gly Ser Ser Gly Leu Arg Val Ser Arg Leu Gly Leu Gly Thr

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Ser Thr Trp Gly	Ser Gly Thr Glu Leu Ala Glu Ala Gly Asp Ile Phe		
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Lys Ala Phe Ile Asn Ser Gly Gly Thr Leu Ile Asp Val Ser Pro Asn			
35	40	45	
Tyr Thr Thr Gly Val Ala Glu Glu Met Leu Gly Thr Met Leu Asp Ala			
50	55	60	
Glu Val Ser Arg Ser Ala Val Val Ile Ser Ser Ser Ala Gly Val Asn			
65	70	75	80
Pro Ala Leu Pro Leu Gly Arg Arg Val Asp Cys Ser Arg Arg Asn Leu			
85	90	95	
Ile Ala Gln Leu Asp Val Thr Leu Arg Ala Leu Asn Thr Asp Tyr Leu			
100	105	110	
Asp Leu Trp Ser Val Gly Tyr Trp Asp Glu Gly Thr Pro Pro His Glu			
115	120	125	
Val Ala Asp Thr Leu Asp Tyr Ala Val Arg Thr Gly Arg Val Arg Tyr			
130	135	140	
Ala Gly Val Arg Gly Tyr Ser Gly Trp Gln Leu Ala Val Thr His Ala			
145	150	155	160
Ala Ser Asn His Ala Ala Ala Ser Ala Arg Pro Val Val Val Ala Gln			
165	170	175	
Asn Glu Tyr Ser Leu Leu Glu Arg Arg Ala Glu Gln Glu Leu Leu Pro			
180	185	190	
Ala Thr Gln His Leu Gly Val Gly Phe Phe Ala Gly Ala Pro Leu Gly			
195	200	205	
Gln Gly Val Leu Thr Ala Lys Tyr Arg Ser Glu Ile Pro His Asp Ser			
210	215	220	
Arg Ala Ala Ser Thr Gly Arg Asp Ala Glu Val Gln Ser Tyr Leu Asp			
225	230	235	240
Asn Arg Gly Arg Ile Ile Val Asp Ala Leu Asp Thr Ala Ala Lys Gly			
245	250	255	
Leu Gly Ile Ser Pro Ala Val Thr Ala Thr Thr Trp Val Arg Asp Arg			
260	265	270	
Pro Gly Val Thr Ala Val Ile Val Gly Ala Arg Thr His Glu Gln Leu			
275	280	285	
Ser His Leu Leu Lys Ala Glu Ser Val Thr Leu Pro Thr Pro Ile Thr			
290	295	300	
Gln Ala Leu Asp Asp Val Ser Leu			
305	310		

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<212> DNA

<213> *Corynebacterium glutamicum*

<220>

<221> CDS

<222> (101)..(724)

<223> RXN02554

<400> 753

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ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag 115
                                         Met Ser His Thr Lys
                                         1                               5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc 163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
                        10                               15                               20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt 211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
                        25                               30                               35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg 259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
                        40                               45                               50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc 307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
                        55                               60                               65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta 355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
                        70                               75                               80                               85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat 403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
                        90                               95                               100

ggg gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att 451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
                        105                               110                               115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac 499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
                        120                               125                               130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att 547
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
                        135                               140                               145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta 595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
                        150                               155                               160                               165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac 643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                        170                               175                               180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat 691

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Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
 185 190 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
 Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
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aac

747

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 <213> Corynebacterium glutamicum

<400> 754
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Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
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Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
 35 40 45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
 50 55 60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65 70 75 80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
 85 90 95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
 100 105 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
 115 120 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
 130 135 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
 145 150 155 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
 165 170 175

Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
 180 185 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
 195 200 205

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<212> DNA

<213> Corynebacterium glutamicum

<220>

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<222> (101)..(910)

<223> RXN01204

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				Met	Lys	Gly	Glu	Phe	
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cac	gcc	ccc	gat	ttg	gac	aaa	gaa	ttt	ttc	ccg	ggg	cac	gta	acc	gat	163
His	Ala	Pro	Asp	Leu	Asp	Lys	Glu	Phe	Phe	Pro	Gly	His	Val	Thr	Asp	
				10					15					20		

agt	ggg	gaa	gtc	gtg	aac	atg	ctg	ttc	acc	gat	ttc	gct	aat	ggg	ttg	211
Ser	Gly	Glu	Val	Val	Asn	Met	Leu	Phe	Thr	Asp	Phe	Ala	Asn	Gly	Trp	
			25					30					35			

ttc	gca	atg	gac	cgc	atc	gta	ttg	atc	cgt	ctt	ctt	atg	acg	gca	gtc	259
Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu	Leu	Met	Thr	Ala	Val	
		40					45					50				

gtt	gtg	gtc	ttc	ttc	ctt	tgg	gct	atg	cgc	aag	cca	aag	ctt	gtt	ccg	307
Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys	Pro	Lys	Leu	Val	Pro	
		55				60					65					

cat	ggc	gtc	cag	aat	ttt	gca	gag	tac	gca	ctc	gat	ttc	gtt	ggg	att	355
His	Gly	Val	Gln	Asn	Phe	Ala	Glu	Tyr	Ala	Leu	Asp	Phe	Val	Gly	Ile	
	70				75					80					85	

cac	atc	gct	gaa	gac	atc	ctc	gga	aag	aag	aaa	ggg	cgt	cgg	ttc	ctg	403
His	Ile	Ala	Glu	Asp	Ile	Leu	Gly	Lys	Lys	Lys	Gly	Arg	Arg	Phe	Leu	
			90						95					100		

ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala	
			105					110					115			

acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499
Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe	
			120				125					130				

cca	atc	gtg	atg	gcg	gta	gct	ggg	tac	atc	gcg	ttt	atc	tac	gca	ggc	547
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly	
		135				140					145					

tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	gtt	gtg	att	595
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile	
	150				155					160				165		

ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	gtt	cca	att	gag	ttc	643
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe	
				170					175					180		

ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met	

185	190	195	
gcc aac ttc ctt gct ggc cac atc atc ctg gtt ctg ctt ttc tcc gca			739
Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val Leu Leu Phe Ser Ala			
200	205	210	
acg aac ttc ttc ttc ttc cag ttc aac gga tgg aca gca atg tcc ggc			787
Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp Thr Ala Met Ser Gly			
215	220	225	
gta acc atc ttg atg gca gta ctc ttc acg gtt tac gag atc att gtt			835
Val Thr Ile Leu Met Ala Val Leu Phe Thr Val Tyr Glu Ile Ile Val			
230	235	240	245
atc ttc ctg cag gca tac atc ttc gct ctg ctg gtc gct gta tac att			883
Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu Val Ala Val Tyr Ile			
250	255	260	
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Glu Leu Ser Leu His Ala Asp Ser His			
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taa			933

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 <213> Corynebacterium glutamicum

<400> 756
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 20 25 30
 Phe Ala Asn Gly Trp Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu
 35 40 45
 Leu Met Thr Ala Val Val Val Val Phe Phe Leu Trp Ala Met Arg Lys
 50 55 60
 Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65 70 75 80
 Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
 85 90 95
 Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
 100 105 110
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
 115 120 125
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
 130 135 140
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
 145 150 155 160

Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
 165 170 175

Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
 180 185 190

Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
 195 200 205

Leu Leu Phe Ser Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
 210 215 220

Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
 225 230 235 240

Tyr Glu Ile Ile Val Ile Phe Leu Gln Ala Tyr Ile Phe Ala Leu Leu
 245 250 255

Val Ala Val Tyr Ile Glu Leu Ser Leu His Ala Asp Ser His
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 Met Lys Gly Glu Phe
 1 5

cac gcc ccc gat ttg gac aaa gaa ttt ttc ccg ggg cac gta acc gat 163
 His Ala Pro Asp Leu Asp Lys Glu Phe Phe Pro Gly His Val Thr Asp
 10 15 20

agt ggt gaa gtc gtg aac atg ctg ttc acc gat ttc gct aat ggt tgg 211
 Ser Gly Glu Val Val Asn Met Leu Phe Thr Asp Phe Ala Asn Gly Trp
 25 30 35

ttc gca atg gac cgc atc gta ttg atc cgt ctt ctt atg acg gca gtc 259
 Phe Ala Met Asp Arg Ile Val Leu Ile Arg Leu Leu Met Thr Ala Val
 40 45 50

gtt gtg gtc ttc ttc ctt tgg gct atg cgc aag cca aag ctt gtt ccg 307
 Val Val Val Phe Phe Leu Trp Ala Met Arg Lys Pro Lys Leu Val Pro
 55 60 65

cat ggc gtc cag aat ttt gca gag tac gca ctc gat ttc gtt ggt att 355
 His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu Asp Phe Val Gly Ile
 70 75 80 85

cac atc gct gaa gac atc ctc gga aag aag aaa ggt cgt cgg ttc ctg 403
 His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys Gly Arg Arg Phe Leu

90										95					100					
ccg	atc	ctg	gcc	acc	atc	ttc	ttc	gcg	gct	ctg	ttg	atg	aac	ctt	gca	451				
Pro	Ile	Leu	Ala	Thr	Ile	Phe	Phe	Ala	Ala	Leu	Leu	Met	Asn	Leu	Ala					
105				110				115												
acg	atc	atc	ccg	gga	cta	aac	atc	tcc	tcc	aac	tca	cgt	att	gca	ttc	499				
Thr	Ile	Ile	Pro	Gly	Leu	Asn	Ile	Ser	Ser	Asn	Ser	Arg	Ile	Ala	Phe					
120				125				130												
cca	atc	gtg	atg	gcg	gta	gct	ggt	tac	atc	gcg	ttt	atc	tac	gca	ggc	547				
Pro	Ile	Val	Met	Ala	Val	Ala	Gly	Tyr	Ile	Ala	Phe	Ile	Tyr	Ala	Gly					
135				140				145												
tct	aag	cgt	tac	gga	ttc	ttc	aaa	tat	gtg	aag	tct	tct	ggt	gtg	att	595				
Ser	Lys	Arg	Tyr	Gly	Phe	Phe	Lys	Tyr	Val	Lys	Ser	Ser	Val	Val	Ile					
150				155				160				165								
ccg	aac	att	cca	cca	gca	ctt	cac	gtc	ttg	gtg	ggt	cca	att	gag	ttc	643				
Pro	Asn	Ile	Pro	Pro	Ala	Leu	His	Val	Leu	Val	Val	Pro	Ile	Glu	Phe					
170				175				180												
ttc	tct	aca	ttc	atc	ttg	agg	cca	gtc	acc	ctg	gca	ctg	cgt	ttg	atg	691				
Phe	Ser	Thr	Phe	Ile	Leu	Arg	Pro	Val	Thr	Leu	Ala	Leu	Arg	Leu	Met					
185				190				195												
gcc	aac	ttc	ctt	gct	ggc	cac	atc	atc	ctg	ggt	ctg	ctt	ttc	ttc	gca	739				
Ala	Asn	Phe	Leu	Ala	Gly	His	Ile	Ile	Leu	Val	Leu	Leu	Phe	Phe	Ala					
200				205				210												
acg	aac	ttc	ttc	ttc	ttc	cag	ttc	aac	gga	tgg	aca	gca	atg	tcc	ggc	787				
Thr	Asn	Phe	Phe	Phe	Phe	Gln	Phe	Asn	Gly	Trp	Thr	Ala	Met	Ser	Gly					
215				220				225												
gta	acc	atc	ttg	atg	gca	gta	ctc	ttc	acg	ggt	tac	gag	atc	att	ggt	835				
Val	Thr	Ile	Leu	Met	Ala	Val	Leu	Phe	Thr	Val	Tyr	Glu	Ile	Ile	Val					
230				235				240				245								
atc	ttc	ctg	cag	gca	tac	atc	ttc	gct								862				
Ile	Phe	Leu	Gln	Ala	Tyr	Ile	Phe	Ala												
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<213> Corynebacterium glutamicum

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		20					25						30		

Phe	Ala	Asn	Gly	Trp	Phe	Ala	Met	Asp	Arg	Ile	Val	Leu	Ile	Arg	Leu
		35					40					45			

Leu	Met	Thr	Ala	Val	Val	Val	Val	Phe	Phe	Leu	Trp	Ala	Met	Arg	Lys
	50					55					60				

Pro Lys Leu Val Pro His Gly Val Gln Asn Phe Ala Glu Tyr Ala Leu
 65 70 75 80
 Asp Phe Val Gly Ile His Ile Ala Glu Asp Ile Leu Gly Lys Lys Lys
 85 90 95
 Gly Arg Arg Phe Leu Pro Ile Leu Ala Thr Ile Phe Phe Ala Ala Leu
 100 105 110
 Leu Met Asn Leu Ala Thr Ile Ile Pro Gly Leu Asn Ile Ser Ser Asn
 115 120 125
 Ser Arg Ile Ala Phe Pro Ile Val Met Ala Val Ala Gly Tyr Ile Ala
 130 135 140
 Phe Ile Tyr Ala Gly Ser Lys Arg Tyr Gly Phe Phe Lys Tyr Val Lys
 145 150 155 160
 Ser Ser Val Val Ile Pro Asn Ile Pro Pro Ala Leu His Val Leu Val
 165 170 175
 Val Pro Ile Glu Phe Phe Ser Thr Phe Ile Leu Arg Pro Val Thr Leu
 180 185 190
 Ala Leu Arg Leu Met Ala Asn Phe Leu Ala Gly His Ile Ile Leu Val
 195 200 205
 Leu Leu Phe Phe Ala Thr Asn Phe Phe Phe Phe Gln Phe Asn Gly Trp
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 Thr Ala Met Ser Gly Val Thr Ile Leu Met Ala Val Leu Phe Thr Val
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 <223> RXA01201

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 Met Ala Glu Leu Thr
 1 5
 atc tcc tcc gat gag atc cgt agc gcg att gcg aac tac acc tcg agc 163
 Ile Ser Ser Asp Glu Ile Arg Ser Ala Ile Ala Asn Tyr Thr Ser Ser
 10 15 20
 tac tcc gcg gag gcc tcc cgt gag gag gtc ggc gtg gtt att tcg gcc 211
 Tyr Ser Ala Glu Ala Ser Arg Glu Glu Val Gly Val Val Ile Ser Ala
 25 30 35

gct gac ggt atc gcc cag gtt tcg ggc ctc ccg tca gta atg gcg aat	259
Ala Asp Gly Ile Ala Gln Val Ser Gly Leu Pro Ser Val Met Ala Asn	
40 45 50	
gag ctc ctc gaa ttc ccg ggc ggc gtc atc ggc gtc gca cag aac ctt	307
Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly Val Ala Gln Asn Leu	
55 60 65	
gaa gct gac cga gtc ggc gtc gtg gtc ctg ggt aac tac gag cta ctt	355
Glu Ala Asp Arg Val Gly Val Val Val Leu Gly Asn Tyr Glu Leu Leu	
70 75 80 85	
aaa gaa ggc gac caa gtt cgt cgt act gga gac gtt ctg tct atc cca	403
Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp Val Leu Ser Ile Pro	
90 95 100	
gtc ggc gag gca ttc ctt ggc cgc gtt atc aac ccc ctt ggc cag cca	451
Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn Pro Leu Gly Gln Pro	
105 110 115	
att gac ggc ctg ggc gaa att gca tcc gaa gag gac cgc gtc ctc gag	499
Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu Asp Arg Val Leu Glu	
120 125 130	
ctt cag gca cca acc gtg ctt gag cgc cag cct gtc gag gag cct ttg	547
Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro Val Glu Glu Pro Leu	
135 140 145	
gca acc ggc atc aag gct atc gat gca atg acc cca atc ggc cgc ggt	595
Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr Pro Ile Gly Arg Gly	
150 155 160 165	
cag cgt cag ctg atc att ggt gac cgt aag act ggc aag acc gca gtc	643
Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr Gly Lys Thr Ala Val	
170 175 180	
tgt gtc gat acc atc ctt aac cag aag gcc aac tgg gag acc ggc gac	691
Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn Trp Glu Thr Gly Asp	
185 190 195	
aag acc aag cag gtt cgc tgc atc tac gtc gca atc ggt cag aag ggc	739
Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala Ile Gly Gln Lys Gly	
200 205 210	
tcc acc att gca gcc ctg cgt aag acc ctc gag gag cag ggc gct ctc	787
Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu Glu Gln Gly Ala Leu	
215 220 225	
gag tac acc acc atc gtg gct gca ccc gct tcc gat gct gca ggc ttc	835
Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser Asp Ala Ala Gly Phe	
230 235 240 245	
aag tgg ctt gca cca ttc gct ggc gct gct ctc gcc cag cac tgg atg	883
Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu Ala Gln His Trp Met	
250 255 260	
tac cag ggc aac cac gtc ctg gtc atc tac gat gat ctg acc aag cag	931
Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp Asp Leu Thr Lys Gln	
265 270 275	

gct gag gca tac cgt gct atc tcc ctg ctg ctg cgt cgc cca ccg ggc	979
Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu Arg Arg Pro Pro Gly	
280 285 290	
cgc gaa gca tac cca ggt gac gtc ttc tac ctg cac tcc cgt ctg ctg	1027
Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu His Ser Arg Leu Leu	
295 300 305	
gag cgc gct gcg aag ctg tcc gat gaa cta ggc gca ggt tct att aca	1075
Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly Ala Gly Ser Ile Thr	
310 315 320 325	
gca ctg cca atc att gag acc aag gct aat gac gtt tcc gcc ttc att	1123
Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp Val Ser Ala Phe Ile	
330 335 340	
cct acc aac gtg att tcc atc acc gac ggt cag gta ttc ctt gag tcc	1171
Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln Val Phe Leu Glu Ser	
345 350 355	
gac ctg ttc aac cgt ggc gtt cgc ccg gcg atc aac gtc ggt gta tcc	1219
Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile Asn Val Gly Val Ser	
360 365 370	
gtc tcc cgt gtc ggt ggc gca gct cag acc aag ggt atg aag aag gtt	1267
Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys Gly Met Lys Lys Val	
375 380 385	
gcc ggt tct ctc cgt ctg gat ctg gct gca ttc cgc gac ctg gaa gca	1315
Ala Gly Ser Leu Arg Leu Asp Leu Ala Ala Phe Arg Asp Leu Glu Ala	
390 395 400 405	
ttc gct acc ttc gca tct gac ttg gat gct gca tcc aag tct cag ctt	1363
Phe Ala Thr Phe Ala Ser Asp Leu Asp Ala Ala Ser Lys Ser Gln Leu	
410 415 420	
gag cgt ggc cag cgc ctc gtt cag ctg ttg att cag tct gag aac gca	1411
Glu Arg Gly Gln Arg Leu Val Gln Leu Leu Ile Gln Ser Glu Asn Ala	
425 430 435	
cct cag gct gtt gag tac cag atc att tct ctc tgg ctt gca ggc gaa	1459
Pro Gln Ala Val Glu Tyr Gln Ile Ile Ser Leu Trp Leu Ala Gly Glu	
440 445 450	
ggc gca ttc gac aac gtt cct gtt gaa gat gtt cgt cgc ttc gag tcc	1507
Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val Arg Arg Phe Glu Ser	
455 460 465	
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Glu Leu His Glu Tyr Leu Gly Ser Asn Ala Ala Gln Val Tyr Glu Gln	
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Ile Ala Gly Gly Ala Gln Leu Ser Asp Glu Ser Lys Glu Thr Leu Leu	
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aag gca acc gaa gat ttc aag agc gct ttc cag acc acc gat ggc acc	1651
Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln Thr Thr Asp Gly Thr	
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Pro Val Ile Asn Glu Pro Glu Val Glu Ala Leu Asp Ala Gly Gln Val
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aag aaa gac cag ctc acc gtt tcc cgc aag gtc agc aag aag 1741
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<213> Corynebacterium glutamicum

<400> 760

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 35 40 45

Ser Val Met Ala Asn Glu Leu Leu Glu Phe Pro Gly Gly Val Ile Gly
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Val Ala Gln Asn Leu Glu Ala Asp Arg Val Gly Val Val Val Leu Gly
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Asn Tyr Glu Leu Leu Lys Glu Gly Asp Gln Val Arg Arg Thr Gly Asp
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Val Leu Ser Ile Pro Val Gly Glu Ala Phe Leu Gly Arg Val Ile Asn
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Pro Leu Gly Gln Pro Ile Asp Gly Leu Gly Glu Ile Ala Ser Glu Glu
 115 120 125

Asp Arg Val Leu Glu Leu Gln Ala Pro Thr Val Leu Glu Arg Gln Pro
 130 135 140

Val Glu Glu Pro Leu Ala Thr Gly Ile Lys Ala Ile Asp Ala Met Thr
 145 150 155 160

Pro Ile Gly Arg Gly Gln Arg Gln Leu Ile Ile Gly Asp Arg Lys Thr
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Gly Lys Thr Ala Val Cys Val Asp Thr Ile Leu Asn Gln Lys Ala Asn
 180 185 190

Trp Glu Thr Gly Asp Lys Thr Lys Gln Val Arg Cys Ile Tyr Val Ala
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Ile Gly Gln Lys Gly Ser Thr Ile Ala Ala Leu Arg Lys Thr Leu Glu
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Glu Gln Gly Ala Leu Glu Tyr Thr Thr Ile Val Ala Ala Pro Ala Ser
 225 230 235 240

Asp Ala Ala Gly Phe Lys Trp Leu Ala Pro Phe Ala Gly Ala Ala Leu
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 Ala Gln His Trp Met Tyr Gln Gly Asn His Val Leu Val Ile Tyr Asp
 260 265 270
 Asp Leu Thr Lys Gln Ala Glu Ala Tyr Arg Ala Ile Ser Leu Leu Leu
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 Arg Arg Pro Pro Gly Arg Glu Ala Tyr Pro Gly Asp Val Phe Tyr Leu
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 His Ser Arg Leu Leu Glu Arg Ala Ala Lys Leu Ser Asp Glu Leu Gly
 305 310 315 320
 Ala Gly Ser Ile Thr Ala Leu Pro Ile Ile Glu Thr Lys Ala Asn Asp
 325 330 335
 Val Ser Ala Phe Ile Pro Thr Asn Val Ile Ser Ile Thr Asp Gly Gln
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 Val Phe Leu Glu Ser Asp Leu Phe Asn Arg Gly Val Arg Pro Ala Ile
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 Asn Val Gly Val Ser Val Ser Arg Val Gly Gly Ala Ala Gln Thr Lys
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 Trp Leu Ala Gly Glu Gly Ala Phe Asp Asn Val Pro Val Glu Asp Val
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 Lys Glu Thr Leu Leu Lys Ala Thr Glu Asp Phe Lys Ser Ala Phe Gln
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 Asp Ala Gly Gln Val Lys Lys Asp Gln Leu Thr Val Ser Arg Lys Val
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 Ser Lys Lys
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Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp Leu Phe Leu Glu Met	
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Glu Glu Met Gly Val Leu Gln Asp Thr Ala Leu Val Phe Gly Gln Met	
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Leu Leu Gly Arg Met Pro Ser Ala Val Gly Tyr Gln Pro Thr Leu Ala	
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Asp Glu Met Gly Val Leu Gln Glu Arg Ile Thr Ser Thr Lys Gly Arg	
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Asp Pro Ala Pro Ala Thr Thr Phe Ala His Leu Asp Ala Thr Thr Glu	
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Leu Thr Ser Thr Ser Arg Ile Leu Glu Pro Ala Ile Val Gly Glu Arg	
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cac tac gag gtt tct cag cgt gtc atc ggc att ctg cag aag aac aag	1267
His Tyr Glu Val Ser Gln Arg Val Ile Gly Ile Leu Gln Lys Asn Lys	
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Glu Leu Gln Asp Ile Ile Ala Ile Leu Gly Met Asp Glu Leu Ser Glu	
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Glu Asp Lys Ile Thr Val Ala Arg Ala Arg Arg Ile Glu Arg Phe Leu	
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Gly Gln Asn Phe Phe Val Ala Glu Lys Phe Thr Gly Leu Pro Gly Ser
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 Tyr Val Pro Leu Thr Asp Thr Val Asp Ala Phe Glu Arg Ile Cys Asn
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 Gly Asp Phe Asp His Tyr Pro Glu Lys Ala Phe Asn Gly Leu Gly Gly
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Gly Asp Asn Leu Ile Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu
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Val Arg Gly Ala Ala Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro
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Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
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Leu Asp Asp Val Ser Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly
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Ile His Arg Glu Pro Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu
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Ile Leu Glu Thr Gly Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val
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Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
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Thr Ser Val Phe Ala Gly Val Gly Glu Arg Thr Arg Glu Gly Thr Asp

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Tyr	Phe	Arg	Asp	Val	Gln	Asn	Gln	Asp	Val	Leu	Leu	Phe	Ile	Asp	Asn	
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Ser	Leu	Gln	Ala	Val	Tyr	Val	Pro	Ala	Asp	Asp	Tyr	Thr	Asp	Pro	Ala	
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Pro	Ala	Thr	Thr	Phe	Ala	His	Leu	Asp	Ala	Thr	Thr	Glu	Leu	Asp	Arg	
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Ser	Ile	Ala	Ser	Lys	Gly	Ile	Tyr	Pro	Ala	Val	Asn	Pro	Leu	Thr	Ser	
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Asp	Ile	Ile	Ala	Ile	Leu	Gly	Met	Asp	Glu	Leu	Ser	Glu	Glu	Asp	Lys	
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Ile	Thr	Val	Ala	Arg	Ala	Arg	Arg	Ile	Glu	Arg	Phe	Leu	Gly	Gln	Asn	
		175					180					185				
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Phe	Phe	Val	Ala	Glu	Lys	Phe	Thr	Gly	Leu	Pro	Gly	Ser	Tyr	Val	Pro	
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ctg	acc	gac	acc	gtc	gac	gct	ttc	gag	cgt	att	tgc	aac	ggc	gac	ttc	674
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Lys	Gly	Ile	Tyr	Pro	Ala	Val	Asn	Pro	Leu	Thr	Ser	Thr	Ser	Arg	Ile
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Ile	Leu	Gly	Met	Asp	Glu	Leu	Ser	Glu	Glu	Asp	Lys	Ile	Thr	Val	Ala
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Arg	Ala	Arg	Arg	Ile	Glu	Arg	Phe	Leu	Gly	Gln	Asn	Phe	Phe	Val	Ala
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Glu	Lys	Phe	Thr	Gly	Leu	Pro	Gly	Ser	Tyr	Val	Pro	Leu	Thr	Asp	Thr
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gtc att ggt gcg gtc gtc gac gtg gag ttt ccc cgc ggc gag ctg cca 211
 Val Ile Gly Ala Val Val Asp Val Glu Phe Pro Arg Gly Glu Leu Pro
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gca ctg tac aac gca ctt act gta gag gta acc ctc gaa tca gtt aag 259
 Ala Leu Tyr Asn Ala Leu Thr Val Glu Val Thr Leu Glu Ser Val Lys
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aag acc gtt gtt ctc gag gtt gct cag cac ctc ggc gac aac ctc atc 307
 Lys Thr Val Val Leu Glu Val Ala Gln His Leu Gly Asp Asn Leu Ile
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 Arg Thr Ile Ala Met Ala Pro Thr Asp Gly Leu Val Arg Gly Ala Ala
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gta acc gat act gca cgc cca att tcc gta cca gtg ggc gat gtt gtt 403
 Val Thr Asp Thr Ala Arg Pro Ile Ser Val Pro Val Gly Asp Val Val
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 Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys Leu Asp Asp Val Ser
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 Leu Asn Asn Asn Pro Glu Ile Glu Arg Trp Gly Ile His Arg Glu Pro
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cca tca ttc gat cag ctt gag ggt aag acc gag atc ctg gaa aca ggc 547
 Pro Ser Phe Asp Gln Leu Glu Gly Lys Thr Glu Ile Leu Glu Thr Gly
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Ile Lys Val Ile Asp Leu Leu Thr Pro Tyr Val Lys Gly Gly Lys Ile
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 Val Gly Asp Val Val Lys Gly His Val Phe Asn Ala Leu Gly Asp Cys
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 Lys Gly Gly Lys Ile Gly Leu Phe Gly Gly Ala Gly Val Gly Lys Thr
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 Val Leu Ile Gln Glu Met Ile Thr Arg Ile Ala Arg Glu Phe Ser Gly
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Leu Phe Leu Glu Met
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Met Asn Glu Ile Ile
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Leu Ala Gln Asp Ala Thr Glu Ser Thr Ile Thr Gly Leu Gly Ala Val
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Gly Tyr Gly Ile Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu
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Val Gly Lys Ala Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly
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Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu
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gca ctg atc ggc ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga 360
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 <222> (101)..(280)
 <223> FRXA02821

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 Val Gly Tyr Gly Ile
 1 5
 gca acc atc gga cct ggc ctc ggc atc ggc atc ttg gtt ggt aag gct 163
 Ala Thr Ile Gly Pro Gly Leu Gly Ile Gly Ile Leu Val Gly Lys Ala
 10 15 20
 ctc gag ggt atg gca cgt cag cct gag atg gct gga cag ctc cgt acc 211
 Leu Glu Gly Met Ala Arg Gln Pro Glu Met Ala Gly Gln Leu Arg Thr
 25 30 35
 acc atg ttc ctg ggc atc gcc ttc gtt gag gcc ctg gca ctg atc ggc 259
 Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala Leu Ala Leu Ile Gly
 40 45 50
 ctt gtt gct ggc ttc ctg ttc taatcagcta acttaaccga aag 303
 Leu Val Ala Gly Phe Leu Phe
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<210> 770
 <211> 60
 <212> PRT
 <213> Corynebacterium glutamicum

<400> 770
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 Gly Gln Leu Arg Thr Thr Met Phe Leu Gly Ile Ala Phe Val Glu Ala
 35 40 45
 Leu Ala Leu Ile Gly Leu Val Ala Gly Phe Leu Phe
 50 55 60

<210> 771
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 <223> RXA01200

<400> 771
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 Gly Cys Leu Arg Trp Lys Ser Glu Pro Ser Val Leu Glu Val Leu Lys
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 gac gcc gca gag cag acc tgg tcc act cca cgc gag ttc cgc gct gga 96
 Asp Ala Ala Glu Gln Thr Trp Ser Thr Pro Arg Glu Phe Arg Ala Gly
 20 25 30
 cta gtc caa ctt ggc cgt cgc gcc ctt ctt cgc tct gcg gag aaa cag 144
 Leu Val Gln Leu Gly Arg Arg Ala Leu Leu Arg Ser Ala Glu Lys Gln
 35 40 45
 ggt cag ctt ggt cag gtg gaa gat gaa ctg ttc cga ctc agc cga atc 192
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 ctg gat cgc gaa agc aag ctg act cag ctt ctt tca gat cgc act cag 240
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 gaa att ggc ggt cga cgt gac ctc ctg gct aag gtg ctc tac ggc aag 288
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 gta act gct gtt acc gaa gcc ctc gca ctg cag gct att ggt cgc cct 336
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 gag cac aac cca att gac gat atc gca gct ttg gct ggc gct gta gca 384
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 gag cta cag ggt cgt tcc gtt gca cat gtc gtt acc gca gtt gaa ctc 432
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 aac gag gga cag caa caa gcg cta gct gaa aag ctg gga cgt att tat 480
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 ggt cgt gcg atg agc atc cac tcc gag gtt gat acc agc ctc ctc ggt 528
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 gga atg atc atc cgc gtc gga gac gaa gta att gac ggc agc acc tcg 576
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
 ggc aaa ctc gag cgt ctg cgg gca agc ttc gca taaagacacg acgaattaga 629
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala

195

200

caa

632

<210> 772
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 <212> PRT
 <213> Corynebacterium glutamicum

<400> 772
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 35 40 45
 Gly Gln Leu Gly Gln Val Glu Asp Glu Leu Phe Arg Leu Ser Arg Ile
 50 55 60
 Leu Asp Arg Glu Ser Lys Leu Thr Gln Leu Leu Ser Asp Arg Thr Gln
 65 70 75 80
 Glu Ile Gly Gly Arg Arg Asp Leu Leu Ala Lys Val Leu Tyr Gly Lys
 85 90 95
 Val Thr Ala Val Thr Glu Ala Leu Ala Leu Gln Ala Ile Gly Arg Pro
 100 105 110
 Glu His Asn Pro Ile Asp Asp Ile Ala Ala Leu Ala Gly Ala Val Ala
 115 120 125
 Glu Leu Gln Gly Arg Ser Val Ala His Val Val Thr Ala Val Glu Leu
 130 135 140
 Asn Glu Gly Gln Gln Gln Ala Leu Ala Glu Lys Leu Gly Arg Ile Tyr
 145 150 155 160
 Gly Arg Ala Met Ser Ile His Ser Glu Val Asp Thr Ser Leu Leu Gly
 165 170 175
 Gly Met Ile Ile Arg Val Gly Asp Glu Val Ile Asp Gly Ser Thr Ser
 180 185 190
 Gly Lys Leu Glu Arg Leu Arg Ala Ser Phe Ala
 195 200

<210> 773
 <211> 495
 <212> DNA
 <213> Corynebacterium glutamicum

<220>
 <221> CDS
 <222> (101)..(472)
 <223> RXA01194

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				1				5	
gtt gaa ctg gtg tct gta gag cgc atg ctg tgg gcc ggc cag gcc tcc	163								
Val Glu Leu Val Ser Val Glu Arg Met Leu Trp Ala Gly Gln Ala Ser									
	10				15			20	
atc gtg act gca cag acc acc gag ggt gag atc ggc gtg ctg ccc gat	211								
Ile Val Thr Ala Gln Thr Thr Glu Gly Glu Ile Gly Val Leu Pro Asp									
	25				30			35	
cac gag cct ctt ctc ggc caa ttg gtt gag aac ggt gtc gtg acc atc	259								
His Glu Pro Leu Leu Gly Gln Leu Val Glu Asn Gly Val Val Thr Ile									
	40				45			50	
cag ccg atc gac ggc gaa aag ctt atc gcc ggc gtt tcg gat gga ttc	307								
Gln Pro Ile Asp Gly Glu Lys Leu Ile Ala Gly Val Ser Asp Gly Phe									
	55				60			65	
ctc tcc gta tct aag gaa aag gtg acg atc ctc gcg gac ttc gcc gtc	355								
Leu Ser Val Ser Lys Glu Lys Val Thr Ile Leu Ala Asp Phe Ala Val									
	70				75			80	85
tgg gcg aat gag gtt gat acc gca tcc gcc gag gct gac ctt aat tcg	403								
Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu Ala Asp Leu Asn Ser									
	90				95			100	
gac gac gag ctg gcc aag gca cac gcc gag gct ggg ctg cgc gcg gtc	451								
Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala Gly Leu Arg Ala Val									
	105				110			115	
cgc cgc agc agc gaa ggt ctc taaacctccg tttagctgaa gta	495								
Arg Arg Ser Ser Glu Gly Leu									
	120								

<213> Corynebacterium glutamicum

Met	Ala	Glu	Ile	Thr	Val	Glu	Leu	Val	Ser	Val	Glu	Arg	Met	Leu	Trp
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			20					25					30		
Gly	Val	Leu	Pro	Asp	His	Glu	Pro	Leu	Leu	Gly	Gln	Leu	Val	Glu	Asn
		35				40						45			
Gly	Val	Val	Thr	Ile	Gln	Pro	Ile	Asp	Gly	Glu	Lys	Leu	Ile	Ala	Gly
	50					55					60				
Val	Ser	Asp	Gly	Phe	Leu	Ser	Val	Ser	Lys	Glu	Lys	Val	Thr	Ile	Leu
65					70					75					80

Ala Asp Phe Ala Val Trp Ala Asn Glu Val Asp Thr Ala Ser Ala Glu
85 90 95

Ala Asp Leu Asn Ser Asp Asp Glu Leu Ala Lys Ala His Ala Glu Ala
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Gly Leu Arg Ala Val Arg Arg Ser Ser Glu Gly Leu
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<210> 775

<211> 1098

<212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1075)

<223> RXA01202

<400> 775

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taaagtactg tccaagcaac tgaagggagg cgtgtgaacc atg gca aca att cgt 115
Met Ala Thr Ile Arg
1 5

gaa ttg cgt gac cga att cgt tcg gtt aac tca acc aag aag atc acc 163
Glu Leu Arg Asp Arg Ile Arg Ser Val Asn Ser Thr Lys Lys Ile Thr
10 15 20

aag gct caa gag ctc atc gcc acc tct cgc atc acc aag gca cag ggt 211
Lys Ala Gln Glu Leu Ile Ala Thr Ser Arg Ile Thr Lys Ala Gln Gly
25 30 35

cgc gtc gcg gca gct gcg ccg tac gcc gag gaa atc cag cgc gtg ctg 259
Arg Val Ala Ala Ala Pro Tyr Ala Glu Glu Ile Gln Arg Val Leu
40 45 50

gag cgc ctc gcg tcg gca agc tcc cta gac cac cca atg ctg cgt gag 307
Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His Pro Met Leu Arg Glu
55 60 65

cgt gaa ggc ggc aag cga gcc gcc gtg ctc gtg gtt act tct gac cgc 355
Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val Val Thr Ser Asp Arg
70 75 80 85

ggc atg gct ggt ggc tac aac cac aac gtt ctg aaa aag gca gcg gag 403
Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu Lys Lys Ala Ala Glu
90 95 100

ctg gaa aag ctt ctt gct gaa agt gga tac gaa gtg gtt cgt tat gtc 451
Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu Val Val Arg Tyr Val
105 110 115

acc ggc aaa aag ggc gtc gac tac tac aag ttc cgc gct gaa gat gtg 499
Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe Arg Ala Glu Asp Val
120 125 130

gct ggc acc tgg act gga ttc tca cag gat cca gac tgg gca gct acc 547
Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro Asp Trp Ala Ala Thr

135	140	145	
cac aac gtg cgc cgt	cac ctc att gat ggt	ttc acc gcc agc tct gaa	595
His Asn Val Arg Arg	His Leu Ile Asp Gly	Phe Thr Ala Ser Ser Glu	
150	155	160	165
ggt gaa gct gca tgg	cgc gag gga ctg aac	cta cca gaa ggc cag gat	643
Gly Glu Ala Ala Trp	Arg Glu Gly Leu Asn	Leu Pro Glu Gly Gln Asp	
	170	175	180
atc cag ggc ttc gac	cag gtt cac gtg gtc	tac acc gag ttc atc tcc	691
Ile Gln Gly Phe Asp	Gln Val His Val Val	Tyr Thr Glu Phe Ile Ser	
	185	190	195
atg ctg act caa aac	cca gta gtg cac caa	ctg ctg cct gtt gag cca	739
Met Leu Thr Gln Asn	Pro Val Val His Gln	Leu Leu Pro Val Glu Pro	
	200	205	210
gtc atc gaa gat gaa	att ttc gaa aaa ggc	gag gat ctg ctg tcc tct	787
Val Ile Glu Asp Glu	Ile Phe Glu Lys Gly	Glu Asp Leu Leu Ser Ser	
	215	220	225
tcc ggc gaa gtc gaa	ccc gac tac gag ttc	gag ccg gat gca gac act	835
Ser Gly Glu Val Glu	Pro Asp Tyr Glu Phe	Glu Pro Asp Ala Asp Thr	
	230	235	240
ctg ctt gag gca ctg	ctt ccg cag tac gtc	tct cgt agg ctg ttc tcc	883
Leu Leu Glu Ala Leu	Leu Pro Gln Tyr Val	Ser Arg Arg Leu Phe Ser	
	250	255	260
atc ttc ttg gag gct	gca gct gca gag tcc	gct tca cgt cga aac gcg	931
Ile Phe Leu Glu Ala	Ala Ala Ala Glu Ser	Ala Ser Arg Arg Asn Ala	
	265	270	275
atg aag tct gcg act	gac aac gct acg gaa	ctg gtc aag gac ctg tcc	979
Met Lys Ser Ala Thr	Asp Asn Ala Thr Glu	Leu Val Lys Asp Leu Ser	
	280	285	290
cgt gtg gcc aac cag	gca cgt cag gca cag	atc acc cag gaa atc aca	1027
Arg Val Ala Asn Gln	Ala Arg Gln Ala Gln	Ile Thr Gln Glu Ile Thr	
	295	300	305
gag att gtt ggt ggc	gca ggc gcg ctc gcc	gac agc gga gaa agt gac	1075
Glu Ile Val Gly Gly	Ala Gly Ala Leu Ala	Asp Ser Gly Glu Ser Asp	
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<210> 776

<211> 325

<212> PRT

<213> Corynebacterium glutamicum

<400> 776

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Thr	Lys	Lys	Ile	Thr	Lys	Ala	Gln	Glu	Leu	Ile	Ala	Thr	Ser	Arg	Ile
			20					25					30		

Thr Lys Ala Gln Gly Arg Val Ala Ala Ala Ala Pro Tyr Ala Glu Glu
 35 40 45
 Ile Gln Arg Val Leu Glu Arg Leu Ala Ser Ala Ser Ser Leu Asp His
 50 55 60
 Pro Met Leu Arg Glu Arg Glu Gly Gly Lys Arg Ala Ala Val Leu Val
 65 70 75 80
 Val Thr Ser Asp Arg Gly Met Ala Gly Gly Tyr Asn His Asn Val Leu
 85 90 95
 Lys Lys Ala Ala Glu Leu Glu Lys Leu Leu Ala Glu Ser Gly Tyr Glu
 100 105 110
 Val Val Arg Tyr Val Thr Gly Lys Lys Gly Val Asp Tyr Tyr Lys Phe
 115 120 125
 Arg Ala Glu Asp Val Ala Gly Thr Trp Thr Gly Phe Ser Gln Asp Pro
 130 135 140
 Asp Trp Ala Ala Thr His Asn Val Arg Arg His Leu Ile Asp Gly Phe
 145 150 155 160
 Thr Ala Ser Ser Glu Gly Glu Ala Ala Trp Arg Glu Gly Leu Asn Leu
 165 170 175
 Pro Glu Gly Gln Asp Ile Gln Gly Phe Asp Gln Val His Val Val Tyr
 180 185 190
 Thr Glu Phe Ile Ser Met Leu Thr Gln Asn Pro Val Val His Gln Leu
 195 200 205
 Leu Pro Val Glu Pro Val Ile Glu Asp Glu Ile Phe Glu Lys Gly Glu
 210 215 220
 Asp Leu Leu Ser Ser Ser Gly Glu Val Glu Pro Asp Tyr Glu Phe Glu
 225 230 235 240
 Pro Asp Ala Asp Thr Leu Leu Glu Ala Leu Leu Pro Gln Tyr Val Ser
 245 250 255
 Arg Arg Leu Phe Ser Ile Phe Leu Glu Ala Ala Ala Ala Glu Ser Ala
 260 265 270
 Ser Arg Arg Asn Ala Met Lys Ser Ala Thr Asp Asn Ala Thr Glu Leu
 275 280 285
 Val Lys Asp Leu Ser Arg Val Ala Asn Gln Ala Arg Gln Ala Gln Ile
 290 295 300
 Thr Gln Glu Ile Thr Glu Ile Val Gly Gly Ala Gly Ala Leu Ala Asp
 305 310 315 320
 Ser Gly Glu Ser Asp
 325

<210> 777
 <211> 1773
 <212> DNA

<213> Corynebacterium glutamicum

<220>

<221> CDS

<222> (101)..(1750)

<223> RXN02434

<400> 777

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                                         Met Arg Thr Phe Ala
                                         1           5

gct tat att gcc att gat ggc ctc agc ttt tcc tac ccc aac acc cac 163
Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser Tyr Pro Asn Thr His
                10                15                20

gtt tta agc gat att tcg ctc acc gtt gcc aat ggc gat atc gcc gga 211
Val Leu Ser Asp Ile Ser Leu Thr Val Ala Asn Gly Asp Ile Ala Gly
                25                30                35

ctg att ggt gaa aac ggc gca gga aaa tcc acc ctg ctc agc ctc atc 259
Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr Leu Leu Ser Leu Ile
                40                45                50

gct ggc gtc atg gaa ccc gac cag ggc agg att tac ctc ccc gaa cgc 307
Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile Tyr Leu Pro Glu Arg
                55                60                65

acc gga ttc atc gcc caa gaa aca gac tta ccg ttt gaa caa ccc gtg 355
Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro Phe Glu Gln Pro Val
                70                75                80                85

cag tcg ctt atc gac gcc gcc gtc gcc cca gtg cgc gcg gtc gat gcc 403
Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val Arg Ala Val Asp Ala
                90                95                100

gcg att aca gat ttg tcc acc aag ctt ggc gac gcc tcc ctc agc gcc 451
Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp Ala Ser Leu Ser Ala
                105                110                115

gaa gag cag gcg caa gtc gcc aca gat ttc gat gca gcg cta ggc gct 499
Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp Ala Ala Leu Gly Ala
                120                125                130

gca gaa gaa ctc gga ctg tgg gaa tta gat gca cgt att gaa acc atc 547
Ala Glu Glu Leu Gly Leu Trp Glu Leu Asp Ala Arg Ile Glu Thr Ile
                135                140                145

gtc gcg ggt ctc ggc ctt gcc gag gtg gat cgc agc act ccc att ggt 595
Val Ala Gly Leu Gly Leu Ala Glu Val Asp Arg Ser Thr Pro Ile Gly
                150                155                160                165

gag ctt tcc ggc ggt cag cgc cgc aga ttc gca ttg gca gcg ctg ctg 643
Glu Leu Ser Gly Gly Gln Arg Arg Arg Phe Ala Leu Ala Ala Leu Leu
                170                175                180

ttg gaa cca cac gat gct ctg att ttc gat gag ccc acc aac cac ctc 691
Leu Glu Pro His Asp Ala Leu Ile Phe Asp Glu Pro Thr Asn His Leu
                185                190                195

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gac	gac	aca	gcc	gta	gat	ttc	ctc	atc	tcg	gag	att	tcc	cgt	ttc	aaa	739
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		200					205					210				
ggt	cca	gtg	ctg	atc	gcc	agc	cac	gat	cgc	ttc	ttc	ctc	gac	tcc	gtc	787
Gly	Pro	Val	Leu	Ile	Ala	Ser	His	Asp	Arg	Phe	Phe	Leu	Asp	Ser	Val	
	215					220					225					
tgt	acc	gag	tta	atc	gac	ctc	gat	cct	gca	ctt	gga	cct	gag	ggc	gga	835
Cys	Thr	Glu	Leu	Ile	Asp	Leu	Asp	Pro	Ala	Leu	Gly	Pro	Glu	Gly	Gly	
230					235					240					245	
tcc	ggc	gaa	gaa	gta	aaa	caa	gcc	gtg	tct	ttt	ggt	ggt	gga	ttt	tct	883
Ser	Gly	Glu	Glu	Val	Lys	Gln	Ala	Val	Ser	Phe	Gly	Gly	Gly	Phe	Ser	
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Glu	Tyr	Ile	Lys	Glu	Arg	Glu	Thr	Arg	Arg	Thr	Arg	Trp	Ala	Gln	Leu	
			265					270					275			
tac	acc	gca	caa	gaa	acc	gag	cgg	gaa	aaa	ctc	gaa	gaa	acc	acc	ggc	979
Tyr	Thr	Ala	Gln	Glu	Thr	Glu	Arg	Glu	Lys	Leu	Glu	Glu	Thr	Thr	Gly	
		280					285					290				
acc	acc	gaa	tcg	gat	att	ttc	cac	agc	tcg	gtt	tcc	aaa	tcg	gaa	gct	1027
Thr	Thr	Glu	Ser	Asp	Ile	Phe	His	Ser	Ser	Val	Ser	Lys	Ser	Glu	Ala	
		295				300					305					
aaa	atc	acc	gcg	aaa	ttt	tac	gca	gac	cgg	gca	gct	aaa	act	caa	ggc	1075
Lys	Ile	Thr	Ala	Lys	Phe	Tyr	Ala	Asp	Arg	Ala	Ala	Lys	Thr	Gln	Gly	
310					315					320					325	
aac	cgc	gtc	cgc	tcc	gcc	aaa	aac	cgc	ctg	aag	gaa	ttg	gaa	cgc	tat	1123
Asn	Arg	Val	Arg	Ser	Ala	Lys	Asn	Arg	Leu	Lys	Glu	Leu	Glu	Arg	Tyr	
				330					335					340		
gaa	atc	cca	gca	cct	cca	aag	cca	ctg	gaa	ttc	caa	ggc	atc	cca	gaa	1171
Glu	Ile	Pro	Ala	Pro	Pro	Lys	Pro	Leu	Glu	Phe	Gln	Gly	Ile	Pro	Glu	
			345					350					355			
gcc	tcc	gga	aac	ggt	cac	ggt	gaa	aca	cta	gaa	gtg	cgg	gct	att	gct	1219
Ala	Ser	Gly	Asn	Gly	His	Gly	Glu	Thr	Leu	Glu	Val	Arg	Ala	Ile	Ala	
		360					365					370				
gtg	gaa	aac	agg	ctt	caa	ccc	ttg	act	ttc	cac	atc	gat	ccc	ggc	gac	1267
Val	Glu	Asn	Arg	Leu	Gln	Pro	Leu	Thr	Phe	His	Ile	Asp	Pro	Gly	Asp	
	375					380					385					
cac	atc	ctg	gtc	gaa	ggc	ccc	aac	ggt	gtc	ggt	aaa	tcc	acc	ctg	ctg	1315
His	Ile	Leu	Val	Glu	Gly	Pro	Asn	Gly	Val	Gly	Lys	Ser	Thr	Leu	Leu	
390					395					400					405	
agc	gtt	ctg	gaa	ggc	gtg	ctt	gaa	cca	acc	gaa	ggt	gaa	ttg	atc	gtc	1363
Ser	Val	Leu	Glu	Gly	Val	Leu	Glu	Pro	Thr	Glu	Gly	Glu	Leu	Ile	Val	
				410					415					420		
ccc	gaa	ggg	ctg	aaa	gtt	gcg	cgc	ctg	aaa	cag	gac	gat	cag	tgg	acg	1411
Pro	Glu	Gly	Leu	Lys	Val	Ala	Arg	Leu	Lys	Gln	Asp	Asp	Gln	Trp	Thr	
			425					430					435			

gaa aag cag ttg aac acc ccc gtc gac gaa ctg ttc gcc gcc cta tcg 1459
 Glu Lys Gln Leu Asn Thr Pro Val Asp Glu Leu Phe Ala Ala Leu Ser
 440 445 450

aaa ggt ccg gtc gga ctc aac ctc gtg gag atg ggg ctg ttg agg gag 1507
 Lys Gly Pro Val Gly Leu Asn Leu Val Glu Met Gly Leu Leu Arg Glu
 455 460 465

acg tcg caa agc agc ccg cta cgg gcc cta tcg ctc ggc caa cgc cgg 1555
 Thr Ser Gln Ser Ser Pro Leu Arg Ala Leu Ser Leu Gly Gln Arg Arg
 470 475 480 485

cgc gtc tcg ctc ggg ctc atc ctg gcg agc cca cca gat ctt ttg ctt 1603
 Arg Val Ser Leu Gly Leu Ile Leu Ala Ser Pro Pro Asp Leu Leu Leu
 490 495 500

ctt gac gag ccc acc aac cac ctc tcc ctc gcg ctg agc gaa gaa ctc 1651
 Leu Asp Glu Pro Thr Asn His Leu Ser Leu Ala Leu Ser Glu Glu Leu
 505 510 515

gag tcg gcg ata gaa aaa ttc ccc ggt cgc gtt att ctg gcc agc cac 1699
 Glu Ser Ala Ile Glu Lys Phe Pro Gly Arg Val Ile Leu Ala Ser His
 520 525 530

gat agg tgg atc aga aaa cgt tgg acg ggg aag aaa atc agc ctg agc 1747
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 535 540 545

cgt taaaccctac tgaacaggaa cct 1773
 Arg
 550

<210> 778

<211> 550

<212> PRT

<213> *Corynebacterium glutamicum*

<400> 778

Met Arg Thr Phe Ala Ala Tyr Ile Ala Ile Asp Gly Leu Ser Phe Ser
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 20 25 30

Gly Asp Ile Ala Gly Leu Ile Gly Glu Asn Gly Ala Gly Lys Ser Thr
 35 40 45

Leu Leu Ser Leu Ile Ala Gly Val Met Glu Pro Asp Gln Gly Arg Ile
 50 55 60

Tyr Leu Pro Glu Arg Thr Gly Phe Ile Ala Gln Glu Thr Asp Leu Pro
 65 70 75 80

Phe Glu Gln Pro Val Gln Ser Leu Ile Asp Ala Ala Val Ala Pro Val
 85 90 95

Arg Ala Val Asp Ala Ala Ile Thr Asp Leu Ser Thr Lys Leu Gly Asp
 100 105 110

Ala Ser Leu Ser Ala Glu Glu Gln Ala Gln Val Ala Thr Asp Phe Asp

115					120					125					
Ala	Ala	Leu	Gly	Ala	Ala	Glu	Glu	Leu	Gly	Leu	Trp	Glu	Leu	Asp	Ala
130					135					140					
Arg	Ile	Glu	Thr	Ile	Val	Ala	Gly	Leu	Gly	Leu	Ala	Glu	Val	Asp	Arg
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Ala	Lys	Thr	Gln	Gly	Asn	Arg	Val	Arg	Ser	Ala	Lys	Asn	Arg	Leu	Lys
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Glu	Leu	Glu	Arg	Tyr	Glu	Ile	Pro	Ala	Pro	Pro	Lys	Pro	Leu	Glu	Phe
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Gln	Gly	Ile	Pro	Glu	Ala	Ser	Gly	Asn	Gly	His	Gly	Glu	Thr	Leu	Glu
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Val	Arg	Ala	Ile	Ala	Val	Glu	Asn	Arg	Leu	Gln	Pro	Leu	Thr	Phe	His
		370					375					380			
Ile	Asp	Pro	Gly	Asp	His	Ile	Leu	Val	Glu	Gly	Pro	Asn	Gly	Val	Gly
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Lys	Ser	Thr	Leu	Leu	Ser	Val	Leu	Glu	Gly	Val	Leu	Glu	Pro	Thr	Glu
				405					410					415	
Gly	Glu	Leu	Ile	Val	Pro	Glu	Gly	Leu	Lys	Val	Ala	Arg	Leu	Lys	Gln
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 Phe Pro Ala Tyr Lys Glu Leu Arg Gln Glu Glu Pro Val Met Phe Asp
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 Glu Arg Ile Gly Tyr Trp Val Thr Lys Tyr Asp Asp Ile Lys Thr
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Ala	Leu	Glu	Pro	Asp	Ile	Arg	Ala	Met	Val	Ile	Asp	Arg	Val	Glu	Lys		
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Met	Leu	Ala	Asn	Asp	Gln	His	Val	Gly	Asp	Met	Val	Ser	Asp	Leu	Ala		
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Tyr	Asp	Ile	Pro	Thr	Ile	Thr	Ile	Leu	Thr	Leu	Ile	Gly	Ala	Asp	Ile		
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Phe	Met	Val	Val	Thr	Tyr	Lys	Arg	Trp	Ser	Asp	Ser	Arg	Ala	Ala	Met		
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Thr	Trp	Gly	Asp	Leu	Ser	Asp	Glu	Glu	Gln	Ile	Pro	His	Ala	His	Asn		
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Ser Ala Asn Arg Asp Glu Ala Arg Phe Glu Asn Gly Glu Glu Phe Asp			
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Ile Ser Arg Ala Asn Ala Arg Glu His Leu Ser Phe Gly Phe Gly Ile			
360	365	370	
cac tat tgc cta gga aac atg ctg gcc aaa ctt caa gcc aag atc tgt			1267
His Tyr Cys Leu Gly Asn Met Leu Ala Lys Leu Gln Ala Lys Ile Cys			
375	380	385	
ctc gag gaa gtc acc agg ctt gtt cct tcc ctg cac ttg gtt gcg gac			1315
Leu Glu Glu Val Thr Arg Leu Val Pro Ser Leu His Leu Val Ala Asp			
390	395	400	405
aaa gct atc ggg ttc cgg gag aac ctc tcc ttc cgc gtc ccc act tct			1363
Lys Ala Ile Gly Phe Arg Glu Asn Leu Ser Phe Arg Val Pro Thr Ser			
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Pro Val Met Phe Asp Glu Arg Ile Gly Tyr Trp Val Val Thr Lys Tyr	
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Met Thr Asp Gly Gly Phe Thr Ala Tyr Ser Gly Leu Ser Ala Arg Ile	
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115 120 125	
Pro Arg Arg Tyr Lys Ala Leu Glu Pro Asp Ile Arg Ala Met Val Ile	
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